



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 152206

TO: Patricia Duffy
Location: rem/3b05/3c18
Art Unit: 1645
Wednesday, May 11, 2005

Case Serial Number: 10/063692

From: Toby Port

Location: Biotech-Chem Library
REM1-A59

Phone: 272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Duffy,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port

This Page Blank (uspto)

STIC-Biotech/ChemLib

~~152206~~ 152206

From: Duffy, Patricia
Sent: Monday, May 02, 2005 1:02 PM
To: STIC-Biotech/ChemLib
Subject: SPDI 10/063,692

PLEASE SEARCH SEQ ID NOS:37, 38 AND OLIGOMERS THEREOF.
PLEASE RUN THE AA OF SEQ ID NO:38 AGAINST THE NA DATABASE.

STANDARD SPDI OUTPUT.

Patricia A. Duffy, Ph.D.
Art Unit 1645
Remsen 3B05; Mailbox 3C18
571-272-0855

RECEIVED
MAY - 2 2005
STIC

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

This Page Blank (usp10)

Run on: May 6, 2005, 13:05:52 ; Search time 994 Seconds
(without alignments)
16949.280 Million cell updates/sec

Title: US-10-063-692-37
Perfect score: 2846
Sequence: 1 cgtctgggaccagcgccgg.....aaaaaaaaaaaaaaaaaaaaa 2846
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 4390206 segs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%

Database : N_Geneseq_16Dec04:*
Listing first 1500 summaries
Maximum Match 100%

No.	Score	Match	Length	DB	ID	Description
1	2846	100.0%	2846	BP	AAZ65034	standard; cDNA; 2846 BP.
2	2846	100.0%	2846	BP	DE	Membrane-bound protein PRO1344 encoding cDNA.
3	2846	100.0%	2846	BP	PN	WO963088-A2.
4	2846	100.0%	2846	BP	PD	09-DEC-2001.
5	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
6	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
7	2846	100.0%	2846	BP	PN	WO200168848-A2.
8	2846	100.0%	2846	BP	PD	20-SEP-2001.
9	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
10	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
11	2846	100.0%	2846	BP	PN	WO200168848-A2.
12	2846	100.0%	2846	BP	PD	20-SEP-2001.
13	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
14	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
15	2846	100.0%	2846	BP	PN	WO200168848-A2.
16	2846	100.0%	2846	BP	PD	20-SEP-2001.
17	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
18	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
19	2846	100.0%	2846	BP	PN	WO200168848-A2.
20	2846	100.0%	2846	BP	PD	20-SEP-2001.
21	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
22	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
23	2846	100.0%	2846	BP	PN	WO200168848-A2.
24	2846	100.0%	2846	BP	PD	20-SEP-2001.
25	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
26	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
27	2846	100.0%	2846	BP	PN	WO200168848-A2.
28	2846	100.0%	2846	BP	PD	20-SEP-2001.
29	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
30	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
31	2846	100.0%	2846	BP	PN	WO200168848-A2.
32	2846	100.0%	2846	BP	PD	20-SEP-2001.
33	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
34	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
35	2846	100.0%	2846	BP	PN	WO200168848-A2.
36	2846	100.0%	2846	BP	PD	20-SEP-2001.
37	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
38	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
39	2846	100.0%	2846	BP	PN	WO200168848-A2.
40	2846	100.0%	2846	BP	PD	20-SEP-2001.
41	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
42	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
43	2846	100.0%	2846	BP	PN	WO200168848-A2.
44	2846	100.0%	2846	BP	PD	20-SEP-2001.
45	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
46	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
47	2846	100.0%	2846	BP	PN	WO200168848-A2.
48	2846	100.0%	2846	BP	PD	20-SEP-2001.
49	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
50	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
51	2846	100.0%	2846	BP	PN	WO200168848-A2.
52	2846	100.0%	2846	BP	PD	20-SEP-2001.
53	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
54	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
55	2846	100.0%	2846	BP	PN	WO200168848-A2.
56	2846	100.0%	2846	BP	PD	20-SEP-2001.
57	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
58	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
59	2846	100.0%	2846	BP	PN	WO200168848-A2.
60	2846	100.0%	2846	BP	PD	20-SEP-2001.
61	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
62	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
63	2846	100.0%	2846	BP	PN	WO200168848-A2.
64	2846	100.0%	2846	BP	PD	20-SEP-2001.
65	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
66	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
67	2846	100.0%	2846	BP	PN	WO200168848-A2.
68	2846	100.0%	2846	BP	PD	20-SEP-2001.
69	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
70	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
71	2846	100.0%	2846	BP	PN	WO200168848-A2.
72	2846	100.0%	2846	BP	PD	20-SEP-2001.
73	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
74	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
75	2846	100.0%	2846	BP	PN	WO200168848-A2.
76	2846	100.0%	2846	BP	PD	20-SEP-2001.
77	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
78	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
79	2846	100.0%	2846	BP	PN	WO200168848-A2.
80	2846	100.0%	2846	BP	PD	20-SEP-2001.
81	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
82	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
83	2846	100.0%	2846	BP	PN	WO200168848-A2.
84	2846	100.0%	2846	BP	PD	20-SEP-2001.
85	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
86	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
87	2846	100.0%	2846	BP	PN	WO200168848-A2.
88	2846	100.0%	2846	BP	PD	20-SEP-2001.
89	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
90	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
91	2846	100.0%	2846	BP	PN	WO200168848-A2.
92	2846	100.0%	2846	BP	PD	20-SEP-2001.
93	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
94	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
95	2846	100.0%	2846	BP	PN	WO200168848-A2.
96	2846	100.0%	2846	BP	PD	20-SEP-2001.
97	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
98	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
99	2846	100.0%	2846	BP	PN	WO200168848-A2.
100	2846	100.0%	2846	BP	PD	20-SEP-2001.
101	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
102	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
103	2846	100.0%	2846	BP	PN	WO200168848-A2.
104	2846	100.0%	2846	BP	PD	20-SEP-2001.
105	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
106	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
107	2846	100.0%	2846	BP	PN	WO200168848-A2.
108	2846	100.0%	2846	BP	PD	20-SEP-2001.
109	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
110	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
111	2846	100.0%	2846	BP	PN	WO200168848-A2.
112	2846	100.0%	2846	BP	PD	20-SEP-2001.
113	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
114	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
115	2846	100.0%	2846	BP	PN	WO200168848-A2.
116	2846	100.0%	2846	BP	PD	20-SEP-2001.
117	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
118	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
119	2846	100.0%	2846	BP	PN	WO200168848-A2.
120	2846	100.0%	2846	BP	PD	20-SEP-2001.
121	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
122	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
123	2846	100.0%	2846	BP	PN	WO200168848-A2.
124	2846	100.0%	2846	BP	PD	20-SEP-2001.
125	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
126	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
127	2846	100.0%	2846	BP	PN	WO200168848-A2.
128	2846	100.0%	2846	BP	PD	20-SEP-2001.
129	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
130	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
131	2846	100.0%	2846	BP	PN	WO200168848-A2.
132	2846	100.0%	2846	BP	PD	20-SEP-2001.
133	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
134	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
135	2846	100.0%	2846	BP	PN	WO200168848-A2.
136	2846	100.0%	2846	BP	PD	20-SEP-2001.
137	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
138	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
139	2846	100.0%	2846	BP	PN	WO200168848-A2.
140	2846	100.0%	2846	BP	PD	20-SEP-2001.
141	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
142	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
143	2846	100.0%	2846	BP	PN	WO200168848-A2.
144	2846	100.0%	2846	BP	PD	20-SEP-2001.
145	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
146	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
147	2846	100.0%	2846	BP	PN	WO200168848-A2.
148	2846	100.0%	2846	BP	PD	20-SEP-2001.
149	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
150	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
151	2846	100.0%	2846	BP	PN	WO200168848-A2.
152	2846	100.0%	2846	BP	PD	20-SEP-2001.
153	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
154	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
155	2846	100.0%	2846	BP	PN	WO200168848-A2.
156	2846	100.0%	2846	BP	PD	20-SEP-2001.
157	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
158	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
159	2846	100.0%	2846	BP	PN	WO200168848-A2.
160	2846	100.0%	2846	BP	PD	20-SEP-2001.
161	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
162	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
163	2846	100.0%	2846	BP	PN	WO200168848-A2.
164	2846	100.0%	2846	BP	PD	20-SEP-2001.
165	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
166	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
167	2846	100.0%	2846	BP	PN	WO200168848-A2.
168	2846	100.0%	2846	BP	PD	20-SEP-2001.
169	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
170	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
171	2846	100.0%	2846	BP	PN	WO200168848-A2.
172	2846	100.0%	2846	BP	PD	20-SEP-2001.
173	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
174	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
175	2846	100.0%	2846	BP	PN	WO200168848-A2.
176	2846	100.0%	2846	BP	PD	20-SEP-2001.
177	2846	100.0%	2846	BP	PA	(GETH) GENENTECH INC.
178	2846	100.0%	2846	BP	DE	Human DNA encoding PRO polypeptide sequence #85.
179	2846	100.0%	2846	BP	PN	WO200168848-A2.
180	2846	100.0%	2846	BP	PD	20-SEP-2001.
181						

DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 16
ID ACF13032 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 17
ID ACD25135 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 18
ID ACF00184 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 19
ID ACA60381 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 20
ID ACA72241 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 21
ID ACD04765 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 22
ID ACD18226 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 23
ID ACD08233 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 24
ID ACA88667 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 25
ID ACA70109 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.

PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 26
ID ACD12331 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 27
ID ACC74246 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 28
ID ACD15874 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 29
ID ACD25442 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 30
ID ACD17919 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 31
ID ACC88206 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 32
ID ACD21560 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 33
ID ACD18627 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 34
ID ACA58828 standard; cDNA; 2846 BP.
DE cDNA encoding human secreted polypeptide PRO1344.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 35
ID ABX98237 standard; cDNA; 2846 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 169.
PN US2003036156-A1.

PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 36
ID ACD13988 standard; cDNA; 2846 BP.
DE Human secreted polypeptide #85.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 37
ID ACD09768 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 38
ID ACC98513 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 39
ID ACD21253 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 40
ID ABX75625 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1344.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 41
ID ACA64004 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 42
ID ABX97828 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 43
ID ACA97304 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 44
ID ACA57767 standard; cDNA; 2846 BP.
DE Human PRO1344 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 45
ID ACD14295 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032130-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 46
ID ACC91078 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 47
ID ACC98820 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 48
ID ACD07017 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 49
ID ACA67468 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 50
ID ACC81523 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 51
ID ACA91268 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 52
ID ACC99127 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 53
ID ACC86483 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 54
ID ACC99741 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 55
ID ACC92920 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032135-A1.
PD 13-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 56
ID ACB80775 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein cDNA, #94.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 57
ID ACB72548 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 58
ID ACA89066 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 59
ID ACA69802 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 60
ID ACA96945 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 61
ID ACA90941 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 62
ID ACA70723 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 63
ID ACA95233 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 64
ID ACD44284 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 65
ID ACC86176 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027263-A1.
PD 06-FEB-2003.

Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 66
ID ACD45167 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane polypeptide PRO1344 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 67
ID ACC90048 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 68
ID ACD12656 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 69
ID ACF19886 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 70
ID ABX76830 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 71
ID ACA73162 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 72
ID ACA68705 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 73
ID ACA74549 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 74
ID ACA70416 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 75
ID ACD14602 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 76
ID ACA93715 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 77
ID ACA68274 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 78
ID ABX98739 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 79
ID ACC81216 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 80
ID ACA95540 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 81
ID ACD04458 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 82
ID ACC97899 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 83
ID ACF12561 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 84
ID ACH66262 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 85
ID ABX79455 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein cDNA, #94.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 86
ID ACA936276 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 87
ID ACA65050 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 88
ID ACA73776 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 89
ID ACA74188 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 90
ID ACA96583 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 91
ID ACD10689 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 92
ID ACC91385 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 93
ID ACA93476 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 94
ID ACD02720 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 95
ID ACC87285 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 96
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;

ID ACC85869 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027362-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 97
ID ABX81158 standard; DNA; 2846 BP.
DE Human secreted or transmembrane protein related PCR primer #50.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 98
ID ACA65357 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 99
ID ACA94174 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 100
ID ACA97918 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 101
ID ACA91420 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 102
ID ACA90634 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 103
ID ACD16181 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 104
ID ACD17342 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 105
ID ACC91999 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 106
ID ACD02316 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2002183493-A1.

PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 107
ID ACA74856 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 108
ID ACA91727 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 109
ID ACA71371 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 110
ID ACC90771 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 111
ID ACA65781 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO protein #85.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 112
ID ACA68944 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 113
ID ACA92974 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 114
ID ACA94926 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 115
ID ACD16488 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 116
ID ACD15567 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036152-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 2846; DB 8; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 117
 ID AC98466 standard; cDNA; 2846 BP.
 DE Human PRO polynucleotide #19.
 PN US2003027993-Al.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2846; DB 8; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 118
 ID ABX17058 standard; cDNA; 2846 BP.
 DE Human PRO polynucleotide #65.
 PN US2002123463-Al.
 PD 05-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2846; DB 8; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 119
 ID ABX16670 standard; cDNA; 2846 BP.
 DE Human cDNA encoding secreted/transmembrane protein #85.
 PN US2002127584-Al.
 PD 12-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2846; DB 8; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 120
 ID AC67913 standard; cDNA; 2846 BP.
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.
 PN US2002177164-Al.
 PD 28-NOV-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2846; DB 9; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 121
 ID AC63391 standard; cDNA; 2846 BP.
 DE cDNA encoding human PRO polypeptide #19.
 PN US2003023042-Al.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2846; DB 9; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 122
 ID AC97611 standard; cDNA; 2846 BP.
 DE Human PRO polynucleotide #85.
 PN US2003032115-Al.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2846; DB 9; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 123
 ID AC99060 standard; cDNA; 2846 BP.
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.
 PN US2003032140-Al.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2846; DB 9; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 124
 ID ACC91692 standard; cDNA; 2846 BP.
 DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
 PN US2003040076-Al.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2846; DB 9; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 125
 ID ACD1103 standard; cDNA; 2846 BP.
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.
 PN US2003008352-Al.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2846; DB 9; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 126

ID ACD14953 standard; cDNA; 2846 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #85.
 PN US2003044922-Al.
 PD 06-MAR-2003.
 Query Match 100.0%; Score 2846; DB 9; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 127
 ID AC98362 standard; cDNA; 2846 BP.
 DE Human secreted and transmembrane polypeptide PRO1344 cDNA.
 PN US2002197615-Al.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2846; DB 9; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 128
 ID AC981869 standard; cDNA; 2846 BP.
 DE cDNA encoding human PRO1344 polypeptide.
 PN US2003017981-Al.
 PD 23-JAN-2003.
 Query Match 100.0%; Score 2846; DB 9; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 129
 ID ACD11717 standard; cDNA; 2846 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #85.
 PN US2003032118-Al.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 2846; DB 9; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 130
 ID AC95846 standard; cDNA; 2846 BP.
 DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
 PN US2003036135-Al.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 2846; DB 9; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 131
 ID ACF16409 standard; cDNA; 2846 BP.
 DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
 PN US2003054455-Al.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2846; DB 9; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 132
 ID ACF02527 standard; cDNA; 2846 BP.
 DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
 PN US2003049741-Al.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2846; DB 9; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 133
 ID ACF02834 standard; cDNA; 2846 BP.
 DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
 PN US2003049743-Al.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2846; DB 9; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 134
 ID ACF21421 standard; cDNA; 2846 BP.
 DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
 PN US2003049769-Al.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2846; DB 9; Length 2846;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 135
 ID ACF10105 standard; cDNA; 2846 BP.
 DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
 PN US2003068743-Al.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 136
ID ACF77998 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 137
ID ACD46703 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 138
ID ACD49466 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 139
ID ACF28233 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 140
ID ACD88923 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 141
ID ACD84318 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 142
ID ACD99092 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 143
ID ADA77921 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 144
ID ACF48834 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 145
ID ACD09154 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 146
ID ACF11947 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 147
ID ACF41181 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 148
ID ACF15795 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 149
ID ACF16102 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 150
ID ADB17094 standard; cDNA; 2846 BP.
DE Human cDNA clone (SeqID 37) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 151
ID ACD31929 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 152
ID ACF18737 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 153
ID ACF09184 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 154
ID ACF78305 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054473-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 155
ID ACF51904 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003064440-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 156
ID ACF26391 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 157
ID ACF24184 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 158
ID ACF63495 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 159
ID ACF50369 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 160
ID ACH07840 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 161
ID ACF13646 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 162
ID ACD41572 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 163
ID ADA37741 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
FN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 164
ID ACF31985 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 165
ID ACF23263 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 166
ID ACF39953 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 167
ID ACD45475 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 168
ID ACF53132 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 169
ID ACF27312 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 170
ID ACF45150 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 171
ID ACF29768 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 172
ID ACD89844 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;

```
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 173
ID ACD84625 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 174
ID ACD98785 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 175
ID ACF77077 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 176
ID ACF76770 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 177
ID ACF49755 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 178
ID ACF50062 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 179
ID ADA21427 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1344.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 180
ID ACD09461 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 181
ID ACD08540 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 182
ID ACH03594 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 183
ID ACF12254 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 184
ID ACC94762 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 185
ID ACD22481 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 186
ID ACF15181 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 187
ID ACC97276 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 188
ID ACC92306 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 189
ID ACF13953 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 190
ID ACF14260 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 191
ID ADA10214 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1344.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
Pred. No. 0;
RESULT 192
ID ACF09491 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
```

PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 193
ID ACD45782 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 194
ID ACD47931 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 195
ID ACD67662 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 196
ID ACF25470 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 197
ID ACF29154 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 198
ID ACD84932 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 199
ID ACD84011 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 200
ID ACD88002 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 201
ID ACF30689 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003069407-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 202
ID ACF32292 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 203
ID ACH11952 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 204
ID ACH12259 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 205
ID ADA19899 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 206
ID ACD40651 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 207
ID ADB17282 standard; cDNA; 2846 BP.
DE Human cDNA clone (SeqID 37) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 208
ID ADA17758 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 209
ID ACF18123 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 210
ID ACF08570 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 211
ID ACF31371 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 212
ID ACF52211 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 213
ID ACD50080 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 214
ID ACF38783 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 215
ID ACF26698 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 216
ID ACF24798 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 217
ID ACF46378 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 218
ID ACF27926 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 219
ID ACD89230 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 220
ID ACF63802 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 221
ID ACF60442 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 222
ID ACHI2566 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 223
ID ACH09989 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 224
ID ACD03844 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 225
ID ACD10382 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 226
ID ACD12024 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 227
ID ACF42409 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 228
ID ADA27866 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 229
ID ACF18430 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 230
ID ACF02220 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 231
ID ACF21728 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 232
ID ACF10412 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 233
ID ACF33864 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 234
ID ACF44826 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 235
ID ACD90458 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 236
ID ACD91071 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 237
ID ACF30382 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 238
ID ACD87081 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 239
ID ACF60135 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 240
ID ACF46685 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 241
ID ACF75542 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 242
ID ADA79713 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 243
ID ACF17202 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 244
ID ACF22956 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 245
ID ACF07956 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 246
ID ACF08263 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 247
ID ACF40567 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 248
ID ACF53746 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064456-A1.
PD 03-APR-2003.

```
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 249
ID ACD47010 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 250
ID ACF47913 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 251
ID ACF47299 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 252
ID ACF46071 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 253
ID ACD86160 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 254
ID ACF52518 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 255
ID ACF52825 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 256
ID ACF64818 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 257
ID ACF76463 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 258
ID ACF61363 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 259
ID ACF61670 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 260
ID ACD30701 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 261
ID ACD31622 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 262
ID ACD32543 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 263
ID ADA20071 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 264
ID ACD82108 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 265
ID ACF17509 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 266
ID ADA94446 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 267
ID ACF07342 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049753-A1.
```


PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 268
ID ACF20500 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 269
ID ACF20807 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 270
ID ACF21114 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 271
ID ACD47624 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 272
ID ACF47606 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 273
ID ACF53439 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 274
ID ACD86774 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 275
ID ACH05022 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 276
ID ACF44519 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 277
ID ADA81440 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 278
ID ACD22174 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 279
ID ACD24521 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 280
ID ACD39724 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 281
ID ACD40031 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 282
ID ACF13339 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 283
ID ACF03141 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 284
ID ACF78612 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 285
ID ACF11333 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 286
ID ACF50676 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032121-A1.

PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 296
ID ACH07226 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 297
ID ACH07533 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 298
ID ACH08147 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 299
ID ACH11338 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 300
ID ACH11645 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 301
ID ACH10296 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 302
ID ACF01299 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 303
ID ACF40874 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 304
ID ACD24214 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 305
ID ACD31315 standard; cDNA; 2846 BP.

PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 297
ID ACF34171 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 298
ID ACD46396 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 299
ID ACD48238 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 300
ID ACF27619 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 301
ID ACF24491 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 302
ID ACD85546 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 303
ID ACD90151 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 304
ID ACD83704 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 305
ID ACF49141 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;

DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 306
ID ACF17816 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 307
ID ADA38671 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 308
ID ACF32599 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 309
ID ACF40260 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 310
ID ACF48220 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 311
ID ACF38169 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 312
ID ACF25105 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 313
ID ACF27005 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 314
ID ACF29461 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 315
ID ACD87695 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 316
ID ACF76156 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 317
ID ACF49448 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 318
ID ACF43905 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 319
ID ACH06250 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 320
ID ACH06557 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 321
ID ADA83238 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 322
ID ACC92613 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 323
ID ACC93227 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 324
ID ACF19272 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 325
ID ACD12963 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 326
ID ACF06421 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 327
ID ACC94455 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 328
ID ACC97883 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US200304932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 329
ID ACC94148 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 330
ID ACF42102 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 331
ID ACD31108 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 332
ID ACD43037 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 333
ID ACD43344 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 334
ID ACF14874 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003045700-A1.
PD 06-MAR-2003.

DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 335
ID ADA92792 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 336
ID ACF01606 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 337
ID ACF31678 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 338
ID ACD67355 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 339
ID ACD48545 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 340
ID ACD48852 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 341
ID ACF51290 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 342
ID ACF54053 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 343
ID ACF25777 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003045700-A1.
PD 06-MAR-2003.

ID ACC96460 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 363
ID ACC98490 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 364
ID ACF41795 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 365
ID ACF16716 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 366
ID ACD32236 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PD US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 367
ID ACD30394 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PD US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 368
ID ACD41265 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PD US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 369
ID ACF07649 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 370
ID ACF31064 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 371
ID ACF77384 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 372
ID ACF11026 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 373
ID ACF32906 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 374
ID ACF26084 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 375
ID ACD83397 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PD US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 376
ID ACF23570 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 377
ID ACF42984 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 378
ID ACF43291 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 379
ID ACH05943 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PD US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 380
ID ACH08761 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PD US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 381
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 400
ID ACD10075 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003036158-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 27-FEB-2003.
RESULT 401
ID ACD16800 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
FN US2003036151-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 27-FEB-2003.
RESULT 402
ID ACH65430 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
FN US2003044806-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 27-FEB-2003.
RESULT 403
ID ACC99097 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003040067-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 27-FEB-2003.
RESULT 404
ID ACF00491 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003054456-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 20-MAR-2003.
RESULT 405
ID ACD40958 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003054482-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 20-MAR-2003.
RESULT 406
ID ACF14567 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003054457-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 20-MAR-2003.
RESULT 407
ID ACF22342 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003059883-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 27-MAR-2003.
RESULT 408
ID ACF78919 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049764-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 13-MAR-2003.
RESULT 409
ID ACF11640 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003073177-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 17-APR-2003.
RESULT 410
ID ADA22353 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1344.
FN US2003040473-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 27-FEB-2003.
RESULT 411
ID ACF51597 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003064442-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 03-APR-2003.
RESULT 412
ID ACF33520 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003064450-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 03-APR-2003.
RESULT 413
ID ACD49773 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003068731-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 10-APR-2003.
RESULT 414
ID ACF37555 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068683-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 10-APR-2003.
RESULT 415
ID ACF28540 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068754-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 10-APR-2003.
RESULT 416
ID ACD88616 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003068681-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 10-APR-2003.
RESULT 417
ID ACF75235 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003096351-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 22-MAY-2003.
RESULT 418
ID ACF61056 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003096358-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 22-MAY-2003.
RESULT 419
ID ACF44212 standard; cDNA; 2846 BP.

DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 420
ID ACF07035 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 421
ID ACF39420 standard; cDNA; 2846 BP.
DE Human PRO 1344 PCR primer #1.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 422
ID ACC93841 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036122-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 423
ID ACD20946 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 424
ID ACF06728 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040065-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 425
ID ACD20639 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044919-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 426
ID ACD22788 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040077-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 427
ID ACF41488 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044928-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 428
ID ADA06519 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #65.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 429
ID ADA39212 standard; cDNA; 2846 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003059782-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 430
ID ACF07035 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 431
ID ACF77691 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 432
ID ACD46089 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 433
ID ACF46992 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 434
ID ACF54360 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 435
ID ACF45764 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 436
ID ACF45457 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 437
ID ACF38476 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 438
ID ACD89537 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068694-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 439
ID ACD85239 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 440
ID ACD85853 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 441
ID ACF75849 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 442
ID ACF60749 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 443
ID ACH05636 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 444
ID ADA82604 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 445
ID ADB85610 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 446
ID ADB96238 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 447
ID ACF55895 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 448
ID ACF55281 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 449
ID ADB85912 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 450
ID ACF56202 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 451
ID ACF56509 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 452
ID ADB68289 standard; cDNA; 2846 BP.
DE Human PRO1344 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 453
ID ADB68096 standard; cDNA; 2846 BP.
DE Human PRO1344 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 454
ID ACF55588 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 455
ID ACF54974 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 456
ID ADB90913 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;

```
RESULT 457
ID ADC57710 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 458
ID ADC55074 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 459
ID ADC11941 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 460
ID ADC06993 standard; cDNA; 2846 BP.
DE Human PRO1344 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 461
ID ADC56363 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 462
ID ADC17172 standard; cDNA; 2846 BP.
DE cDNA sequence encoding a PRO polypeptide (seqID 37).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 463
ID ADC07418 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 464
ID ADC11408 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 465
ID ADC14870 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 466
ID ADC52365 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US200313882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 467
ID ADC14530 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 468
ID ADD08062 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 469
ID ADC81887 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 470
ID ADD07529 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 471
ID ADC82420 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 472
ID ADD05642 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 473
ID ADD08600 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 474
ID ADD06849 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 475
ID ADC83096 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 476
ID ADD55203 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
```

```
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 477
ID ADD36041 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 478
ID ADD56161 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 479
ID ADD54599 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 480
ID ADE26753 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 481
ID ADE26220 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 482
ID ADF67157 standard; cDNA; 2846 BP.
DE Human PRO1344 nucleotide sequence SEQ ID NO:230.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 483
ID ADG01042 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 484
ID ADG08595 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 485
ID ADG02637 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 486
ID ADG01344 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 487
ID ADF95519 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 488
ID ADF95216 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 489
ID ADG12334 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 490
ID ADH24069 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 491
ID ADH34095 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 492
ID ADH29928 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 493
ID ADH23899 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 494
ID ADH08994 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 495
ID ADG85303 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
```

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 496
ID ADH24579 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 497
ID ADH37435 standard; cDNA; 2846 BP.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 498
ID ADH2024 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 499
ID ADH37605 standard; cDNA; 2846 BP.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 500
ID ADG85643 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 501
ID ADH24239 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 502
ID ADH38533 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 503
ID ADG83654 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 504
ID ADH29462 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 505
ID ADH27578 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 506
ID ADH37775 standard; cDNA; 2846 BP.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 507
ID ADH37952 standard; cDNA; 2846 BP.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 508
ID ADH57372 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 509
ID ADH53514 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 510
ID ADH53684 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 511
ID ADH52020 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 512
ID ADH49875 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 513
ID ADI25385 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;

```
Best Local Similarity 100.0%; Pred. No. 0;
ID ADH90178 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 514
ID ADH90178 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 515
ID ADI25555 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 516
ID ADH97729 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 517
ID ADI35411 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 518
ID ADI03577 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 519
ID ADI11934 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 520
ID ADH90008 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 521
ID ADH99903 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 522
ID ADH98409 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 523
ID ADI11084 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 524
ID ADI11594 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 525
ID ADH98239 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 526
ID ADH98579 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 527
ID ADH98069 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 528
ID ABX78612 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 529
ID ACA75584 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 530
ID ACA71064 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 531
ID ACC87592 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 532
ID ACC86978 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
```

RESULT 533
ID ACD04151 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 534
ID ABX77859 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 535
ID ABX80271 standard; DNA; 2846 BP.
DE Human secreted or transmembrane protein related PCR primer #50.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 536
ID ACAG9177 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 537
ID ACA69482 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 538
ID ACA90327 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 539
ID ACC89434 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 540
ID ABX90248 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein cDNA, #94.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 541
ID ACA98225 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 542
ID ACAG93867 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 543
ID ACD15260 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 544
ID ACD08847 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 545
ID ACC96767 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 546
ID ACF15488 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 547
ID ABX64094 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 548
ID ACA72855 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 549
ID ACD03027 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 550
ID ACD01842 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 551
ID ACA92034 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 552
ID ADI05057 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 553

ID ADI03407 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 554
ID ADI04802 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 555
ID ADH78256 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 556
ID ADI19600 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 557
ID ADH90348 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 558
ID ADI03067 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 559
ID ADH77916 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 560
ID ADH97899 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 561
ID ADI01284 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 562
ID ADI01979 standard; cDNA; 2846 BP.

DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 563
ID ADI03237 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 564
ID ADI11424 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 565
ID ADI02326 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 566
ID ADI11764 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 567
ID ADI05401 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 568
ID ADH79473 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 569
ID ADI19430 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 570
ID ADI05231 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 571
ID ADH79643 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.

PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 572
ID ADI01469 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 573
ID ADI01639 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 574
ID ADI01809 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 575
ID ADH79813 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 576
ID ADI04631 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 577
ID ADI02767 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 578
ID ADH78086 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 579
ID ADI25725 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 580
ID ADI25895 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181671-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 581
ID ADH98749 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 582
ID ADH79990 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 583
ID ADL32775 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 11; Length 2846;
RESULT 584
ID ADM30309 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 11; Length 2846;
RESULT 585
ID ADL93721 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 11; Length 2846;
RESULT 586
ID ADC52175 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 587
ID ADE74306 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 588
ID ADE74918 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003211574-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 589
ID ADF35356 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;

RESULT 590
ID ADG11606 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 591
ID ADF96131 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003215909-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 592
ID ADG04402 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 593
ID ADG00562 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 594
ID ADH06607 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 595
ID ADH06437 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 596
ID ADG68858 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 597
ID ADH27748 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 598
ID ADH25089 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 599
ID ADH33721 standard; cDNA; 2846 BP.

DE Human PRO polynucleotide #19.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 600
ID ADG82818 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 601
ID ADH02364 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 602
ID ADH07971 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 603
ID ADG69368 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 604
ID ADH39189 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 605
ID ADH26099 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 606
ID ADG83929 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 607
ID ADH19476 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 608
ID ADG85473 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.

Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 627
ID ADH20009 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 628
ID ADH02534 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 629
ID ADG69028 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 630
ID ADH07631 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 631
ID ADG86153 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 632
ID ADH24749 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 633
ID ADH25797 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 634
ID ADH38363 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 635
ID ADH57202 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 636
ID ADH52190 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 637
ID ADH49556 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 638
ID ADH90518 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 639
ID ADI11254 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 640
ID ADH98919 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 641
ID ADI02149 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 642
ID ADH90688 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 643
ID ADJ54807 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 644
ID ADJ98563 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 645
ID ADJ98733 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 646
ID ADJ78892 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 647
ID ADJ99126 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 648
ID ADJ99296 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 649
ID ADJ98914 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 650
ID ADJ79062 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 651
ID ADK00922 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 652
ID ADK14443 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 653
ID ADJ64578 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 654

ID ADM31474 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 655
ID ADM36521 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 656
ID ADM40326 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 657
ID ADM80892 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 658
ID ADM37934 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 659
ID ADK65407 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 2844.4; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 660
ID ACA89307 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.7%; Score 2838; DB 8; Length 2846;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 661
ID ADA00368 standard; cDNA; 2843 BP.
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.5%; Score 2832; DB 9; Length 2843;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 662
ID ACA67289 standard; cDNA; 2848 BP.
DE cDNA encoding human secreted polypeptide PRO1344.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.2%; Score 2824; DB 8; Length 2848;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 663
ID AAA39951 standard; cDNA; 2747 BP.

DE Human TANGO 215 cDNA.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 95.7%; Score 2724.6; DB 3; Length 2747;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 664
ID AB235533 standard; cDNA; 2845 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 644.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match 95.4%; Score 2714.4; DB 6; Length 2845;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 665
ID AAH47256 standard; cDNA; 2784 BP.
DE Human serine protease-like protein encoding cDNA (hc-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 92.6%; Score 2636.8; DB 4; Length 2784;
Best Local Similarity 98.0%; Pred. No. 0;
RESULT 666
ID AAH15142 standard; cDNA; 2784 BP.
DE Human cDNA sequence SEQ ID NO:13201.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 92.6%; Score 2636.8; DB 4; Length 2784;
Best Local Similarity 98.0%; Pred. No. 0;
RESULT 667
ID ADN04639 standard; cDNA; 2784 BP.
DE Anticoporiatic cDNA sequence #529.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 92.6%; Score 2636.8; DB 12; Length 2784;
Best Local Similarity 98.0%; Pred. No. 0;
RESULT 668
ID ADS85021 standard; DNA; 2784 BP.
DE Human atopic dermatitis-related gene sequence SeqID23.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (YUJU-) UNIV JUNTENDO.
Query Match 92.6%; Score 2636.8; DB 13; Length 2784;
Best Local Similarity 98.0%; Pred. No. 0;
RESULT 669
ID ADS85033 standard; DNA; 2784 BP.
DE Human atopic dermatitis-related gene sequence SeqID35.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (YUJU-) UNIV JUNTENDO.
Query Match 92.6%; Score 2636.8; DB 13; Length 2784;
Best Local Similarity 98.0%; Pred. No. 0;
RESULT 670
ID ADL06663 standard; DNA; 2650 BP.
DE Human 3T3 cell conversion promoter FP938 DNA.
PN CN1403477-A.
PD 19-MAR-2003.
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
Query Match 92.4%; Score 2630.6; DB 10; Length 2650;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 671
ID ADL06661 standard; cDNA; 2650 BP.
DE Human 3T3 cell conversion promoter FP938 cDNA.
PN CN1403477-A.
PD 19-MAR-2003.
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
Query Match 92.4%; Score 2630.6; DB 10; Length 2650;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 672

ID ADR41309 standard; cDNA; 2311 BP.
DE Human CD-like molecule HSXDF41 cDNA, SEQ ID NO:108.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 80.8%; Score 2298.8; DB 7; Length 2311;
Best Local Similarity 99.6%; Pred. No. 0;
RESULT 673
ID AAD30584 standard; cDNA; 2632 BP.
DE Human protease, PRYS-17 cDNA.
PN WO200208396-A2.
PD 31-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 80.5%; Score 2292.4; DB 6; Length 2632;
Best Local Similarity 92.2%; Pred. No. 0;
RESULT 674
ID ABK30334 standard; cDNA; 2886 BP.
DE Human G-prtein-coupled protease #104.
PN US6331427-B1.
PD 18-DEC-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 79.4%; Score 2259.4; DB 6; Length 2886;
Best Local Similarity 96.9%; Pred. No. 1.1e-311;
RESULT 675
ID AAF74433 standard; cDNA; 2306 BP.
DE Human PRO2 nucleotide sequence SEQ ID NO:3.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 77.2%; Score 2197.6; DB 4; Length 2306;
Best Local Similarity 99.8%; Pred. No. 6.5e-303;
RESULT 676
ID AAS01222 standard; cDNA; 2306 BP.
DE DNA encoding human secreted protein, POLY13.
PN WO200119856-A2.
PD 22-MAR-2001.
PA (CURA-) CURAGEN CORP.
Query Match 77.2%; Score 2197.6; DB 5; Length 2306;
Best Local Similarity 99.8%; Pred. No. 6.5e-303;
RESULT 677
ID ADH89027 standard; cDNA; 2305 BP.
DE Human POLYX polynucleotide #13.
PN US2003198958-A1.
PD 23-OCT-2003.
PA (SHIM/) SHIMKETS R. A.
PA (FERN/) FERNANDES E.
PA (HERR/) HERRMANN J L.
PA (LIUX/) LIU X.
PA (YANG/) YANG M.
PA (BOLD/) BOLDOG F L.
PA (SMIT/) SMITHSON G.
PA (RAST/) RASTELLI L.
Query Match 76.8%; Score 2185.6; DB 12; Length 2305;
Best Local Similarity 99.8%; Pred. No. 3.3e-301;
RESULT 678
ID AAA39952 standard; cDNA; 2163 BP.
DE Human TANGO 215 coding sequence cDNA.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 75.7%; Score 2155; DB 3; Length 2163;
Best Local Similarity 99.8%; Pred. No. 7.2e-297;
RESULT 679
ID AAC90025 standard; cDNA; 2259 BP.
DE Clone HFPBY75 coding sequence.
PN WO200061774-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 75.3%; Score 2142.2; DB 3; Length 2259;
Best Local Similarity 97.6%; Pred. No. 4.7e-295;
RESULT 680
ID AAH47258 standard; cDNA; 2289 BP.
DE Human serine protease-like protein coding sequence.

PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 73.6%; Score 2095.8; DB 4; Length 2289;
Best Local Similarity 97.6%; Pred. No. 1.8e-288;
RESULT 681
ID AAD33261 standard; cDNA; 2022 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:35.
PD WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 70.5%; Score 2007.8; DB 6; Length 2022;
Best Local Similarity 99.7%; Pred. No. 5.4e-276;
RESULT 682
ID AAI59076 standard; cDNA; 2144 BP.
DE Human polynucleotide SEQ ID NO 1279.
PD WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 69.9%; Score 1988.4; DB 4; Length 2144;
Best Local Similarity 97.1%; Pred. No. 3e-273;
RESULT 683
ID ADQ99299 standard; cDNA; 2144 BP.
DE DNA encoding human GPCR-like protein seqid 969.
PD US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 69.9%; Score 1988.4; DB 5; Length 2144;
Best Local Similarity 97.1%; Pred. No. 3e-273;
RESULT 684
ID ADB49059 standard; cDNA; 2144 BP.
DE Novel human cDNA SEQ ID NO 969.
PD US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRNA/) DRMANAC R T.
Query Match 69.9%; Score 1988.4; DB 9; Length 2144;
Best Local Similarity 97.1%; Pred. No. 3e-273;
RESULT 685
ID AAI59113 standard; cDNA; 2142 BP.
DE Human polynucleotide SEQ ID NO 1316.
PD WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 69.7%; Score 1984.8; DB 4; Length 2142;
Best Local Similarity 97.0%; Pred. No. 9.9e-273;
RESULT 686
ID ADQ99336 standard; cDNA; 2142 BP.
DE DNA encoding human GPCR-like protein seqid 1006.
PD US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 69.7%; Score 1984.8; DB 5; Length 2142;
Best Local Similarity 97.0%; Pred. No. 9.9e-273;
RESULT 687
ID ADB49096 standard; cDNA; 2142 BP.
DE Novel human cDNA SEQ ID NO 1006.
PD US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRNA/) DRMANAC R T.
Query Match 69.7%; Score 1984.8; DB 9; Length 2142;
Best Local Similarity 97.0%; Pred. No. 9.9e-273;
RESULT 688
ID AAI60862 standard; cDNA; 2040 BP.
DE Human polynucleotide SEQ ID NO 4851.
PD WO200153312-A1.

PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 67.7%; Score 1928; DB 4; Length 2040;
Best Local Similarity 97.5%; Pred. No. 1.1e-264;
RESULT 689
ID AAA39985 standard; cDNA; 2823 BP.
DE Murine TANGO 215 cDNA.
PD WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 65.4%; Score 1862.4; DB 3; Length 2823;
Best Local Similarity 80.3%; Pred. No. 2.2e-255;
RESULT 690
ID AAF74432 standard; cDNA; 1867 BP.
DE Human PRO1 nucleotide sequence SEQ ID NO:1.
PD WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 60.5%; Score 1722; DB 4; Length 1867;
Best Local Similarity 99.2%; Pred. No. 1.8e-235;
RESULT 691
ID AAH47257 standard; cDNA; 2244 BP.
DE Murine serine protease-like protein encoding cDNA (mc-PLACE1009992).
PD WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 59.5%; Score 1692.6; DB 4; Length 2244;
Best Local Similarity 85.5%; Pred. No. 2.7e-231;
RESULT 692
ID AAD33241 standard; cDNA; 1101 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:15.
PD WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 30.9%; Score 879.8; DB 6; Length 1101;
Best Local Similarity 94.4%; Pred. No. 5e-116;
RESULT 693
ID AAH99144 standard; cDNA; 1058 BP.
DE Human EST-derived coding sequence SEQ ID NO: 1001.
PD WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 23.7%; Score 674.2; DB 4; Length 1058;
Best Local Similarity 94.3%; Pred. No. 7.2e-87;
RESULT 694
ID AAS86826 standard; cDNA; 1058 BP.
DE DNA encoding novel human diagnostic protein #22630.
PD WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 23.7%; Score 674.2; DB 5; Length 1058;
Best Local Similarity 94.3%; Pred. No. 7.2e-87;
RESULT 695
ID AAH08069 standard; cDNA; 705 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:4904.
PD EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 22.8%; Score 648; DB 4; Length 705;
Best Local Similarity 98.5%; Pred. No. 3.8e-83;
RESULT 696
ID AB234917 standard; cDNA; 548 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 29.
PD WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match 18.9%; Score 538.8; DB 6; Length 548;
Best Local Similarity 98.5%; Pred. No. 1.2e-67;
RESULT 697
ID ABK30409 standard; cDNA; 505 BP.
DE Human G-protein-coupled protease #179.
PD US6331427-B1.
PD 18-DEC-2001.

PA (MILL-) MILLENNIUM PHARM INC.
Query Match 16.8%; Score 479.4; DB 6; Length 505;
Best Local Similarity 99.4%; Pred. No. 3.1e-59;
RESULT 698
ID AAI60899 standard; cDNA; 438 BP.
DE Human polynucleotide SEQ ID NO 4888.
PN WO200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.6%; Score 414.6; DB 4; Length 438;
Best Local Similarity 98.8%; Pred. No. 4.9e-50;
RESULT 699
ID ABN74148 standard; cDNA; 997 BP.
DE Bovine embryonic germ (EG) cell cDNA EST #199.
PN WO200194550-A2.
PD 13-DEC-2001.
PA (INFI-) INFIGEN INC.
Query Match 14.4%; Score 409.4; DB 6; Length 997;
Best Local Similarity 83.9%; Pred. No. 2.6e-49;
RESULT 700
ID AAHL3031 standard; cDNA; 532 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:9866.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 14.3%; Score 408.2; DB 4; Length 532;
Best Local Similarity 88.5%; Pred. No. 3.9e-49;
RESULT 701
ID ABL63519 standard; DNA; 337 BP.
DE Breast cancer related gene sequence SEQ ID NO:1856.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 11.8%; Score 337; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 5e-39;
RESULT 702
ID ABL63953 standard; DNA; 337 BP.
DE Breast cancer related gene sequence SEQ ID NO:2290.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 11.8%; Score 337; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 5e-39;
RESULT 703
ID AAX40465 standard; cDNA; 340 BP.
DE Human secreted protein 5' EST SEQ ID No: 65.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 11.7%; Score 332; DB 2; Length 340;
Best Local Similarity 98.5%; Pred. No. 2.6e-38;
RESULT 704
ID AAD33260 standard; cDNA; 477 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:34.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.3%; Score 321; DB 6; Length 477;
Best Local Similarity 99.1%; Pred. No. 9.1e-37;
RESULT 705
ID ACH19532 standard; cDNA; 403 BP.
DE Human adult lung cDNA #535.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 9.9%; Score 283; DB 9; Length 403;
Best Local Similarity 97.6%; Pred. No. 2.3e-31;
RESULT 706
ID ABN73761 standard; cDNA; 432 BP.

DE Bovine embryonic germ (EG) cell cDNA EST 990928a CONTIG 32.
PN WO200194550-A2.
PD 13-DEC-2001.
PA (INFI-) INFIGEN INC.
Query Match 8.9%; Score 253.8; DB 6; Length 432;
Best Local Similarity 85.5%; Pred. No. 3.1e-27;
RESULT 707
ID ADQ21818 standard; DNA; 286 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4638.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.7%; Score 218.4; DB 12; Length 286;
Best Local Similarity 99.5%; Pred. No. 3.3e-22;
RESULT 708
ID AAD37042 standard; DNA; 369 BP.
DE Mouse limulus-clotting factor protease-like EST gene.
PN WO200203787-A2.
PD 17-JAN-2002.
PA (DELT-) DELTAGEN INC.
Query Match 7.5%; Score 213.6; DB 6; Length 369;
Best Local Similarity 82.7%; Pred. No. 1.6e-21;
RESULT 709
ID AAZ43781 standard; cDNA; 2685 BP.
DE Human fetal brain cDNA clone vb6_1.
PN WO9955721-A1.
PD 04-NOV-1999.
PA (ALPH-) ALPHAGENE INC.
Query Match 5.2%; Score 148; DB 3; Length 2685;
Best Local Similarity 84.7%; Pred. No. 2.9e-12;
RESULT 710
ID AAD07722 standard; cDNA; 938 BP.
DE Human secreted protein-encoding gene 18 cDNA clone HLYDU43, SEQ ID NO:28.
PN WO200134800-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.1%; Score 146.2; DB 5; Length 938;
Best Local Similarity 78.5%; Pred. No. 5.4e-12;
RESULT 711
ID ACN58522 standard; cDNA; 476 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-010-Q6-K6-C11, SEQ:13303.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 5.1%; Score 145.8; DB 13; Length 476;
Best Local Similarity 85.7%; Pred. No. 6.4e-12;
RESULT 712
ID ADR62569 standard; cDNA; 1423 BP.
DE Cotton cDNA sequence, SEQ ID 3350.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match 5.1%; Score 145.8; DB 13; Length 1423;
Best Local Similarity 85.7%; Pred. No. 6.1e-12;
RESULT 713
ID AAF72803 standard; DNA; 2057 BP.
DE Secreted protein gene #5.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.1%; Score 145.6; DB 4; Length 2057;
Best Local Similarity 79.6%; Pred. No. 6.4e-12;
RESULT 714
ID AAI87708 standard; cDNA; 903 BP.
DE Human polynucleotide SEQ ID NO 7768.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.

Query Match 5.1%; Score 145.4; DB 4; Length 903;
Best Local Similarity 90.6%; Pred. No. 7.1e-12;
RESULT 715
ID ACN45855 standard; cDNA; 608 BP.
DE Cotton primed seed EST Clone ID: LIB3825-009-Q1-K6-G7, SEQ:636.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 5.1%; Score 144.8; DB 13; Length 608;
Best Local Similarity 87.8%; Pred. No. 8.8e-12;
RESULT 716
ID ACN61841 standard; cDNA; 483 BP.
DE Cotton gynecium tissue EST Clone ID: LIB3829-021-Q6-N6-F9, SEQ:16622.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 5.1%; Score 144.4; DB 13; Length 483;
Best Local Similarity 84.0%; Pred. No. 1e-11;
RESULT 717
ID ABA93725 standard; cDNA; 3028 BP.
DE Human differentiation/development cDNA clone amy2_2b19.
PN WO200198454-A2.
PD 27-DEC-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.1%; Score 144.2; DB 6; Length 3028;
Best Local Similarity 75.5%; Pred. No. 9.9e-12;
RESULT 718
ID ACF34512 standard; DNA; 3028 BP.
DE Gene encoding angiogenesis protein BN0146.
PN WO2003027285-A1.
PD 03-APR-2003.
PA (BION-) BIONOMICS LTD.
Query Match 5.1%; Score 144.2; DB 8; Length 3028;
Best Local Similarity 75.5%; Pred. No. 9.9e-12;
RESULT 719
ID ABV58662 standard; cDNA; 381 BP.
DE Human prostate expression marker cDNA 58653.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 144; DB 5; Length 381;
Best Local Similarity 84.4%; Pred. No. 1.2e-11;
RESULT 720
ID ACN45357 standard; cDNA; 597 BP.
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-A11, SEQ:138.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 5.1%; Score 144; DB 13; Length 597;
Best Local Similarity 84.4%; Pred. No. 1.1e-11;
RESULT 721
ID ABV44911 standard; cDNA; 375 BP.
DE Human prostate expression marker cDNA 44902.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 143.8; DB 5; Length 375;
Best Local Similarity 87.7%; Pred. No. 1.2e-11;
RESULT 722
ID ACN56273 standard; cDNA; 517 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-N6-E7, SEQ:11054.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 5.1%; Score 143.8; DB 13; Length 517;
Best Local Similarity 83.6%; Pred. No. 1.2e-11;
RESULT 723
ID ACN33890 standard; cDNA; 547 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-F10, SEQ:8671.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 5.1%; Score 143.8; DB 13; Length 547;
Best Local Similarity 90.1%; Pred. No. 1.2e-11;
RESULT 724
ID ADN95834 standard; DNA; 1999 BP.
DE Human BEC/LEC-related gene sequence SeqID758.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 5.1%; Score 143.8; DB 11; Length 1999;
Best Local Similarity 83.6%; Pred. No. 1.2e-11;
RESULT 725
ID ADQ24947 standard; DNA; 1999 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7767.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.1%; Score 143.8; DB 12; Length 1999;
Best Local Similarity 83.6%; Pred. No. 1.2e-11;
RESULT 726
ID ADP23790 standard; cDNA; 1999 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:968.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 5.1%; Score 143.8; DB 13; Length 1999;
Best Local Similarity 83.6%; Pred. No. 1.2e-11;
RESULT 727
ID ADP23585 standard; cDNA; 733 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:763.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 143.4; DB 13; Length 733;
Best Local Similarity 88.1%; Pred. No. 1.4e-11;
RESULT 728
ID ACN51414 standard; cDNA; 547 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-K6-G6, SEQ:6195.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 5.0%; Score 143.2; DB 13; Length 547;
Best Local Similarity 87.2%; Pred. No. 1.5e-11;
RESULT 729
ID ADI43251 standard; DNA; 2226 BP.
DE Plant transcription factor polynucleotide #1150.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER-) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.

PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J.
 PA (BROU/) BROUN M E.
 PA (PILG/) PILGRIM M L.
 PA (DUBE/) DUBELL A N.
 PA (PINE/) PINEDA O.
 PA (YUGG/) YU G.
 Query Match
 Best Local Similarity 5.0%; Score 143; DB 12; Length 2226;
 RESULT 730
 ID ADO02941 standard; cDNA; 2226 BP.
 DE Soybean orthologue of Thalecress transcription factor, cDNA #174.
 PN US2004045049-A1.
 PD 04-MAR-2004.
 PA (ZHAN/) ZHANG J.
 PA (FROM/) FROMM M E.
 PA (HEAR/) HEARD J E.
 PA (RIEC/) RIECHMANN J L.
 PA (ADAM/) ADAM L J.
 PA (BROU/) BROUN P E.
 PA (PINE/) PINEDA O.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J S.
 PA (YUGG/) YU G.
 PA (JIAN/) JIANG C.
 PA (SAMA/) SAMAHA R S.
 PA (PILG/) PILGRIM M L.
 PA (CREE/) CREELMAN R A.
 PA (DUBE/) DUBELL A N.
 PA (RATC/) RATCLIFFE O.
 PA (KUMI/) KUMIMOTO R.
 PA (SHER/) SHERMAN B K.
 Query Match
 Best Local Similarity 5.0%; Score 143; DB 12; Length 2226;
 RESULT 731
 ID ACN56223 standard; cDNA; 458 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-N6-A12, SEQ:11004.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 5.0%; Score 142.8; DB 13; Length 458;
 RESULT 732
 ID ACN47028 standard; cDNA; 528 BP.
 DE Cotton primed seed EST Clone ID: LIB3825-006-Q1-N6-B12, SEQ:1809.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 5.0%; Score 142.8; DB 13; Length 528;
 RESULT 733
 ID ACN56344 standard; cDNA; 565 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-034-Q6-N6-B10, SEQ:11125.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 5.0%; Score 142.8; DB 13; Length 565;
 RESULT 734
 ID AAC59297 standard; cDNA; 887 BP.
 DE Human secreted protein cDNA #21.
 PN WO200056753-A1.
 PD 28-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match
 Best Local Similarity 5.0%; Score 142.8; DB 3; Length 887;
 RESULT 735
 ID ACN82109 standard; cDNA; 547 BP.
 DE Cotton gynoeceum tissue EST Clone ID: LIB3829-025-Q6-N6-C2, SEQ:16890.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 5.0%; Score 142.6; DB 13; Length 547;
 RESULT 736
 ID AAQ04107 standard; cDNA; 2427 BP.
 DE Human pro-urokinase cDNA of clone pcUK176.
 PN EP365894-A.
 PD 02-MAY-1990.
 PA (FARM) FARMITALIA ERBA SPA CARLO.
 Query Match
 Best Local Similarity 5.0%; Score 142.6; DB 2; Length 2427;
 RESULT 737
 ID ABV23160 standard; cDNA; 2922 BP.
 DE Human prostate expression marker cDNA 23151.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 5.0%; Score 142.6; DB 5; Length 2922;
 RESULT 738
 ID ACN47472 standard; cDNA; 560 BP.
 DE Cotton primed seed EST Clone ID: LIB3825-011-Q1-N6-C9, SEQ:2253.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 5.0%; Score 142.4; DB 13; Length 560;
 RESULT 739
 ID ABX48619 standard; cDNA; 397 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #13784.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match
 Best Local Similarity 5.0%; Score 142.2; DB 8; Length 397;
 RESULT 740
 ID ABK34899 standard; cDNA; 409 BP.
 DE Human cDNA encoding secreted protein #37.
 PN WO200177288-A2.
 PD 18-OCT-2001.
 PA (GEMY) GENETICS INST INC.
 Query Match
 Best Local Similarity 5.0%; Score 142.2; DB 6; Length 409;
 RESULT 741
 ID ABV56624 standard; cDNA; 544 BP.
 DE Human prostate expression marker cDNA 56615.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 5.0%; Score 142.2; DB 5; Length 544;
 RESULT 742
 ID AAS62239 standard; cDNA; 681 BP.
 DE cDNA sequence #26 encoding novel human secreted protein.
 PN WO200177291-A2.
 PD 18-OCT-2001.
 PA (GEMY) GENETICS INST INC.

Query Match 5.0%; Score 142.2; DB 6; Length 681;
Best Local Similarity 92.0%; Pred. No. 2e-11;
RESULT 743
ID ABZ82489 standard; cDNA; 805 BP.
DE Human secreted protein cDNA #SEQ ID 36.
PN WO200268628-A1.
PD 06-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.0%; Score 142.2; DB 6; Length 805;
Best Local Similarity 92.0%; Pred. No. 2e-11;
RESULT 744
ID ACN62281 standard; cDNA; 496 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-027-Q6-N6-E4, SEQ:17062.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 5.0%; Score 142; DB 13; Length 496;
Best Local Similarity 91.0%; Pred. No. 2.2e-11;
RESULT 745
ID ADQ22434 standard; DNA; 1215 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5254.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.0%; Score 142; DB 12; Length 1215;
Best Local Similarity 76.1%; Pred. No. 2.1e-11;
RESULT 746
ID ADL26832 standard; cDNA; 12178 BP.
DE Rat L-NAME-related actin-associated cytoskeleton protein LACS cDNA.
PN WO2004022753-A1.
PD 18-MAR-2004.
PA (ANGE-) ANGES MG INC.
Query Match 5.0%; Score 142; DB 13; Length 12178;
Best Local Similarity 91.0%; Pred. No. 1.9e-11;
RESULT 747
ID ABX43725 standard; cDNA; 257 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #8890.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 5.0%; Score 141.8; DB 8; Length 257;
Best Local Similarity 87.6%; Pred. No. 2.4e-11;
RESULT 748
ID ADQ24863 standard; DNA; 2575 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7683.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.0%; Score 141.8; DB 12; Length 2575;
Best Local Similarity 81.6%; Pred. No. 2.2e-11;
RESULT 749
ID ACN48060 standard; cDNA; 487 BP.
DE Cotton primed seed EST Clone ID: LIB3825-018-Q1-N6-F4, SEQ:2841.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 5.0%; Score 141.6; DB 13; Length 487;
Best Local Similarity 80.5%; Pred. No. 2.5e-11;
RESULT 750
ID ADK57243 standard; DNA; 774 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4626.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.

PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 5.0%; Score 141.6; DB 10; Length 774;
Best Local Similarity 91.5%; Pred. No. 2.5e-11;
RESULT 751
ID ABL33490 standard; DNA; 8392 BP.
DE Human immune system associated gene SEQ ID NO: 1463.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 141.6; DB 6; Length 8392;
Best Local Similarity 86.7%; Pred. No. 2.2e-11;
RESULT 752
ID ABL32118 standard; DNA; 11416 BP.
DE Human immune system associated gene SEQ ID NO: 91.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 141.6; DB 6; Length 11416;
Best Local Similarity 84.6%; Pred. No. 2.2e-11;
RESULT 753
ID ABL70135 standard; DNA; 11416 BP.
DE Chemically treated cell signalling DNA sequence#13.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 141.6; DB 6; Length 11416;
Best Local Similarity 84.6%; Pred. No. 2.2e-11;
RESULT 754
ID AAS61063 standard; DNA; 11416 BP.
DE Human gene regulation-associated gene oligonucleotide #18.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 141.6; DB 6; Length 11416;
Best Local Similarity 84.6%; Pred. No. 2.2e-11;
RESULT 755
ID ABL33404 standard; DNA; 16033 BP.
DE Human immune system associated gene SEQ ID NO: 1377.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 141.6; DB 6; Length 16033;
Best Local Similarity 84.6%; Pred. No. 2.2e-11;
RESULT 756
ID ABX48177 standard; cDNA; 286 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13342.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 5.0%; Score 141.4; DB 8; Length 286;
Best Local Similarity 90.4%; Pred. No. 2.7e-11;
RESULT 757
ID AA187526 standard; cDNA; 382 BP.
DE Human polynucleotide SEQ ID NO 7586.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.0%; Score 141.2; DB 4; Length 382;
Best Local Similarity 87.1%; Pred. No. 2.9e-11;
RESULT 758
ID ABQ67159 standard; DNA; 6775 BP.
DE Human angiotensin associated polynucleotide SEQ ID NO 189.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 141.2; DB 6; Length 6775;
Best Local Similarity 87.1%; Pred. No. 2.6e-11;
RESULT 759
ID ADS89685 standard; DNA; 8900 BP.
DE Oligonucleotide of the invention SEQ ID NO:701.

PD WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 141.2; DB 13; Length 8900;
Best Local Similarity 87.1%; Pred. No. 2.5e-11;
RESULT 760
ID ADS89411 standard; DNA; 8900 BP.
DE Oligonucleotide of the invention SEQ ID NO:427.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 141.2; DB 13; Length 8900;
Best Local Similarity 87.1%; Pred. No. 2.5e-11;
RESULT 761
ID AAI88514 standard; cDNA; 389 BP.
DE Human polynucleotide SEQ ID NO 8574.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYGE-) HYSEQ INC.
Query Match 5.0%; Score 141; DB 4; Length 389;
Best Local Similarity 86.2%; Pred. No. 3.1e-11;
RESULT 762
ID AAC59098 standard; cDNA; 667 BP.
DE Human secreted protein coding sequence SEQ ID NO: 60.
PN WO200055171-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.0%; Score 141; DB 3; Length 667;
Best Local Similarity 76.0%; Pred. No. 3e-11;
RESULT 763
ID ADQ22371 standard; DNA; 4824 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5191.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.0%; Score 141; DB 12; Length 4824;
Best Local Similarity 90.9%; Pred. No. 2.8e-11;
RESULT 764
ID AAK89974 standard; DNA; 165 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3550.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 4; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 765
ID AAK90168 standard; DNA; 165 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3744.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 4; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 766
ID AAK89381 standard; DNA; 165 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2957.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 4; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 767
ID AAK73944 standard; DNA; 165 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28756.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 4; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 768
ID AAK78761 standard; DNA; 165 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33573.
PN WO200157182-A2.

PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 4; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 769
ID AAK81312 standard; DNA; 165 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36124.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 4; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 770
ID AAK79574 standard; DNA; 165 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34386.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 4; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 771
ID AAL07127 standard; DNA; 165 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9815.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 4; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 772
ID AAL04803 standard; DNA; 165 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7491.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 4; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 773
ID ABA08161 standard; DNA; 165 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 956.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 4; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 774
ID ABL97697 standard; DNA; 165 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2349.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 4; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 775
ID AAS29235 standard; DNA; 165 BP.
DE Genomic sequence #78 encoding novel human DNA-binding protein.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 5; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 776
ID ABA17044 standard; DNA; 165 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9375.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 5; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 777
ID ABA17044 standard; DNA; 165 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9375.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 5; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 778
ID AAD16672 standard; DNA; 165 BP.
DE Human pancreatic related protein-encoding exon, SEQ ID NO:36.
PN WO200155327-A2.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 5; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 778
ID AAS39812 standard; DNA; 165 BP.
DE Genomic sequence #231 encoding human colon associated polypeptide.
PN WO200155302-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 5; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 779
ID ABS68375 standard; DNA; 165 BP.
DE Human DNA-binding protein genomic DNA sequence #78.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.9%; Score 140.8; DB 6; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 780
ID ADB32772 standard; DNA; 165 BP.
DE Human novel colon related polypeptide DNA SEQ ID NO 709.
PN US2003050231-A1.
PD 13-MAR-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.9%; Score 140.8; DB 9; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 781
ID ADC25497 standard; cDNA; 165 BP.
DE Human cDNA from extracellular matrix gene 80 #9.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.8; DB 10; Length 165;
Best Local Similarity 95.4%; Pred. No. 3.4e-11;
RESULT 782
ID ACN56670 standard; cDNA; 341 BP.
DE Cotton primed seed EST Clone ID: LIB3825-007-Q1-K6-C8, SEQ:451.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 140.8; DB 13; Length 341;
Best Local Similarity 83.3%; Pred. No. 3.3e-11;
RESULT 783
ID ACN53869 standard; cDNA; 355 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-B10, SEQ:8650.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 140.8; DB 13; Length 355;
Best Local Similarity 87.5%; Pred. No. 3.3e-11;
RESULT 784
ID ACN51993 standard; cDNA; 478 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-E1, SEQ:6774.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 140.8; DB 13; Length 478;
Best Local Similarity 83.3%; Pred. No. 3.3e-11;
RESULT 785

ID ACN54384 standard; cDNA; 489 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-004-Q1-K6-F9, SEQ:9165.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 140.8; DB 13; Length 489;
Best Local Similarity 91.4%; Pred. No. 3.3e-11;
RESULT 786
ID ABV57765 standard; cDNA; 502 BP.
DE Human prostate expression marker cDNA 57756.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 140.8; DB 5; Length 502;
Best Local Similarity 87.0%; Pred. No. 3.3e-11;
RESULT 787
ID ACN62215 standard; cDNA; 516 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-026-Q6-N6-F3, SEQ:16996.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 140.8; DB 13; Length 516;
Best Local Similarity 83.3%; Pred. No. 3.3e-11;
RESULT 788
ID ACN55333 standard; cDNA; 517 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-K6-E7, SEQ:10114.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 140.8; DB 13; Length 517;
Best Local Similarity 89.9%; Pred. No. 3.3e-11;
RESULT 789
ID ACN52090 standard; cDNA; 571 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-B9, SEQ:6871.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 140.8; DB 13; Length 571;
Best Local Similarity 83.3%; Pred. No. 3.2e-11;
RESULT 790
ID AAD50017 standard; cDNA; 1696 BP.
DE Human secreted protein cDNA.
PN WO200283914-A2.
PD 24-OCT-2002.
PA (PEKE) PE CORP NY.
Query Match 4.9%; Score 140.8; DB 8; Length 1696;
Best Local Similarity 87.5%; Pred. No. 3.1e-11;
RESULT 791
ID AAA48576 standard; cDNA; 2604 BP.
DE cDNA encoding wheat protein phosphatase 2A regulatory subunit A.
PN WO200036121-A2.
PD 22-JUN-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.9%; Score 140.8; DB 3; Length 2604;
Best Local Similarity 92.5%; Pred. No. 3e-11;
RESULT 792
ID ABL92313 standard; DNA; 8079 BP.
DE Chemically treated DNA repair gene fragment complementary to #61.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.

Query Match 4.9%; Score 140.8; DB 6; Length 8079;
Best Local Similarity 85.3%; Pred. No. 2.9e-11;
RESULT 793
ID ACN62049 standard; cDNA; 469 BP.
DE Coton gynoecium tissue EST Clone ID: LIB3829-024-Q6-N6-E4, SEQ:16830.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FING/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 140.6; DB 13; Length 469;
Best Local Similarity 86.6%; Pred. No. 3.5e-11;
RESULT 794
ID ADD69623 standard; cDNA; 1343 BP.
DE Human REMAP cDNA - SEQ ID 52.
PN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.9%; Score 140.6; DB 10; Length 1343;
Best Local Similarity 86.6%; Pred. No. 3.3e-11;
RESULT 795
ID ADD69624 standard; cDNA; 1464 BP.
DE Human REMAP cDNA - SEQ ID 53.
PN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.9%; Score 140.6; DB 10; Length 1464;
Best Local Similarity 86.6%; Pred. No. 3.3e-11;
RESULT 796
ID ADR25589 standard; DNA; 1521 BP.
DE Breast cancer prognosis marker #1450.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 4.9%; Score 140.6; DB 13; Length 1521;
Best Local Similarity 86.6%; Pred. No. 3.3e-11;
RESULT 797
ID ADP55051 standard; cDNA; 1521 BP.
DE Human PRO cDNA sequence SEQ ID NO:1027.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.9%; Score 140.6; DB 13; Length 1521;
Best Local Similarity 86.6%; Pred. No. 3.3e-11;
RESULT 798
ID ADQ22988 standard; DNA; 1576 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5808.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.9%; Score 140.6; DB 12; Length 1576;
Best Local Similarity 88.9%; Pred. No. 3.3e-11;
RESULT 799
ID ADI42816 standard; DNA; 1803 BP.
DE Plant transcription factor polynucleotide #820.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.

PA (YUGG/) YU G.
Query Match 4.9%; Score 140.6; DB 12; Length 1803;
Best Local Similarity 86.6%; Pred. No. 3.3e-11;
RESULT 800
ID ADO03025 standard; cDNA; 1803 BP.
DE Corn orthologue of Thalecress transcription factor, cDNA #126.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 4.9%; Score 140.6; DB 12; Length 1803;
Best Local Similarity 86.6%; Pred. No. 3.3e-11;
RESULT 801
ID ADR24479 standard; DNA; 2809 BP.
DE Breast cancer prognosis marker #340.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 4.9%; Score 140.6; DB 13; Length 2809;
Best Local Similarity 86.6%; Pred. No. 3.2e-11;
RESULT 802
ID ADK00688 standard; DNA; 3226 BP.
DE HOMO protein encoding sequence #33.
PN WO2004014946-A1.
PD 19-FEB-2004.
PA (NEWO-) NEWORGEN LTD.
Query Match 4.9%; Score 140.6; DB 12; Length 3226;
Best Local Similarity 86.6%; Pred. No. 3.2e-11;
RESULT 803
ID ADJ48200 standard; DNA; 3505 BP.
DE Maize oil-associated gene #18.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 4.9%; Score 140.6; DB 12; Length 3505;
Best Local Similarity 88.9%; Pred. No. 3.2e-11;
RESULT 804
ID ABK31495 standard; DNA; 15954 BP.
DE Signal transduction associated gene modified complementary DNA #169.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 140.6; DB 6; Length 15954;
Best Local Similarity 91.4%; Pred. No. 3e-11;
RESULT 805
ID ABL70468 standard; DNA; 15954 BP.
DE Chemically treated cell signalling DNA sequence complementary to#179.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 140.6; DB 6; Length 15954;
Best Local Similarity 91.4%; Pred. No. 3e-11;

RESULT 806
ID ABX39465 standard; cDNA; 327 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4630.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.9%; Score 140.4; DB 8; Length 327;
Best Local Similarity 90.4%; Pred. No. 3.8e-11;
RESULT 807
ID ACN55708 standard; cDNA; 381 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-027-Q6-N6-E10, SEQ:10489.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 140.4; DB 13; Length 381;
Best Local Similarity 90.4%; Pred. No. 3.8e-11;
RESULT 808
ID ACN47898 standard; cDNA; 495 BP.
DE Cotton primed seed EST Clone ID: LIB3825-016-Q1-N6-E4, SEQ:2679.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 140.4; DB 13; Length 495;
Best Local Similarity 81.4%; Pred. No. 3.7e-11;
RESULT 809
ID AAF91902 standard; cDNA; 1198 BP.
DE Human secreted protein-encoding gene 45 cDNA clone HRAC126, SEQ ID NO:55.
PN WO200118022-A1.
PD 15-MAR-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.4; DB 4; Length 1198;
Best Local Similarity 87.9%; Pred. No. 3.6e-11;
RESULT 810
ID AAX33181 standard; DNA; 6644 BP.
DE Base sequence of the plasmid prx-ires-bsr.
PN WO913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 4.9%; Score 140.4; DB 2; Length 6644;
Best Local Similarity 71.0%; Pred. No. 3.3e-11;
RESULT 811
ID AAX33182 standard; DNA; 7372 BP.
DE Base sequence of the plasmid prx-Bcl-xl-bsr.
PN WO913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 4.9%; Score 140.4; DB 2; Length 7372;
Best Local Similarity 71.0%; Pred. No. 3.3e-11;
RESULT 812
ID AAX33180 standard; DNA; 7797 BP.
DE Cowpox virus bsr full length gene sequence.
PN WO913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 4.9%; Score 140.4; DB 2; Length 7797;
Best Local Similarity 71.0%; Pred. No. 3.3e-11;
RESULT 813
ID AAX33184 standard; DNA; 7996 BP.
DE Base sequence of the plasmid prx-Bcl 2-i-hcd 25.
PN WO913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 4.9%; Score 140.4; DB 2; Length 7996;
Best Local Similarity 71.0%; Pred. No. 3.3e-11;

RESULT 814
ID ABX32895 standard; DNA; 11729 BP.
DE Human immune system associated gene SEQ ID NO: 868.
PN WO20020928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 140.4; DB 6; Length 11729;
Best Local Similarity 85.7%; Pred. No. 3.2e-11;
RESULT 815
ID AAT76782 standard; DNA; 240 BP.
DE Staphylococcus aureus exfoliative toxin A gene capture probe.
PN US5627054-A.
PD 06-MAY-1997.
PA (USAA) US SEC OF ARMY.
Query Match 4.9%; Score 140; DB 2; Length 240;
Best Local Similarity 86.1%; Pred. No. 4.4e-11;
RESULT 816
ID ABX38708 standard; cDNA; 242 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3873.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.9%; Score 140; DB 8; Length 242;
Best Local Similarity 88.4%; Pred. No. 4.4e-11;
RESULT 817
ID ACN53191 standard; cDNA; 564 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-003-Q1-N6-B10, SEQ:7972.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 140; DB 13; Length 564;
Best Local Similarity 88.4%; Pred. No. 4.2e-11;
RESULT 818
ID ABV29481 standard; cDNA; 760 BP.
DE Human prostate expression marker cDNA 29472.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 140; DB 5; Length 760;
Best Local Similarity 86.1%; Pred. No. 4.2e-11;
RESULT 819
ID ABV28953 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 28944.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 140; DB 5; Length 1603;
Best Local Similarity 82.1%; Pred. No. 4e-11;
RESULT 820
ID ABV22100 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 22091.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 140; DB 5; Length 1603;
Best Local Similarity 82.1%; Pred. No. 4e-11;
RESULT 821
ID ABV23114 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 23105.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 140; DB 5; Length 1603;
Best Local Similarity 82.1%; Pred. No. 4e-11;
RESULT 822
ID ABV27940 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 27931.

PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.9%; Score 140; DB 5; Length 1603;
 Best Local Similarity 82.1%; Pred. No. 4e-11;
 RESULT 823
 ID ADQ22192 standard; DNA; 3931 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5012.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 4.9%; Score 140; DB 12; Length 3931;
 Best Local Similarity 86.1%; Pred. No. 3.9e-11;
 RESULT 824
 ID ABL32171 standard; DNA; 3973 BP.
 DE Human immune system associated gene SEQ ID NO: 144.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.9%; Score 140; DB 6; Length 3973;
 Best Local Similarity 84.0%; Pred. No. 3.9e-11;
 RESULT 825
 ID ABQ67149 standard; DNA; 40324 BP.
 DE Human angiogenesis associated polynucleotide SEQ ID NO 179.
 PN WO200246454-A2.
 PD 13-JUN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.9%; Score 140; DB 6; Length 40324;
 Best Local Similarity 90.9%; Pred. No. 3.5e-11;
 RESULT 826
 ID ACN52108 standard; cDNA; 545 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-P7, SEQ:6889.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.9%; Score 139.8; DB 13; Length 545;
 Best Local Similarity 83.2%; Pred. No. 4.5e-11;
 RESULT 827
 ID ACN53565 standard; cDNA; 619 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-K6-C10, SEQ:8346.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.9%; Score 139.8; DB 13; Length 619;
 Best Local Similarity 83.2%; Pred. No. 4.5e-11;
 RESULT 828
 ID AA64638 standard; DNA; 801 BP.
 DE Partial sequence MEL3 associated with melanoma and thyroid tumors.
 PN WO200050595-A2.
 PD 31-AUG-2000.
 PA (GOUT/) GOUT I.
 PA (RODN/) RODIN N.
 PA (FILO/) FILOENKO V.
 PA (MATS/) MATSUKA G.
 PA (SCAN/) SCANLAN M.
 PA (OLDL/) OLD L.
 PA (BILY/) BILYNSKY B.
 Query Match 4.9%; Score 139.8; DB 3; Length 801;
 Best Local Similarity 92.9%; Pred. No. 4.4e-11;
 RESULT 829
 ID ADE40468 standard; DNA; 1047 BP.
 DE Human granzyme H (gene ID 1793) DNA.
 PN WO200307083-A2.
 PD 28-AUG-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 4.9%; Score 139.8; DB 10; Length 1047;
 Best Local Similarity 89.8%; Pred. No. 4.4e-11;

RESULT 830
 ID ADN39370 standard; cDNA; 1416 BP.
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:B54.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 4.9%; Score 139.8; DB 11; Length 1416;
 Best Local Similarity 89.8%; Pred. No. 4.3e-11;
 RESULT 831
 ID ACN41008 standard; cDNA; 1416 BP.
 DE Tumour-associated antigenic target (TAT) cDNA DNA327030, SEQ ID NO:6163.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH-) GENENTECH INC.
 Query Match 4.9%; Score 139.8; DB 13; Length 1416;
 Best Local Similarity 89.8%; Pred. No. 4.3e-11;
 RESULT 832
 ID ADQ24552 standard; DNA; 7115 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7372.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 4.9%; Score 139.8; DB 12; Length 7115;
 Best Local Similarity 83.2%; Pred. No. 4e-11;
 RESULT 833
 ID ABV57059 standard; cDNA; 490 BP.
 DE Human prostate expression marker cDNA 57050.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.9%; Score 139.6; DB 5; Length 490;
 Best Local Similarity 91.4%; Pred. No. 4.8e-11;
 RESULT 834
 ID ACN55464 standard; cDNA; 540 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-024-Q6-N6-A3, SEQ:10245.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.9%; Score 139.6; DB 13; Length 540;
 Best Local Similarity 82.5%; Pred. No. 4.8e-11;
 RESULT 835
 ID ACN51318 standard; cDNA; 545 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-P6, SEQ:6099.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.9%; Score 139.6; DB 13; Length 545;
 Best Local Similarity 76.1%; Pred. No. 4.8e-11;
 RESULT 836
 ID ACN52669 standard; cDNA; 578 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-017-Q1-N6-A11, SEQ:7450.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.9%; Score 139.6; DB 13; Length 578;
 Best Local Similarity 76.1%; Pred. No. 4.8e-11;
 RESULT 837
 ID AAK88206 standard; cDNA; 698 BP.
 DE Human digestive system antigen coding sequence SEQ ID NO: 522.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.9%; Score 139.6; DB 4; Length 698;
 Best Local Similarity 83.5%; Pred. No. 4.8e-11;

RESULT 838
ID AAS29150 standard; cDNA; 698 BP.
DE cDNA encoding for human DNA-binding protein #121.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 139.6; DB 5; Length 698;
Best Local Similarity 83.5%; Pred. No. 4.8e-11;
RESULT 839
ID AAD16659 standard; cDNA; 698 BP.
DE Human novel protein-encoding cDNA clone HVAET61, SEQ ID NO:13.
PN WO200155327-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 139.6; DB 5; Length 698;
Best Local Similarity 83.5%; Pred. No. 4.8e-11;
RESULT 840
ID ABS68290 standard; cDNA; 698 BP.
DE cDNA encoding human DNA-binding protein #121.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.9%; Score 139.6; DB 6; Length 698;
Best Local Similarity 83.5%; Pred. No. 4.8e-11;
RESULT 841
ID ADC25284 standard; cDNA; 698 BP.
DE Human cDNA from extracellular matrix gene 121.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 139.6; DB 10; Length 698;
Best Local Similarity 83.5%; Pred. No. 4.8e-11;
RESULT 842
ID AAC68125 standard; cDNA; 809 BP.
DE Human secreted protein cDNA sequence #45.
PN WO200059335-A1.
PD 05-OCT-2000.
PA (ROSE/) ROSEN C A.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 139.6; DB 3; Length 809;
Best Local Similarity 91.4%; Pred. No. 4.7e-11;
RESULT 843
ID AAA64642 standard; DNA; 905 BP.
DE Partial sequence MEL7 associated with melanoma and thyroid tumors.
PN WO200050595-A2.
PD 31-AUG-2000.
PA (GOUT/) GOUT I.
PA (RODN/) RODIN N.
PA (FILO/) FILOENKO V.
PA (MATS/) MATSUKA G.
PA (SCAN/) SCANLAN M.
PA (OLDL/) OLD L.
PA (BILY/) BILYNSKY B.
Query Match 4.9%; Score 139.6; DB 3; Length 905;
Best Local Similarity 65.9%; Pred. No. 4.7e-11;
RESULT 844
ID ADQ22618 standard; DNA; 2499 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5439.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.9%; Score 139.6; DB 12; Length 2499;
Best Local Similarity 82.5%; Pred. No. 4.5e-11;
RESULT 845
ID ADQ32662 standard; DNA; 15749 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6482.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.9%; Score 139.6; DB 12; Length 15749;
Best Local Similarity 91.4%; Pred. No. 4.2e-11;

RESULT 846
ID ACN51926 standard; cDNA; 509 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-N6-G11, SEQ:6707.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 139.4; DB 13; Length 509;
Best Local Similarity 81.7%; Pred. No. 5.1e-11;
RESULT 847
ID ACN55753 standard; cDNA; 516 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-N6-B12, SEQ:10534.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 139.4; DB 13; Length 516;
Best Local Similarity 85.6%; Pred. No. 5.1e-11;
RESULT 848
ID ACN62570 standard; cDNA; 552 BP.
DE Cotton developing fibre EST Clone ID: LIB3830-001-Q1-N6-A1, SEQ:17351.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 139.4; DB 13; Length 552;
Best Local Similarity 90.3%; Pred. No. 5.1e-11;
RESULT 849
ID ABZ71285 standard; cDNA; 667 BP.
DE Secreted protein-encoding gene 5 cDNA clone HADDE71, SEQ ID NO:15.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 139.4; DB 8; Length 667;
Best Local Similarity 75.5%; Pred. No. 5.1e-11;
RESULT 850
ID ABT16763 standard; DNA; 667 BP.
DE Human secreted protein gene sequence - SEQ ID NO 12.
PN WO200277188-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 139.4; DB 10; Length 667;
Best Local Similarity 75.5%; Pred. No. 5.1e-11;
RESULT 851
ID ABZ66896 standard; cDNA; 667 BP.
DE Human secreted protein encoding cDNA SEQ ID NO 16.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 139.4; DB 10; Length 667;
Best Local Similarity 75.5%; Pred. No. 5.1e-11;
RESULT 852
ID AAD05318 standard; cDNA; 671 BP.
DE Human secreted protein-encoding gene 19 cDNA clone HWLFQ64, SEQ ID NO:29.
PN WO200134626-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 139.4; DB 4; Length 671;
Best Local Similarity 90.3%; Pred. No. 5.1e-11;
RESULT 853
ID ACN60479 standard; cDNA; 431 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-023-Q6-K6-D10, SEQ:15260.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.

PA (ZIEG/) ZIEGLER T E.
 Query Match 4.9%; Score 139.2; DB 13; Length 431;
 Best Local Similarity 91.9%; Pred. No. 5.5e-11;
 RESULT 854
 ID ACN52334 standard; cDNA; 571 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-E11, SEQ:7115.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.9%; Score 139.2; DB 13; Length 571;
 Best Local Similarity 82.8%; Pred. No. 5.5e-11;
 RESULT 855
 ID AAC80551 standard; cDNA; 658 BP.
 DE Human secreted protein gene 21 SEQ ID NO:31.
 PN WO200058467-A1.
 PD 05-OCT-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.9%; Score 139.2; DB 3; Length 658;
 Best Local Similarity 84.8%; Pred. No. 5.4e-11;
 RESULT 856
 ID ABV78042 standard; DNA; 1071 BP.
 DE Hypoxia-regulated protein coding sequence #62.
 PN WO200246465-A2.
 PD 13-JUN-2002.
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 Query Match 4.9%; Score 139.2; DB 6; Length 1071;
 Best Local Similarity 81.0%; Pred. No. 5.3e-11;
 RESULT 857
 ID ABQ92014 standard; cDNA; 4236 BP.
 DE Human polynucleotide SEQ ID NO 11.
 PN US2002065394-A1.
 PD 30-MAY-2002.
 PA (JACO/) JACOBS K.
 PA (MCCO/) MCCOY J M.
 PA (LAVA/) LAVALLIE E R.
 PA (COLL/) COLLINS-RACIE L A.
 PA (EVAN/) EVANS C.
 PA (MERB/) MERBERG D.
 PA (TREAC/) TREACY M.
 PA (SPAU/) SPAULDING V.
 Query Match 4.9%; Score 139.2; DB 6; Length 4236;
 Best Local Similarity 82.8%; Pred. No. 5e-11;
 RESULT 858
 ID AAS46815 standard; DNA; 21354 BP.
 DE Tumour suppressor gene derived chemically modified sequence #512.
 PN WO200168912-A2.
 PD 20-SEP-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.9%; Score 139.2; DB 4; Length 21354;
 Best Local Similarity 89.3%; Pred. No. 4.7e-11;
 RESULT 859
 ID ABV57512 standard; cDNA; 439 BP.
 DE Human prostate expression marker cDNA 57503.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.9%; Score 139; DB 5; Length 439;
 Best Local Similarity 83.5%; Pred. No. 5.9e-11;
 RESULT 860
 ID ACN52447 standard; cDNA; 537 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-015-Q1-N6-E10, SEQ:7228.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.9%; Score 139; DB 13; Length 537;
 Best Local Similarity 86.0%; Pred. No. 5.9e-11;
 RESULT 861

ID ADQ23617 standard; DNA; 2050 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6437.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 4.9%; Score 139; DB 12; Length 2050;
 Best Local Similarity 86.0%; Pred. No. 5.5e-11;
 RESULT 862
 ID AAF22346 standard; cDNA; 2058 BP.
 DE Human secreted protein gene 31 SEQ ID NO:41.
 PN WO200061748-A1.
 PD 19-OCT-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.9%; Score 139; DB 3; Length 2058;
 Best Local Similarity 89.7%; Pred. No. 5.5e-11;
 RESULT 863
 ID ADJ48201 standard; DNA; 2520 BP.
 DE Maize oil-associated gene #19.
 PN US2004025202-A1.
 PD 05-FEB-2004.
 PA (LAUR/) LAURIE C C.
 PA (RAVA/) RAVANELLO M.
 PA (SAVA/) SAVAGE T.
 PA (LEDE/) LEDEUX J R.
 PA (ROGE/) ROGERS J A.
 Query Match 4.9%; Score 139; DB 12; Length 2520;
 Best Local Similarity 86.0%; Pred. No. 5.5e-11;
 RESULT 864
 ID ABL33662 standard; DNA; 5845 BP.
 DE Human immune system associated gene SEQ ID NO: 1635.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.9%; Score 139; DB 6; Length 5845;
 Best Local Similarity 88.3%; Pred. No. 5.3e-11;
 RESULT 865
 ID ABL33637 standard; DNA; 7306 BP.
 DE Human immune system associated gene SEQ ID NO: 1610.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.9%; Score 139; DB 6; Length 7306;
 Best Local Similarity 90.8%; Pred. No. 5.2e-11;
 RESULT 866
 ID ABL32717 standard; DNA; 12007 BP.
 DE Human immune system associated gene SEQ ID NO: 690.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.9%; Score 139; DB 6; Length 12007;
 Best Local Similarity 88.3%; Pred. No. 5.1e-11;
 RESULT 867
 ID ACN53606 standard; cDNA; 486 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-K6-F5, SEQ:8387.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.9%; Score 138.8; DB 13; Length 486;
 Best Local Similarity 89.8%; Pred. No. 6.3e-11;
 RESULT 868
 ID ACN49328 standard; cDNA; 496 BP.
 DE Cotton primed seed EST Clone ID: LIB3825-031-Q6-K6-E6, SEQ:4109.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.9%; Score 138.8; DB 13; Length 496;
 Best Local Similarity 89.8%; Pred. No. 6.3e-11;
 RESULT 869

RESULT 869
ID AAZ06226 standard; DNA; 936 BP.
DE Human secreted protein gene No. 8.
PN WO9935158-A1.
PD 15-JUL-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 138.8; DB 2; Length 936;
Best Local Similarity 89.8%; Pred. No. 6.1e-11;
RESULT 870
ID ADM32854 standard; DNA; 1084 BP.
DE DNA sequence of a human adenosine monophosphate deaminase (AMPD).
PN WO2004024880-A2.
PD 25-MAR-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 4.9%; Score 138.8; DB 12; Length 1084;
Best Local Similarity 92.4%; Pred. No. 6.1e-11;
RESULT 871
ID AAF91862 standard; cDNA; 2753 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HDP185, SEQ ID NO:15.
PN WO200118022-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 138.8; DB 4; Length 2753;
Best Local Similarity 89.8%; Pred. No. 5.8e-11;
RESULT 872
ID AAS45399 standard; DNA; 15832 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #52.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 138.8; DB 4; Length 15832;
Best Local Similarity 92.4%; Pred. No. 5.4e-11;
RESULT 873
ID ABL33343 standard; DNA; 15832 BP.
DE Human immune system associated gene SEQ ID NO: 1316.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 138.8; DB 6; Length 15832;
Best Local Similarity 92.4%; Pred. No. 5.4e-11;
RESULT 874
ID ABK28244 standard; DNA; 15832 BP.
DE DNA transcription associated complementary genomic DNA #59.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 138.8; DB 6; Length 15832;
Best Local Similarity 92.4%; Pred. No. 5.4e-11;
RESULT 875
ID AAT13475 standard; RNA; 191 BP.
DE Capture probe for detection of target sequence by chimaeric probe.
PN EP707076-A1.
PD 17-APR-1996.
PA (STAD) AMOCO CORP.
Query Match 4.9%; Score 138.6; DB 2; Length 191;
Best Local Similarity 91.3%; Pred. No. 7e-11;
RESULT 876
ID ABV44994 standard; cDNA; 309 BP.
DE Human prostate expression marker cDNA 44985.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 138.6; DB 5; Length 309;
Best Local Similarity 91.3%; Pred. No. 6.8e-11;
RESULT 877
ID ACN58609 standard; cDNA; 313 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-010-Q6-N6-C11, SEQ:13390.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK-) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 138.6; DB 6; Length 14006;
Best Local Similarity 84.3%; Pred. No. 5.8e-11;
RESULT 878
ID ACN60136 standard; cDNA; 481 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-018-Q6-K6-C5, SEQ:14917.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK-) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 138.6; DB 13; Length 481;
Best Local Similarity 88.8%; Pred. No. 6.7e-11;
RESULT 879
ID ACN46089 standard; cDNA; 538 BP.
DE Cotton primed seed EST Clone ID: LIB3825-015-Q1-K6-A6, SEQ:870.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK-) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 138.6; DB 13; Length 538;
Best Local Similarity 82.4%; Pred. No. 6.7e-11;
RESULT 880
ID ADR59353 standard; cDNA; 583 BP.
DE Cotton cDNA sequence, SEQ ID 134.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA-) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match 4.9%; Score 138.6; DB 13; Length 583;
Best Local Similarity 94.1%; Pred. No. 6.6e-11;
RESULT 881
ID ACN54072 standard; cDNA; 640 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-020-Q1-K6-G11, SEQ:8853.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK-) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 138.6; DB 13; Length 640;
Best Local Similarity 94.1%; Pred. No. 6.6e-11;
RESULT 882
ID ABV04793 standard; cDNA; 893 BP.
DE Human prostate expression marker cDNA 4784.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 138.6; DB 5; Length 893;
Best Local Similarity 80.6%; Pred. No. 6.5e-11;
RESULT 883
ID ACN86075 standard; DNA; 893 BP.
DE Breast cancer related marker, seq id 7225.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.9%; Score 138.6; DB 11; Length 893;
Best Local Similarity 65.0%; Pred. No. 6.5e-11;
RESULT 884
ID ABL33958 standard; DNA; 14006 BP.
DE Human immune system associated gene SEQ ID NO: 1931.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 138.6; DB 6; Length 14006;
Best Local Similarity 84.3%; Pred. No. 5.8e-11;
RESULT 885
ID AAF94862 standard; cDNA; 396 BP.
DE Human ovarian cancer associated coding sequence SEQ ID NO: 53.
PN WO200118046-A2.

Query Match 4.9%; Score 138.6; DB 13; Length 313;
Best Local Similarity 84.3%; Pred. No. 6.8e-11;
RESULT 878
ID ACN60136 standard; cDNA; 481 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-018-Q6-K6-C5, SEQ:14917.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK-) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 138.6; DB 13; Length 481;
Best Local Similarity 88.8%; Pred. No. 6.7e-11;
RESULT 879
ID ACN46089 standard; cDNA; 538 BP.
DE Cotton primed seed EST Clone ID: LIB3825-015-Q1-K6-A6, SEQ:870.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK-) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 138.6; DB 13; Length 538;
Best Local Similarity 82.4%; Pred. No. 6.7e-11;
RESULT 880
ID ADR59353 standard; cDNA; 583 BP.
DE Cotton cDNA sequence, SEQ ID 134.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA-) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match 4.9%; Score 138.6; DB 13; Length 583;
Best Local Similarity 94.1%; Pred. No. 6.6e-11;
RESULT 881
ID ACN54072 standard; cDNA; 640 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-020-Q1-K6-G11, SEQ:8853.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK-) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 138.6; DB 13; Length 640;
Best Local Similarity 94.1%; Pred. No. 6.6e-11;
RESULT 882
ID ABV04793 standard; cDNA; 893 BP.
DE Human prostate expression marker cDNA 4784.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 138.6; DB 5; Length 893;
Best Local Similarity 80.6%; Pred. No. 6.5e-11;
RESULT 883
ID ACN86075 standard; DNA; 893 BP.
DE Breast cancer related marker, seq id 7225.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.9%; Score 138.6; DB 11; Length 893;
Best Local Similarity 65.0%; Pred. No. 6.5e-11;
RESULT 884
ID ABL33958 standard; DNA; 14006 BP.
DE Human immune system associated gene SEQ ID NO: 1931.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 138.6; DB 6; Length 14006;
Best Local Similarity 84.3%; Pred. No. 5.8e-11;
RESULT 885
ID AAF94862 standard; cDNA; 396 BP.
DE Human ovarian cancer associated coding sequence SEQ ID NO: 53.
PN WO200118046-A2.

PD 15-MAR-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.9%; Score 138.4; DB 4; Length 396;
Best Local Similarity 79.3%; Pred. No. 7.2e-11;
RESULT 886
ID ABL4812 standard; cDNA; 396 BP.
DE Ovarian carcinoma sequence isolate 24368.
PN US2002004491-A1.
PD 10-JAN-2002.
PA (XUJ/) XU J.
PA (STOL/) STOLK J A.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
Query Match 4.9%; Score 138.4; DB 6; Length 396;
Best Local Similarity 79.3%; Pred. No. 7.2e-11;
RESULT 887
ID ABT03129 standard; cDNA; 396 BP.
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 53.
PN WO200239885-A2.
PD 23-MAY-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.9%; Score 138.4; DB 6; Length 396;
Best Local Similarity 79.3%; Pred. No. 7.2e-11;
RESULT 888
ID ADM10722 standard; cDNA; 396 BP.
DE Human ovarian carcinoma-associated cDNA 24368.
PN US2003206918-A1.
PD 06-NOV-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.9%; Score 138.4; DB 11; Length 396;
Best Local Similarity 79.3%; Pred. No. 7.2e-11;
RESULT 889
ID ADJ11052 standard; cDNA; 396 BP.
DE Representative human ovarian carcinoma cDNA SeqID 53.
PN US2003232056-A1.
PD 18-DEC-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.9%; Score 138.4; DB 12; Length 396;
Best Local Similarity 79.3%; Pred. No. 7.2e-11;
RESULT 890
ID ADM43313 standard; cDNA; 396 BP.
DE Human ovarian carcinoma cDNA #53.
PN US2003129192-A1.
PD 10-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.9%; Score 138.4; DB 12; Length 396;
Best Local Similarity 79.3%; Pred. No. 7.2e-11;
RESULT 891
ID ACN53459 standard; cDNA; 567 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-008-Q1-K6-A7, SEQ:8240.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 138.4; DB 13; Length 567;
Best Local Similarity 85.6%; Pred. No. 7.1e-11;
RESULT 892
ID ACN51300 standard; cDNA; 583 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-C2, SEQ:6081.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 138.4; DB 13; Length 583;
Best Local Similarity 79.9%; Pred. No. 7.1e-11;
RESULT 893
ID AAC77829 standard; cDNA; 2921 BP.
DE Human cancer associated gene sequence SEQ ID NO:223.
PN WO200055350-A1.

PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 138.4; DB 3; Length 2921;
Best Local Similarity 91.8%; Pred. No. 6.6e-11;
RESULT 894
ID ABQ67050 standard; DNA; 6486 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 80.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 138.4; DB 6; Length 6486;
Best Local Similarity 87.8%; Pred. No. 6.4e-11;
RESULT 895
ID ACF62785 standard; DNA; 7369 BP.
DE Colon cancer analysis related genomic DNA SEQ ID NO:34.
PN WO2003014388-A2.
PD 20-FEB-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 138.4; DB 8; Length 7369;
Best Local Similarity 90.2%; Pred. No. 6.4e-11;
RESULT 896
ID ABZ09991 standard; DNA; 7369 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #131.
PN WO20027772-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 138.4; DB 8; Length 7369;
Best Local Similarity 90.2%; Pred. No. 6.4e-11;
RESULT 897
ID AAS46303 standard; DNA; 10369 BP.
DE Tumour suppressor gene derived chemically modified sequence #25.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 138.4; DB 4; Length 10369;
Best Local Similarity 90.2%; Pred. No. 6.3e-11;
RESULT 898
ID ABL32392 standard; DNA; 10369 BP.
DE Human immune system associated gene SEQ ID NO: 365.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 138.4; DB 6; Length 10369;
Best Local Similarity 90.2%; Pred. No. 6.3e-11;
RESULT 899
ID ACN53877 standard; cDNA; 325 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-C7, SEQ:8658.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 138.2; DB 13; Length 325;
Best Local Similarity 86.9%; Pred. No. 7.8e-11;
RESULT 900
ID ADL43689 standard; DNA; 351 BP.
DE Human ovarian cancer DNA marker #17579.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 138.2; DB 5; Length 351;
Best Local Similarity 89.2%; Pred. No. 7.7e-11;
RESULT 901
ID AAI88388 standard; cDNA; 398 BP.
DE Human polynucleotide SEQ ID NO 8448.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.9%; Score 138.2; DB 4; Length 398;
Best Local Similarity 91.8%; Pred. No. 7.7e-11;
RESULT 902
ID ACN49987 standard; cDNA; 452 BP.

DE Cotton primed seed EST Clone ID: LIB3825-033-Q6-N6-F5, SEQ:4768.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 138.2; DB 13; Length 452;
Best Local Similarity 79.2%; Pred. No. 7.7e-11;
RESULT 903
ID ACN52021 standard; cDNA; 485 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-G4, SEQ:6802.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 138.2; DB 13; Length 485;
Best Local Similarity 80.9%; Pred. No. 7.6e-11;
RESULT 904
ID ADM47653 standard; DNA; 1708 BP.
DE Polynucleotide sequence #71 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 4.9%; Score 138.2; DB 12; Length 1708;
Best Local Similarity 86.9%; Pred. No. 7.2e-11;
RESULT 905
ID AAA23441 standard; cDNA; 1954 BP.
DE cDNA encoding human secreted protein vc51_1, SEQ ID NO:37.
PN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 4.9%; Score 138.2; DB 3; Length 1954;
Best Local Similarity 86.9%; Pred. No. 7.2e-11;
RESULT 906
ID ADQ22627 standard; DNA; 2785 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5447.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.9%; Score 138.2; DB 12; Length 2785;
Best Local Similarity 89.2%; Pred. No. 7.1e-11;
RESULT 907
ID AAZ07192 standard; cDNA; 3275 BP.
DE Human lung tumour protein SAL-25 5' cDNA sequence.
PN WO9938973-A2.
PD 05-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 4.9%; Score 138.2; DB 2; Length 3275;
Best Local Similarity 91.8%; Pred. No. 7e-11;
RESULT 908
ID AAC79145 standard; cDNA; 3275 BP.
DE Human lung tumour-specific cDNA #98.
PN WO200060077-A2.
PD 12-OCT-2000.
PA (CORI-) CORIXA CORP.
Query Match 4.9%; Score 138.2; DB 3; Length 3275;
Best Local Similarity 91.8%; Pred. No. 7e-11;
RESULT 909
ID AAD23220 standard; cDNA; 3275 BP.
DE Human lung tumour-specific protein SAL-25 cDNA.
PN WO200172295-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.9%; Score 138.2; DB 4; Length 3275;
Best Local Similarity 91.8%; Pred. No. 7e-11;
RESULT 910
ID ADD66459 standard; cDNA; 3275 BP.
DE Human lung tumour-specific related cDNA, SEQ ID No 151.

PN WO200292001-A2.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.9%; Score 138.2; DB 10; Length 3275;
Best Local Similarity 91.8%; Pred. No. 7e-11;
RESULT 911
ID ADE87713 standard; cDNA; 3275 BP.
DE Human lung tumour antigen cDNA #98.
PN US2003118599-A1.
PD 26-JUN-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.9%; Score 138.2; DB 10; Length 3275;
Best Local Similarity 91.8%; Pred. No. 7e-11;
RESULT 912
ID ADQ23592 standard; DNA; 3454 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6412.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.9%; Score 138.2; DB 12; Length 3454;
Best Local Similarity 86.9%; Pred. No. 7e-11;
RESULT 913
ID ABL32681 standard; DNA; 6436 BP.
DE Human immune system associated gene SEQ ID NO: 654.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 138.2; DB 6; Length 6436;
Best Local Similarity 91.8%; Pred. No. 6.8e-11;
RESULT 914
ID AAI80464 standard; cDNA; 456 BP.
DE Human polynucleotide SEQ ID NO 524.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.8%; Score 138; DB 4; Length 456;
Best Local Similarity 96.6%; Pred. No. 8.2e-11;
RESULT 915
ID ACN46935 standard; cDNA; 499 BP.
DE Cotton primed seed EST Clone ID: LIB3825-005-Q1-N6-D10, SEQ:1716.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 138; DB 13; Length 499;
Best Local Similarity 82.0%; Pred. No. 8.1e-11;
RESULT 916
ID ACN48235 standard; cDNA; 560 BP.
DE Cotton primed seed EST Clone ID: LIB3825-021-Q1-N6-B5, SEQ:3016.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 138; DB 13; Length 560;
Best Local Similarity 82.0%; Pred. No. 8.1e-11;
RESULT 917
ID ACN52610 standard; cDNA; 574 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-N6-G6, SEQ:7391.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 138; DB 13; Length 574;
Best Local Similarity 83.9%; Pred. No. 8.1e-11;
RESULT 918
ID ACN87190 standard; DNA; 592 BP.
DE Breast cancer related marker, seq id 8340.

PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.8%; Score 138; DB 11; Length 592;
Best Local Similarity 78.9%; Pred. No. 8.1e-11;
RESULT 919
ID AAT72860 standard; cDNA; 2771 BP.
DE Human cervical cancer marker nucleic acid 4134.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 138; DB 4; Length 2771;
Best Local Similarity 90.7%; Pred. No. 7.6e-11;
RESULT 920
ID ABL32911 standard; DNA; 8946 BP.
DE Human immune system associated gene SEQ ID NO: 884.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 138; DB 6; Length 8946;
Best Local Similarity 90.7%; Pred. No. 7.2e-11;
RESULT 921
ID ABL34174 standard; DNA; 113515 BP.
DE Human immune system associated gene SEQ ID NO: 2147.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 138; DB 6; Length 113515;
Best Local Similarity 90.7%; Pred. No. 6.4e-11;
RESULT 922
ID ACN46088 standard; cDNA; 522 BP.
DE Cotton primed seed EST Clone ID: LIB3825-015-Q1-K6-A5, SEQ:869.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 137.8; DB 13; Length 522;
Best Local Similarity 87.3%; Pred. No. 8.7e-11;
RESULT 923
ID ADM19286 standard; cDNA; 1167 BP.
DE Novel human channel/transporter gene #83.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 137.8; DB 5; Length 1167;
Best Local Similarity 92.4%; Pred. No. 8.4e-11;
RESULT 924
ID AAS20587 standard; cDNA; 1798 BP.
DE Human methionine aminopeptidase protease cDNA.
PN US6329188-B1.
PD 11-DEC-2001.
PA (PEKE) PE CORP NY.
Query Match 4.8%; Score 137.8; DB 6; Length 1798;
Best Local Similarity 95.3%; Pred. No. 8.2e-11;
RESULT 925
ID ADB54096 standard; DNA; 4316 BP.
DE Pretreated genomic DNA region 20.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 137.8; DB 10; Length 4316;
Best Local Similarity 85.1%; Pred. No. 7.9e-11;
RESULT 926
ID ADS89248 standard; DNA; 4316 BP.
DE Oligonucleotide of the invention SEQ ID NO:264.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 137.8; DB 13; Length 4316;
Best Local Similarity 85.1%; Pred. No. 7.9e-11;
RESULT 927

ID ABL32921 standard; DNA; 5195 BP.
DE Human immune system associated gene SEQ ID NO: 894.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 137.8; DB 6; Length 5195;
Best Local Similarity 85.1%; Pred. No. 7.8e-11;
RESULT 928
ID ABK34027 standard; DNA; 6944 BP.
DE Human DNA for staging of Astrocytomas, complement, #57.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 137.8; DB 6; Length 6944;
Best Local Similarity 85.1%; Pred. No. 7.8e-11;
RESULT 929
ID ADA20447 standard; DNA; 6944 BP.
DE Prostate tumour related genomic DNA complement sample #56.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 137.8; DB 8; Length 6944;
Best Local Similarity 85.1%; Pred. No. 7.8e-11;
RESULT 930
ID ADA84254 standard; DNA; 6944 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:112.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 137.8; DB 8; Length 6944;
Best Local Similarity 85.1%; Pred. No. 7.8e-11;
RESULT 931
ID AAI87804 standard; cDNA; 398 BP.
DE Human polynucleotide SEQ ID NO 7864.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.8%; Score 137.6; DB 4; Length 398;
Best Local Similarity 91.2%; Pred. No. 9.4e-11;
RESULT 932
ID ADL37305 standard; DNA; 406 BP.
DE Human ovarian cancer DNA marker #11195.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 137.6; DB 5; Length 406;
Best Local Similarity 88.0%; Pred. No. 9.4e-11;
RESULT 933
ID ADI72158 standard; DNA; 406 BP.
DE Human ovarian cancer DNA marker #4900.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 137.6; DB 5; Length 406;
Best Local Similarity 88.0%; Pred. No. 9.4e-11;
RESULT 934
ID ACN52913 standard; cDNA; 411 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-019-Q1-N6-D10, SEQ:7694.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 137.6; DB 13; Length 411;
Best Local Similarity 82.3%; Pred. No. 9.4e-11;
RESULT 935
ID ABX46069 standard; cDNA; 419 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11234.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.

PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J. 4.8%; Score 137.6; DB 13; Length 563;
PA (FENG//) FENG P C C. 82.3%; Pred. No. 9.2e-11;
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 4.8%; Score 137.6; DB 13; Length 563;
RESULT 944
ID ADF81828 standard; DNA; 873 BP.
DE Leukaemia-related DNA sequence #2384.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE//) HAFERLACH T.
PA (SCHO//) SCHOCH C.
PA (KERN//) KERN W.
Query Match
Best Local Similarity 4.8%; Score 137.6; DB 10; Length 873;
RESULT 945
ID AAV61487 standard; cDNA; 4237 BP.
DE Human secreted protein fe366_1 cDNA.
PN WO9841539-A2.
PD 24-SEP-1998.
PA (GEMY-) GENETICS INST INC.
Query Match
Best Local Similarity 4.8%; Score 137.6; DB 2; Length 4237;
RESULT 946
ID ABL32788 standard; DNA; 6171 BP.
DE Human immune system associated gene SEQ ID NO: 761.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 137.6; DB 6; Length 6171;
RESULT 947
ID AAI83750 standard; cDNA; 463 BP.
DE Human polynucleotide SEQ ID NO 3810.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.8%; Score 137.4; DB 4; Length 463;
RESULT 948
ID AAH3241 standard; cDNA; 464 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:297.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.8%; Score 137.4; DB 4; Length 464;
RESULT 949
ID ACN47530 standard; cDNA; 506 BP.
DE Cotton primed seed EST Clone ID: LTB3825-012-Q1-K6-F1, SEQ:2311.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J. 4.8%; Score 137.4; DB 4; Length 464;
PA (FENG//) FENG P C C. 65.3%; Pred. No. 9.9e-11;
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 4.8%; Score 137.4; DB 13; Length 506;
RESULT 950
ID ABL70492 standard; DNA; 5241 BP.
DE Chemically-treated cell signalling DNA sequence complementary to#191.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 137.4; DB 6; Length 5241;
RESULT 951
ID AAS61450 standard; DNA; 5241 BP.
DE Human gene regulation-associated gene oligonucleotide #405.

```

PD WO200177375-A2.
PD 18-OCT-2001.
PA (EPIC-) EPIGENOMICS AG.
Query Match 4.8%; Score 137.4; DB 6; Length 5241;
Best Local Similarity 90.2%; Pred. No. 8.9e-11;
RESULT 952
ID ABX39417 standard; cDNA; 393 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4582.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.8%; Score 137.2; DB 8; Length 393;
Best Local Similarity 89.2%; Pred. No. 1.1e-10;
RESULT 953
ID ABX1098 standard; cDNA; 408 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6263.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.8%; Score 137.2; DB 8; Length 408;
Best Local Similarity 89.2%; Pred. No. 1.1e-10;
RESULT 954
ID ACN56650 standard; cDNA; 502 BP.
DE Cotton gynoecium tissue EST clone ID: LIB3829-001-Q1-N6-H7, SEQ:11431.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 137.2; DB 13; Length 502;
Best Local Similarity 89.2%; Pred. No. 1.1e-10;
RESULT 955
ID ACN52320 standard; cDNA; 549 BP.
DE Cotton androecium tissue EST clone ID: LIB3828-014-Q1-N6-B10, SEQ:7101.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 137.2; DB 13; Length 549;
Best Local Similarity 89.2%; Pred. No. 1.1e-10;
RESULT 956
ID ACN54487 standard; cDNA; 671 BP.
DE Cotton androecium tissue EST clone ID: LIB3828-006-Q1-K6-F12, SEQ:9268.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 137.2; DB 13; Length 671;
Best Local Similarity 83.7%; Pred. No. 1e-10;
RESULT 957
ID AAC95569 standard; cDNA; 1036 BP.
DE Human secreted protein gene 49 SEQ ID NO:59.
PN WO200061596-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 4.8%; Score 137.2; DB 3; Length 1036;
Best Local Similarity 83.2%; Pred. No. 1e-10;
RESULT 958
ID ADA98058 standard; cDNA; 1036 BP.
DE Human secreted protein cDNA sequence #152.
PN WO2003004623-A2.

PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 137.2; DB 8; Length 1036;
Best Local Similarity 83.2%; Pred. No. 1e-10;
RESULT 959
ID ADA43944 standard; cDNA; 1036 BP.
DE Human secreted protein cDNA SEQ ID 132.
PN WO200300865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 137.2; DB 8; Length 1036;
Best Local Similarity 83.2%; Pred. No. 1e-10;
RESULT 960
ID ADC20214 standard; DNA; 1036 BP.
DE Human secreted protein coding sequence #153.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 137.2; DB 10; Length 1036;
Best Local Similarity 83.2%; Pred. No. 1e-10;
RESULT 961
ID ADF10630 standard; DNA; 1036 BP.
DE Human secreted protein encoding sequence #83.
PN WO200299085-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 137.2; DB 10; Length 1036;
Best Local Similarity 83.2%; Pred. No. 1e-10;
RESULT 962
ID ADP07638 standard; DNA; 1244 BP.
DE Human secreted protein encoding DNA, seq id 121.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 137.2; DB 12; Length 1244;
Best Local Similarity 91.8%; Pred. No. 1e-10;
RESULT 963
ID ADQ25148 standard; DNA; 1533 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7968.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.8%; Score 137.2; DB 12; Length 1533;
Best Local Similarity 79.1%; Pred. No. 1e-10;
RESULT 964
ID ABX92004 standard; cDNA; 1808 BP.
DE Lung specific nucleic acid (LSNA) #46.
PN WO200268633-A2.
PD 06-SEP-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 4.8%; Score 137.2; DB 6; Length 1808;
Best Local Similarity 89.2%; Pred. No. 1e-10;
RESULT 965
ID AB132651 standard; DNA; 12177 BP.
DE Human immune system associated gene SEQ ID NO: 624.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 4.8%; Score 137.2; DB 6; Length 12177;
Best Local Similarity 89.2%; Pred. No. 9.2e-11;
RESULT 966
ID ACN51559 standard; cDNA; 318 BP.
DE Cotton androecium tissue EST clone ID: LIB3828-004-Q1-N6-B3, SEQ:6340.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 137; DB 13; Length 318;
Best Local Similarity 90.7%; Pred. No. 1.2e-10;
RESULT 967
ID ABV58273 standard; cDNA; 497 BP.
```


DE Human prostate expression marker cDNA 58264.
 PN WO200160860-A2.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.8%; Score 137; DB 5; Length 497;
 Best Local Similarity 88.2%; Pred. No. 1.1e-10;
 RESULT 968
 ID AAF31060 standard; cDNA; 872 BP.
 DE Rat clone 701291473H1 coding sequence.
 PN WO200102557-A1.
 PD 11-JAN-2001.
 PA (JANC) JANSSEN PHARM NV.
 Query Match 4.8%; Score 137; DB 4; Length 872;
 Best Local Similarity 96.6%; Pred. No. 1.1e-10;
 RESULT 969
 ID AAQ04690 standard; cDNA; 1834 BP.
 DE Encodes Mammalian amino acid dehydrogenase activating factor-eta.
 PN JP02111796-A.
 PD 24-APR-1990.
 PA (TOFU) TOA NENRYO KOGYO KK.
 Query Match 4.8%; Score 137; DB 2; Length 1834;
 Best Local Similarity 85.9%; Pred. No. 1.1e-10;
 RESULT 970
 ID ABL59287 standard; cDNA; 1957 BP.
 DE Nucleotide sequence of AA233368 protein (from first ORF).
 PN WO200246362-A2.
 PD 13-JUN-2002.
 PA (GENE-) GENE LOGIC INC.
 PA (NISB) JAPAN TOBACCO INC.
 Query Match 4.8%; Score 137; DB 6; Length 1957;
 Best Local Similarity 88.2%; Pred. No. 1.1e-10;
 RESULT 971
 ID ABL59288 standard; cDNA; 1957 BP.
 DE Nucleotide sequence of AA233368 protein (from second ORF).
 PN WO200246362-A2.
 PD 13-JUN-2002.
 PA (GENE-) GENE LOGIC INC.
 PA (NISB) JAPAN TOBACCO INC.
 Query Match 4.8%; Score 137; DB 6; Length 1957;
 Best Local Similarity 88.2%; Pred. No. 1.1e-10;
 RESULT 972
 ID ADP56341 standard; cDNA; 2401 BP.
 DE Human PRO cDNA sequence SEQ ID NO:2317.
 PN WO2004039956-A2.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 4.8%; Score 137; DB 13; Length 2401;
 Best Local Similarity 78.5%; Pred. No. 1.1e-10;
 RESULT 973
 ID AAV54587 standard; cDNA; 2447 BP.
 DE Human secretory protein encoding cDNA clone CO1020-1.
 PN WO9833916-A2.
 PD 06-AUG-1998.
 PA (GEMY) GENETICS INST INC.
 Query Match 4.8%; Score 137; DB 2; Length 2447;
 Best Local Similarity 84.9%; Pred. No. 1.1e-10;
 RESULT 974
 ID AAZ25607 standard; cDNA; 2447 BP.
 DE Human secreted protein clone CO1020_1 nucleotide sequence.
 PN US965397-A.
 PD 12-OCT-1999.
 PA (GEMY) GENETICS INST INC.
 Query Match 4.8%; Score 137; DB 2; Length 2447;
 Best Local Similarity 84.9%; Pred. No. 1.1e-10;
 RESULT 975
 ID ADQ22306 standard; DNA; 2700 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5126.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 4.8%; Score 137; DB 12; Length 2700;
 Best Local Similarity 88.2%; Pred. No. 1e-10;
 RESULT 976

DE ADD18806 standard; DNA; 3232 BP.
 DE Human disease related protein DNA sequence SeqID238.
 PN WO2003018621-A2.
 PD 06-MAR-2003.
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 Query Match 4.8%; Score 137; DB 10; Length 3232;
 Best Local Similarity 85.9%; Pred. No. 1e-10;
 RESULT 977
 ID ABL34573 standard; DNA; 6172 BP.
 DE Human metastasis associated gene SEQ ID NO: 126.
 PN WO200177376-A2.
 PD 18-OCT-2001.
 PA (EPIC-) EPIGENOMICS AG.
 Query Match 4.8%; Score 137; DB 6; Length 6172;
 Best Local Similarity 88.2%; Pred. No. 1e-10;
 RESULT 978
 ID ADS99834 standard; DNA; 6172 BP.
 DE Complement of bisulphite treated metastasis-associated human gene #63.
 PN US2003148327-A1.
 PD 07-AUG-2003.
 PA (OLEK/) OLEK A.
 PA (PIEP/) PIEPENBROCK C.
 PA (BERL/) BERLIN K.
 Query Match 4.8%; Score 137; DB 7; Length 6172;
 Best Local Similarity 88.2%; Pred. No. 1e-10;
 RESULT 979
 ID ABX40612 standard; cDNA; 241 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #5777.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 4.8%; Score 136.8; DB 8; Length 241;
 Best Local Similarity 85.0%; Pred. No. 1.2e-10;
 RESULT 980
 ID ACNS2877 standard; cDNA; 421 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-N6-H7, SEQ:7658.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.8%; Score 136.8; DB 13; Length 421;
 Best Local Similarity 85.0%; Pred. No. 1.2e-10;
 RESULT 981
 ID ABX44494 standard; cDNA; 456 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #9659.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 4.8%; Score 136.8; DB 8; Length 456;
 Best Local Similarity 95.3%; Pred. No. 1.2e-10;
 RESULT 982
 ID ABV59114 standard; cDNA; 570 BP.
 DE Human prostate expression marker cDNA 59105.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.8%; Score 136.8; DB 5; Length 570;
 Best Local Similarity 95.3%; Pred. No. 1.2e-10;
 RESULT 983
 ID ACNS58226 standard; cDNA; 591 BP.
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-008-Q6-K6-G6, SEQ:13007.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E. 4.8%; Score 136.8; DB 13; Length 591;
Query Match
Best Local Similarity 94.6%; Pred. No. 1.2e-10;
RESULT 984
ID AAX89609 standard; cDNA; 831 BP.
DE Human secreted protein clone bg570_1 encoding cDNA.
PN WO9315253-A1.
PD 15-JUL-1999.
PA (GEMY) GENETICS INST INC.
Query Match 4.8%; Score 136.8; DB 2; Length 831;
Best Local Similarity 89.6%; Pred. No. 1.2e-10;
RESULT 985
ID AAS59240 standard; cDNA; 831 BP.
DE Human cDNA encoding a secreted protein bg570_1.
PN WO200175068-A2.
PD 11-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 4.8%; Score 136.8; DB 4; Length 831;
Best Local Similarity 89.6%; Pred. No. 1.2e-10;
RESULT 986
ID ABA90909 standard; cDNA; 831 BP.
DE Human polynucleotide seq ID NO 67.
PN US2001039335-A1.
PD 08-NOV-2001.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (AGOS/) AGOSTINO M J.
PA (STEI/) STEININGER R J.
PA (SPAU/) SPAULDING V.
PA (WONG/) WONG G G.
PA (CLAR/) CLARK H.
PA (FECH/) FECHTEL K.
Query Match 4.8%; Score 136.8; DB 6; Length 831;
Best Local Similarity 89.6%; Pred. No. 1.2e-10;
RESULT 987
ID ADO23195 standard; DNA; 1091 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6015.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.8%; Score 136.8; DB 12; Length 1091;
Best Local Similarity 89.6%; Pred. No. 1.2e-10;
RESULT 988
ID ABL32411 standard; DNA; 6161 BP.
DE Human immune system associated gene SEQ ID NO: 384.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 136.8; DB 6; Length 6161;
Best Local Similarity 89.6%; Pred. No. 1.1e-10;
RESULT 989
ID ACF62807 standard; DNA; 7369 BP.
DE Colon cancer analysis related genomic DNA SEQ ID NO:56.
PN WO2003014388-A2.
PD 20-FEB-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 136.8; DB 8; Length 7369;
Best Local Similarity 89.6%; Pred. No. 1.1e-10;
RESULT 990
ID ABZ10137 standard; DNA; 7369 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #277.
PN WO20027272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 136.8; DB 8; Length 7369;
Best Local Similarity 89.6%; Pred. No. 1.1e-10;
RESULT 991

ID AAV09036 standard; RNA; 12827 BP.
DE Equine arteritis virus partial RNA genome sequence.
PN WO9802549-A1.
PD 22-JAN-1998.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 4.8%; Score 136.8; DB 2; Length 12827;
Best Local Similarity 98.6%; Pred. No. 1e-10;
RESULT 992
ID AAV09039 standard; DNA; 15528 BP.
DE Equine arteritis virus expression vector pEAV030.
PN WO9802549-A1.
PD 22-JAN-1998.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 4.8%; Score 136.8; DB 2; Length 15528;
Best Local Similarity 98.6%; Pred. No. 1e-10;
RESULT 993
ID ABX49357 standard; cDNA; 220 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #14522.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.8%; Score 136.6; DB 8; Length 220;
Best Local Similarity 88.6%; Pred. No. 1.3e-10;
RESULT 994
ID AAI87163 standard; cDNA; 394 BP.
DE Human polynucleotide seq ID NO 7223.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.8%; Score 136.6; DB 4; Length 394;
Best Local Similarity 86.3%; Pred. No. 1.3e-10;
RESULT 995
ID ABVI3564 standard; cDNA; 394 BP.
DE Human prostate expression marker cDNA 13555.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 136.6; DB 5; Length 394;
Best Local Similarity 90.1%; Pred. No. 1.3e-10;
RESULT 996
ID ABV43535 standard; cDNA; 408 BP.
DE Human prostate expression marker cDNA 43526.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 136.6; DB 5; Length 408;
Best Local Similarity 90.1%; Pred. No. 1.3e-10;
RESULT 997
ID ABV34679 standard; cDNA; 408 BP.
DE Human prostate expression marker cDNA 34670.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 136.6; DB 5; Length 408;
Best Local Similarity 90.1%; Pred. No. 1.3e-10;
RESULT 998
ID ACNS4703 standard; cDNA; 426 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-K6-D2, SEQ:9484.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 136.6; DB 13; Length 426;
Best Local Similarity 97.2%; Pred. No. 1.3e-10;
RESULT 999
ID ABV58008 standard; cDNA; 484 BP.
DE Human prostate expression marker cDNA 57999.
PN WO200160860-A2.

PD, 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 136.6; DB 5; Length 484;
Best Local Similarity 88.6%; Pred. No. 1.3e-10;
RESULT 1000
ID ACN87735 standard; DNA; 599 BP.
DE Breast cancer related marker, seq id 8885.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.8%; Score 136.6; DB 11; Length 599;
Best Local Similarity 85.5%; Pred. No. 1.3e-10;
RESULT 1001
ID ACN45292 standard; cDNA; 627 BP.
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-K6-A11, SEQ:73.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 136.6; DB 13; Length 627;
Best Local Similarity 97.2%; Pred. No. 1.3e-10;
RESULT 1002
ID ADE79027 standard; DNA; 1064 BP.
DE Human protein modification and maintenance molecule (PMM) -7 gene.
Query Match 4.8%; Score 136.6; DB 10; Length 1064;
Best Local Similarity 88.6%; Pred. No. 1.2e-10;
RESULT 1003
ID AAZ52560 standard; cDNA; 2262 BP.
DE Human secreted protein clone yep_1 nucleotide sequence SEQ ID NO:171.
PN WO958642-A2.
PD 18-NOV-1999.
PA (GENY) GENETICS INST INC.
Query Match 4.8%; Score 136.6; DB 3; Length 2262;
Best Local Similarity 91.2%; Pred. No. 1.2e-10;
RESULT 1004
ID ABK28222 standard; DNA; 11394 BP.
DE DNA transcription associated complementary genomic DNA #48.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 136.6; DB 6; Length 11394;
Best Local Similarity 88.6%; Pred. No. 1.1e-10;
RESULT 1005
ID ABX38235 standard; cDNA; 446 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3400.
PN US200237139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.8%; Score 136.4; DB 8; Length 446;
Best Local Similarity 90.1%; Pred. No. 1.4e-10;
RESULT 1006
ID ACN51887 standard; cDNA; 469 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-N6-C10, SEQ:6668.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 136.4; DB 13; Length 469;
Best Local Similarity 83.3%; Pred. No. 1.4e-10;
RESULT 1007
ID ABV55889 standard; cDNA; 516 BP.
DE Human prostate expression marker cDNA 55880.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 136.4; DB 5; Length 516;

Best Local Similarity 90.1%; Pred. No. 1.4e-10;
RESULT 1008
ID ADL43972 standard; DNA; 539 BP.
DE Human ovarian cancer DNA marker #17862.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 136.4; DB 5; Length 539;
Best Local Similarity 83.3%; Pred. No. 1.4e-10;
RESULT 1009
ID ACN53206 standard; cDNA; 553 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-003-Q1-N6-D8, SEQ:7987.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 136.4; DB 13; Length 553;
Best Local Similarity 83.3%; Pred. No. 1.4e-10;
RESULT 1010
ID ACN92384 standard; cDNA; 700 BP.
DE Human colon cancer cell expressed cDNA #796.
PN US2002155438-A1.
PD 24-OCT-2002.
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
Query Match 4.8%; Score 136.4; DB 10; Length 700;
Best Local Similarity 90.1%; Pred. No. 1.4e-10;
RESULT 1011
ID AAL45656 standard; cDNA; 1762 BP.
DE Human cancer cell growth inhibitor related DNA SEQ ID NO: 16.
PN CN1324819-A.
PD 05-DEC-2001.
PA (SHAN-) SHANGHAI CITY INST ONCOLOGY.
Query Match 4.8%; Score 136.4; DB 6; Length 1762;
Best Local Similarity 95.9%; Pred. No. 1.3e-10;
RESULT 1012
ID AAL45657 standard; DNA; 1762 BP.
DE Human cancer cell growth inhibitor related DNA SEQ ID NO: 18.
PN CN1324819-A.
PD 05-DEC-2001.
PA (SHAN-) SHANGHAI CITY INST ONCOLOGY.
Query Match 4.8%; Score 136.4; DB 6; Length 1762;
Best Local Similarity 95.9%; Pred. No. 1.3e-10;
RESULT 1013
ID ADI43478 standard; DNA; 1875 BP.
DE Plant transcription factor polynucleotide #1329.
PN US200401927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 4.8%; Score 136.4; DB 12; Length 1875;
Best Local Similarity 99.3%; Pred. No. 1.3e-10;
RESULT 1014
ID ADB54224 standard; DNA; 4316 BP.
DE Pretreated genomic DNA region 148.
PN WO2003072821-A2.
PD 04-SEP-2003.

PA (EPIC-) EPIGENOMICS AG.
Query Match 4.8%; Score 136.4; DB 10; Length 4316;
Best Local Similarity 85.4%; Pred. No. 1.2e-10;
RESULT 1015
ID ADS89522 standard; DNA; 4316 BP.
DE Oligonucleotide of the invention SEQ ID NO:538.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIC-) EPIGENOMICS AG.
Query Match 4.8%; Score 136.4; DB 13; Length 4316;
Best Local Similarity 85.4%; Pred. No. 1.2e-10;
RESULT 1016
ID ABN80099 standard; DNA; 5368 BP.
DE Human chemically modified disease associated gene SEQ ID NO 116.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 4.8%; Score 136.4; DB 6; Length 5369;
Best Local Similarity 85.4%; Pred. No. 1.2e-10;
RESULT 1017
ID ABK40004 standard; DNA; 5586 BP.
DE Human chemically pretreated gene sequence #43 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 4.8%; Score 136.4; DB 6; Length 5586;
Best Local Similarity 90.1%; Pred. No. 1.2e-10;
RESULT 1018
ID AAS46692 standard; DNA; 24259 BP.
DE Tumour suppressor gene derived chemically modified sequence #415.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIC-) EPIGENOMICS AG.
Query Match 4.8%; Score 136.2; DB 13; Length 249;
Best Local Similarity 88.6%; Pred. No. 1.5e-10;
RESULT 1020
ID ACN49835 standard; cDNA; 450 BP.
DE Cotton primed seed EST Clone ID: LTB3825-031-Q6-N6-E4, SEQ:4616.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 136.2; DB 13; Length 450;
Best Local Similarity 94.6%; Pred. No. 1.5e-10;
RESULT 1021
ID ABV54284 standard; cDNA; 459 BP.
DE Human prostate expression marker cDNA 54275.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 136.2; DB 5; Length 459;
Best Local Similarity 82.5%; Pred. No. 1.5e-10;
RESULT 1022
ID ABV56248 standard; cDNA; 481 BP.
DE Human prostate expression marker cDNA 56239.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 136.2; DB 5; Length 481;
Best Local Similarity 77.5%; Pred. No. 1.5e-10;

RESULT 1023
ID ADR64316 standard; cDNA; 510 BP.
DE Cotton cDNA sequence, SEQ ID 5097.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match 4.8%; Score 136.2; DB 13; Length 510;
Best Local Similarity 94.6%; Pred. No. 1.5e-10;
RESULT 1024
ID ACN49853 standard; cDNA; 518 BP.
DE Cotton primed seed EST Clone ID: LTB3825-031-Q6-N6-G11, SEQ:4634.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 136.2; DB 13; Length 518;
Best Local Similarity 94.6%; Pred. No. 1.5e-10;
RESULT 1025
ID ACN53350 standard; cDNA; 528 BP.
DE Cotton androecium tissue EST Clone ID: LTB3828-006-Q1-N6-F8, SEQ:8131.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 136.2; DB 13; Length 528;
Best Local Similarity 94.6%; Pred. No. 1.5e-10;
RESULT 1026
ID ACN57165 standard; cDNA; 541 BP.
DE Cotton gynoeceum tissue EST Clone ID: LTB3829-014-Q6-N6-G1, SEQ:11946.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 136.2; DB 13; Length 541;
Best Local Similarity 94.6%; Pred. No. 1.5e-10;
RESULT 1027
ID ABN80041 standard; DNA; 5387 BP.
DE Human chemically modified disease associated gene SEQ ID NO 58.
PN WO200200927-A2.
PA (EPIC-) EPIGENOMICS AG.
Query Match 4.8%; Score 136.2; DB 6; Length 5387;
Best Local Similarity 97.9%; Pred. No. 1.3e-10;
RESULT 1028
ID AAS46691 standard; DNA; 24259 BP.
DE Tumour suppressor gene derived chemically modified sequence #414.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIC-) EPIGENOMICS AG.
Query Match 4.8%; Score 136.2; DB 4; Length 24259;
Best Local Similarity 84.5%; Pred. No. 1.2e-10;
RESULT 1029
ID ACN61227 standard; cDNA; 486 BP.
DE Cotton gynoeceum tissue EST Clone ID: LTB3829-034-Q1-N6-A7, SEQ:16008.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 136; DB 13; Length 486;
Best Local Similarity 75.4%; Pred. No. 1.6e-10;
RESULT 1030
ID ACN49736 standard; cDNA; 489 BP.
DE Cotton primed seed EST Clone ID: LTB3825-026-Q6-N6-B11, SEQ:4517.

PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 4.8%; Score 136; DB 13; Length 489;
 RESULT 1031
 ID ACN50622 standard; cDNA; 508 BP.
 DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-N6-E9, SEQ:5403.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 4.8%; Score 136; DB 13; Length 508;
 RESULT 1032
 ID ACN59983 standard; cDNA; 526 BP.
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-036-Q1-N6-A4, SEQ:14764.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 4.8%; Score 136; DB 13; Length 526;
 RESULT 1033
 ID ACN61425 standard; cDNA; 527 BP.
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-015-Q1-N6-H7, SEQ:16206.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 4.8%; Score 136; DB 13; Length 527;
 RESULT 1034
 ID ADRA4025 standard; DNA; 1806 BP.
 DE Human colon tumour associated gene clone-36 SEQ ID NO:35.
 PN WO2004074506-A2.
 PD 02-SEP-2004.
 PA (MERG-) MERGEN LTD.
 Query Match
 Best Local Similarity 4.8%; Score 136; DB 13; Length 1806;
 RESULT 1035
 ID ADN05367 standard; cDNA; 1913 BP.
 DE Antipsoriatic cDNA sequence #906.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 4.8%; Score 136; DB 12; Length 1913;
 RESULT 1036
 ID ADQ08601 standard; DNA; 3030 BP.
 DE Ciona intestinalis nervous system associated gene SeqID3.
 PN JP2004057127-A.
 PD 26-FEB-2004.
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 Query Match
 Best Local Similarity 4.8%; Score 136; DB 12; Length 3030;
 RESULT 1037
 ID ABV57596 standard; cDNA; 396 BP.
 DE Human prostate expression marker cDNA 57587.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 4.8%; Score 135.8; DB 5; Length 396;
 RESULT 1038
 ID ACN52033 standard; cDNA; 443 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-H4, SEQ:6814.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 4.8%; Score 135.8; DB 13; Length 443;
 RESULT 1039
 ID ABV5662 standard; cDNA; 549 BP.
 DE Human prostate expression marker cDNA 56653.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 4.8%; Score 135.8; DB 5; Length 549;
 RESULT 1040
 ID ACN56366 standard; cDNA; 574 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-034-Q6-N6-D1, SEQ:11147.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 4.8%; Score 135.8; DB 13; Length 574;
 RESULT 1041
 ID ACN52339 standard; cDNA; 593 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-F10, SEQ:7120.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 4.8%; Score 135.8; DB 13; Length 593;
 RESULT 1042
 ID ADM47812 standard; DNA; 1383 BP.
 DE Polynucleotide sequence #230 useful in producing transgenic plants.
 PN US2003233670-A1.
 PD 18-DEC-2003.
 PA (EDGE/) EDGERTON M D.
 PA (CHOM/) CHOMET P S.
 PA (LACC/) LACCRETI L B.
 Query Match
 Best Local Similarity 4.8%; Score 135.8; DB 12; Length 1383;
 RESULT 1043
 ID ACN39804 standard; cDNA; 2074 BP.
 DE Tumour-associated antigenic target (TAT) cDNA DNA325989, SEQ ID NO:4174.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 4.8%; Score 135.8; DB 13; Length 2074;
 RESULT 1044
 ID ABZ10078 standard; DNA; 2501 BP.
 DE Haematopoietic cell proliferation disorder related DNA sequence #218.
 PN WO20027272-A2.
 PD 03-OCT-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match
 Best Local Similarity 4.8%; Score 135.8; DB 8; Length 2501;
 RESULT 1045
 ID ABZ10224 standard; DNA; 2501 BP.
 DE Haematopoietic cell proliferation disorder related DNA sequence #364.
 PN WO20027272-A2.
 PD 03-OCT-2002.
 PA (EPIG-) EPIGENOMICS AG.

Query Match
Best Local Similarity 4.8%; Score 135.8; DB 8; Length 2501;
RESULT 1046
ID ABK33928 standard; DNA; 4001 BP.
DE Human DNA for staging of Astrocytomas, complement, #5.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 4001;
RESULT 1047
ID ADA20431 standard; DNA; 4001 BP.
DE Prostate tumour related genomic DNA complement sample #48.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 135.8; DB 8; Length 4001;
RESULT 1048
ID ADA84238 standard; DNA; 4001 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:96.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 135.8; DB 8; Length 4001;
RESULT 1049
ID ABL32511 standard; DNA; 5306 BP.
DE Human immune system associated gene SEQ ID NO: 484.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 5306;
RESULT 1050
ID ABOQ7140 standard; DNA; 6134 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 170.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 6134;
RESULT 1051
ID ABL32996 standard; DNA; 7061 BP.
DE Human immune system associated gene SEQ ID NO: 969.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 7061;
RESULT 1052
ID ABL70247 standard; DNA; 7061 BP.
DE Chemically treated cell signalling DNA sequence#69.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 7061;
RESULT 1053
ID AAS61188 standard; DNA; 7061 BP.
DE Human gene regulation-associated gene oligonucleotide #143.
PN WO20017375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 7061;
RESULT 1054
ID ABL33032 standard; DNA; 14798 BP.
DE Human immune system associated gene SEQ ID NO: 1005.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 14798;

Best Local Similarity 98.6%; Pred. No. 1.4e-10;
RESULT 1055
ID ABN80146 standard; DNA; 14920 BP.
DE Human chemically modified disease associated gene SEQ ID NO 163.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 14920;
RESULT 1056
ID ABN79984 standard; DNA; 16633 BP.
DE Human chemically modified disease associated gene SEQ ID NO 1.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 16633;
RESULT 1057
ID ABL33719 standard; DNA; 17934 BP.
DE Human immune system associated gene SEQ ID NO: 1692.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 17934;
RESULT 1058
ID ABZ09958 standard; DNA; 35962 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #98.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 135.8; DB 8; Length 35962;
RESULT 1059
ID ABZ10104 standard; DNA; 35962 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #244.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 135.8; DB 8; Length 35962;
RESULT 1060
ID AAI85202 standard; cDNA; 390 BP.
DE Human polynucleotide SEQ ID NO 5262.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.8%; Score 135.6; DB 4; Length 390;
RESULT 1061
ID ACH21249 standard; cDNA; 429 BP.
DE Human adult liver cDNA #861.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 4.8%; Score 135.6; DB 9; Length 429;
RESULT 1062
ID ACS53490 standard; cDNA; 468 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-008-Q1-K6-D3, SEQ:8271.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 4.8%; Score 135.6; DB 13; Length 468;
RESULT 1063

ID ACN47785 standard; cDNA; 557 BP.
DE - Cotton primed seed EST Clone ID: LIB3825-015-Q1-N6-A5, SEQ:2566.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 135.6; DB 13; Length 557;
Best Local Similarity 84.1%; Pred. No. 1.8e-10;
RESULT 1064
ID AAL16123 standard; cDNA; 831 BP.
DE Human breast cancer expressed polynucleotide 8580.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 135.6; DB 4; Length 831;
Best Local Similarity 64.8%; Pred. No. 1.7e-10;
RESULT 1065
ID AAD02119 standard; cDNA; 1459 BP.
DE Maize RAD51 orthologue #2 cDNA.
PN WO200068370-A2.
PD 16-NOV-2000.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 4.8%; Score 135.6; DB 4; Length 1459;
Best Local Similarity 97.2%; Pred. No. 1.7e-10;
RESULT 1066
ID ABN80138 standard; DNA; 6484 BP.
DE Human chemically modified disease associated gene SEQ ID NO 155.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 135.6; DB 6; Length 6484;
Best Local Similarity 86.2%; Pred. No. 1.6e-10;
RESULT 1067
ID ABQ67061 standard; DNA; 9095 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 91.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 135.6; DB 6; Length 9095;
Best Local Similarity 82.1%; Pred. No. 1.6e-10;
RESULT 1068
ID ABL70544 standard; DNA; 15649 BP.
DE Chemically treated cell signalling DNA sequence complementary to#217.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 135.6; DB 6; Length 15649;
Best Local Similarity 86.2%; Pred. No. 1.5e-10;
RESULT 1069
ID ABL34072 standard; DNA; 40862 BP.
DE Human immune system associated gene SEQ ID NO: 2045.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 135.6; DB 6; Length 40862;
Best Local Similarity 84.1%; Pred. No. 1.5e-10;
RESULT 1070
ID ABX36136 standard; cDNA; 181 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1301.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.8%; Score 135.4; DB 8; Length 181;
Best Local Similarity 99.3%; Pred. No. 2e-10;
RESULT 1071
ID ABV54282 standard; cDNA; 412 BP.
DE Human prostate expression marker cDNA 54273.
PN WO200160860-A2.

PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 135.4; DB 5; Length 412;
Best Local Similarity 92.8%; Pred. No. 1.9e-10;
RESULT 1072
ID ADH39852 standard; cDNA; 2146 BP.
DE Guayule fructan:fructan 1-fructosyltransferase (1-FFT) cDNA.
PN US2002170086-A1.
PD 14-NOV-2002.
PA (ALLE/) ALLEN S M.
PA (CAIM/) CAIMI P G.
PA (STOO/) STOOP J M.
Query Match 4.8%; Score 135.4; DB 10; Length 2146;
Best Local Similarity 85.3%; Pred. No. 1.8e-10;
RESULT 1073
ID ABK34669 standard; cDNA; 3415 BP.
DE Human cDNA for novel secreted protein, SEQ ID 438.
PN WO200177290-A2.
PD 18-OCT-2001.
PA (GENY) GENETICS INST INC.
Query Match 4.8%; Score 135.4; DB 6; Length 3415;
Best Local Similarity 95.9%; Pred. No. 1.8e-10;
RESULT 1074
ID ABV54241 standard; cDNA; 385 BP.
DE Human prostate expression marker cDNA 54232.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 135.2; DB 5; Length 385;
Best Local Similarity 83.5%; Pred. No. 2.1e-10;
RESULT 1075
ID ABV49895 standard; cDNA; 522 BP.
DE Human prostate expression marker cDNA 49886.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 135.2; DB 5; Length 522;
Best Local Similarity 82.6%; Pred. No. 2e-10;
RESULT 1076
ID ADN04959 standard; cDNA; 1999 BP.
DE Antiprosoriatic cDNA sequence #694.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.8%; Score 135.2; DB 12; Length 1999;
Best Local Similarity 91.7%; Pred. No. 1.9e-10;
RESULT 1077
ID AAF97906 standard; cDNA; 2394 BP.
DE Human secreted protein cDNA, SEQ ID NO: 33.
PN WO200121658-A1.
PD 29-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 135.2; DB 4; Length 2394;
Best Local Similarity 89.0%; Pred. No. 1.9e-10;
RESULT 1078
ID ADP04916 standard; cDNA; 2789 BP.
DE Sea squirt cDNA with tissue specific expression in development Seq 511.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 4.8%; Score 135.2; DB 12; Length 2789;
Best Local Similarity 86.6%; Pred. No. 1.9e-10;
RESULT 1079
ID ACA25512 standard; DNA; 195 BP.
DE Prokaryotic essential gene #7169.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 135; DB 8; Length 195;
Best Local Similarity 93.4%; Pred. No. 2.3e-10;
RESULT 1080
ID ACN50243 standard; cDNA; 368 BP.
DE Cotton non-primed seed EST Clone ID: LIB3826-002-Q1-K6-B12, SEQ:5024.

PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.7%; Score 135; DB 13; Length 368;
 Best Local Similarity 72.8%; Pred. No. 2.2e-10;
 RESULT 1081
 ID AAI83197 standard; cDNA; 403 BP.
 DE Human polynucleotide SEQ ID NO 3257.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.7%; Score 135; DB 4; Length 403;
 Best Local Similarity 81.7%; Pred. No. 2.2e-10;
 RESULT 1082
 ID ABV09124 standard; cDNA; 417 BP.
 DE Human prostate expression marker cDNA 9115.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 135; DB 5; Length 417;
 Best Local Similarity 69.6%; Pred. No. 2.2e-10;
 RESULT 1083
 ID AAI93052 standard; cDNA; 452 BP.
 DE Human polynucleotide SEQ ID NO 3112.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.7%; Score 135; DB 4; Length 452;
 Best Local Similarity 96.5%; Pred. No. 2.2e-10;
 RESULT 1084
 ID ACN53254 standard; cDNA; 578 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-004-Q1-N6-F11, SEQ:8035.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.7%; Score 135; DB 13; Length 578;
 Best Local Similarity 85.7%; Pred. No. 2.2e-10;
 RESULT 1085
 ID AAR23442 standard; cDNA; 1933 BP.
 DE cDNA encoding human secreted protein vcs2_1, SEQ ID NO:39.
 PN WO200011015-A1.
 PD 02-MAR-2000.
 PA (ALPH-) ALPHAGENE INC.
 Query Match 4.7%; Score 135; DB 3; Length 1933;
 Best Local Similarity 96.5%; Pred. No. 2e-10;
 RESULT 1086
 ID ADH61306 standard; DNA; 3420 BP.
 DE INTSIG encoding DNA 7512389CB1, SEQ ID 23.
 PN WO2004001005-A2.
 PD 31-DEC-2003.
 PA (INCY-) INCYTE CORP.
 Query Match 4.7%; Score 135; DB 12; Length 3420;
 Best Local Similarity 88.0%; Pred. No. 2e-10;
 RESULT 1087
 ID ABX49356 standard; cDNA; 411 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #14521.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 4.7%; Score 134.8; DB 8; Length 411;
 Best Local Similarity 92.2%; Pred. No. 2.3e-10;
 RESULT 1088
 ID ACN56895 standard; cDNA; 435 BP.
 DE Cotton gynoeceum tissue EST Clone ID: LIB3829-011-Q6-N6-E2, SEQ:11676.

PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.7%; Score 134.8; DB 13; Length 435;
 Best Local Similarity 89.5%; Pred. No. 2.3e-10;
 RESULT 1089
 ID ABV54519 standard; cDNA; 515 BP.
 DE Human prostate expression marker cDNA 54510.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 134.8; DB 5; Length 515;
 Best Local Similarity 84.8%; Pred. No. 2.3e-10;
 RESULT 1090
 ID ADQ22502 standard; DNA; 1389 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5322.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 4.7%; Score 134.8; DB 12; Length 1389;
 Best Local Similarity 92.2%; Pred. No. 2.2e-10;
 RESULT 1091
 ID AAD05087 standard; cDNA; 2297 BP.
 DE Human secreted protein-encoding gene 7 cDNA clone HHMM74, SEQ ID NO: 45.
 PN WO200134768-A2.
 PD 17-MAY-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 134.8; DB 4; Length 2297;
 Best Local Similarity 78.4%; Pred. No. 2.2e-10;
 RESULT 1092
 ID ADA40350 standard; cDNA; 2297 BP.
 DE Human secreted protein encoding cDNA.
 PN WO2002102993-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 134.8; DB 8; Length 2297;
 Best Local Similarity 78.4%; Pred. No. 2.2e-10;
 RESULT 1093
 ID ADA56516 standard; DNA; 2297 BP.
 DE Gene encoding human secreted protein #223.
 PN WO2002102994-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 134.8; DB 10; Length 2297;
 Best Local Similarity 78.4%; Pred. No. 2.2e-10;
 RESULT 1094
 ID ACN53258 standard; cDNA; 353 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-004-Q1-N6-F9, SEQ:8039.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.7%; Score 134.6; DB 13; Length 353;
 Best Local Similarity 80.2%; Pred. No. 2.5e-10;
 RESULT 1095
 ID ABV59054 standard; cDNA; 360 BP.
 DE Human prostate expression marker cDNA 59045.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 134.6; DB 5; Length 360;
 Best Local Similarity 97.2%; Pred. No. 2.5e-10;
 RESULT 1096
 ID ABV08149 standard; cDNA; 391 BP.
 DE Human prostate expression marker cDNA 8140.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 4.7%; Score 134.6; DB 5; Length 391;
 Best Local Similarity 80.0%; Pred. No. 2.5e-10;
 RESULT 1097
 ID ABV58690 standard; cDNA; 579 BP.
 DE Human prostate expression marker cDNA 58681.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 134.6; DB 5; Length 579;
 Best Local Similarity 86.1%; Pred. No. 2.5e-10;
 RESULT 1098
 ID AAC98734 standard; cDNA; 225 BP.
 DE Human colon cancer antigen nucleotide sequence SEQ ID NO:744.
 PN WO200055351-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 134.4; DB 3; Length 225;
 Best Local Similarity 92.8%; Pred. No. 2.7e-10;
 RESULT 1099
 ID ACN53166 standard; cDNA; 319 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-022-Q1-N6-G10, SEQ:7947.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.7%; Score 134.4; DB 13; Length 319;
 Best Local Similarity 81.2%; Pred. No. 2.7e-10;
 RESULT 1100
 ID ACN53082 standard; cDNA; 398 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-021-Q1-N6-F7, SEQ:7863.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.7%; Score 134.4; DB 13; Length 398;
 Best Local Similarity 95.8%; Pred. No. 2.7e-10;
 RESULT 1101
 ID ABV16128 standard; cDNA; 416 BP.
 DE Human prostate expression marker cDNA 16119.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 134.4; DB 5; Length 416;
 Best Local Similarity 76.5%; Pred. No. 2.7e-10;
 RESULT 1102
 ID ACH19935 standard; cDNA; 423 BP.
 DE Human adult lung cDNA #938.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRNA/) DRNANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 4.7%; Score 134.4; DB 9; Length 423;
 Best Local Similarity 77.1%; Pred. No. 2.7e-10;
 RESULT 1103
 ID ACN55408 standard; cDNA; 499 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-023-Q6-N6-C10, SEQ:10189.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.7%; Score 134.4; DB 13; Length 499;
 Best Local Similarity 75.0%; Pred. No. 2.6e-10;
 RESULT 1104
 ID ACN52918 standard; cDNA; 520 BP.

DE Cotton androecium tissue EST Clone ID: LIB3828-019-Q1-N6-D6, SEQ:7699.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.7%; Score 134.4; DB 13; Length 520;
 Best Local Similarity 85.2%; Pred. No. 2.6e-10;
 RESULT 1105
 ID ACN61238 standard; cDNA; 548 BP.
 DE Cotton gynoeceum tissue EST Clone ID: LIB3829-034-Q1-N6-C12, SEQ:16019.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.7%; Score 134.4; DB 13; Length 548;
 Best Local Similarity 81.2%; Pred. No. 2.6e-10;
 RESULT 1106
 ID ADL37588 standard; DNA; 608 BP.
 DE Human ovarian cancer DNA marker #11478.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 134.4; DB 5; Length 608;
 Best Local Similarity 80.6%; Pred. No. 2.6e-10;
 RESULT 1107
 ID ADI72448 standard; DNA; 608 BP.
 DE Human ovarian cancer DNA marker #5190.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 134.4; DB 5; Length 608;
 Best Local Similarity 80.6%; Pred. No. 2.6e-10;
 RESULT 1108
 ID ACN50609 standard; cDNA; 616 BP.
 DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-N6-D5, SEQ:5390.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.7%; Score 134.4; DB 13; Length 616;
 Best Local Similarity 81.2%; Pred. No. 2.6e-10;
 RESULT 1109
 ID ABK47997 standard; DNA; 6409 BP.
 DE Human kinesin motor protein KinI-3 DNA.
 PN WO200226929-A2.
 PD 04-APR-2002.
 PA (CYTO-) CYTOKINETICS INC.
 Query Match 4.7%; Score 134.4; DB 6; Length 6409;
 Best Local Similarity 87.5%; Pred. No. 2.4e-10;
 RESULT 1110
 ID ACAG2846 standard; DNA; 6409 BP.
 DE DNA encoding human kinesin motor protein KinI-3.
 PN US2003036075-A1.
 PD 20-FEB-2003.
 PA (CYTO-) CYTOKINETICS.
 Query Match 4.7%; Score 134.4; DB 8; Length 6409;
 Best Local Similarity 87.5%; Pred. No. 2.4e-10;
 RESULT 1111
 ID ACAG2960 standard; DNA; 6409 BP.
 DE DNA encoding human kinesin motor protein, KinI-3.
 PN US6514738-B1.
 PD 04-FEB-2003.
 PA (CYTO-) CYTOKINETICS INC.
 Query Match 4.7%; Score 134.4; DB 9; Length 6409;
 Best Local Similarity 87.5%; Pred. No. 2.4e-10;
 RESULT 1112
 ID ADF50896 standard; DNA; 11097 BP.

DE Chemically modified promoter region of human melastatin gene (SeqID 4).
PN EP1344832-A1.
PD 17-SEP-2003.
PA (EP1G-) EPIGENOMICS AG.
Query Match 4.7%; Score 134.4; DB 10; Length 11097;
Best Local Similarity 83.2%; Pred. No. 2.3e-10;
RESULT 1113
ID AAF24360 standard; DNA; 160 BP.
DE Retroviral recombination assay coding sequence fragment #5.
PN WO200104360-A2.
PD 18-JAN-2001.
PA (UABR-) UAB RES FOUND.
PA (TRAN-) TRANZYME INC.
Query Match 4.7%; Score 134.2; DB 5; Length 160;
Best Local Similarity 97.8%; Pred. No. 3e-10;
RESULT 1114
ID AAF24361 standard; DNA; 178 BP.
DE Retroviral recombination assay coding sequence fragment #6.
PN WO200104360-A2.
PD 18-JAN-2001.
PA (UABR-) UAB RES FOUND.
PA (TRAN-) TRANZYME INC.
Query Match 4.7%; Score 134.2; DB 5; Length 178;
Best Local Similarity 97.8%; Pred. No. 2.9e-10;
RESULT 1115
ID ADP85921 standard; DNA; 196 BP.
DE Synthetic construct #5.
PN US2004110205-A1.
PD 10-JUN-2004.
PA (WANG/) WANG H.
Query Match 4.7%; Score 134.2; DB 12; Length 196;
Best Local Similarity 97.8%; Pred. No. 2.9e-10;
RESULT 1116
ID AAF24363 standard; DNA; 208 BP.
DE Retroviral recombination assay coding sequence fragment #8.
PN WO200104360-A2.
PD 18-JAN-2001.
PA (UABR-) UAB RES FOUND.
PA (TRAN-) TRANZYME INC.
Query Match 4.7%; Score 134.2; DB 5; Length 208;
Best Local Similarity 97.8%; Pred. No. 2.9e-10;
RESULT 1117
ID . ABX41374 standard; cDNA; 217 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6539.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.7%; Score 134.2; DB 8; Length 217;
Best Local Similarity 97.8%; Pred. No. 2.9e-10;
RESULT 1118
ID ACN53426 standard; cDNA; 403 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-007-Q1-K6-F9, SEQ:8207.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134.2; DB 13; Length 403;
Best Local Similarity 89.0%; Pred. No. 2.8e-10;
RESULT 1119
ID AAI89032 standard; cDNA; 416 BP.
DE Human polynucleotide SEQ ID NO 9092.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 134.2; DB 4; Length 416;
Best Local Similarity 89.0%; Pred. No. 2.8e-10;
RESULT 1120
ID AAI87701 standard; cDNA; 491 BP.

DE Human polynucleotide SEQ ID NO 7761.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 134.2; DB 4; Length 491;
Best Local Similarity 71.9%; Pred. No. 2.8e-10;
RESULT 1121
ID ACH24750 standard; cDNA; 491 BP.
DE Human adult ovary cDNA #3130.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRNA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.7%; Score 134.2; DB 9; Length 491;
Best Local Similarity 71.9%; Pred. No. 2.8e-10;
RESULT 1122
ID ABV59092 standard; cDNA; 501 BP.
DE Human prostate expression marker cDNA 59083.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 134.2; DB 5; Length 501;
Best Local Similarity 97.8%; Pred. No. 2.8e-10;
RESULT 1123
ID ACN56029 standard; cDNA; 529 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-031-Q6-N6-C8, SEQ:10810.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134.2; DB 13; Length 529;
Best Local Similarity 86.5%; Pred. No. 2.8e-10;
RESULT 1124
ID ACN52102 standard; cDNA; 542 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-E12, SEQ:6883.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134.2; DB 13; Length 542;
Best Local Similarity 97.8%; Pred. No. 2.8e-10;
RESULT 1125
ID ACN45362 standard; cDNA; 570 BP.
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-A5, SEQ:143.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134.2; DB 13; Length 570;
Best Local Similarity 97.8%; Pred. No. 2.8e-10;
RESULT 1126
ID ADQ62833 standard; RNA; 1000 BP.
DE Homopoly-A contaminant for RNaseH activity assay.
PN WO2004059012-A1.
PD 15-JUL-2004.
PA (AMHP) WYETH.
Query Match 4.7%; Score 134.2; DB 12; Length 1000;
Best Local Similarity 97.8%; Pred. No. 2.7e-10;
RESULT 1127
ID ADQ62832 standard; RNA; 1000 BP.
DE Homopoly-U contaminant for RNaseH activity assay.
PN WO2004059012-A1.
PD 15-JUL-2004.
PA (AMHP) WYETH.

Query Match 4.7%; Score 134.2; DB 12; Length 1000;
 Best Local Similarity 97.8%; Pred. No. 2.7e-10;
 RESULT 1128
 ID ADP85917 standard; DNA; 1300 BP.
 DE Synthetic construct #1.
 PN US2004110205-A1.
 PD 10-JUN-2004.
 PA (WANG/) WANG H.
 Query Match 4.7%; Score 134.2; DB 12; Length 1300;
 Best Local Similarity 97.8%; Pred. No. 2.7e-10;
 RESULT 1129
 ID ACC50413 standard; cDNA; 1663 BP.
 DE Human secreted protein coding sequence, SEQ ID 80.
 PN WO200295010-A2.
 PD 28-NOV-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 134.2; DB 8; Length 1663;
 Best Local Similarity 97.8%; Pred. No. 2.7e-10;
 RESULT 1130
 ID ABZ71230 standard; cDNA; 1663 BP.
 DE Human secreted protein-encoding gene 41 cDNA clone HDP5H53, SEQ ID NO:51.
 PN WO200276488-A1.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 134.2; DB 8; Length 1663;
 Best Local Similarity 97.8%; Pred. No. 2.7e-10;
 RESULT 1131
 ID ADB91122 standard; cDNA; 1663 BP.
 DE Human secreted protein cDNA #SEQ ID 68.
 PN WO2003004622-A2.
 PD 16-JAN-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 134.2; DB 9; Length 1663;
 Best Local Similarity 97.8%; Pred. No. 2.7e-10;
 RESULT 1132
 ID ADC73466 standard; DNA; 1663 BP.
 DE Human secreted protein-related DNA - SEQ ID 99.
 PN WO2003038063-A2.
 PD 08-MAY-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 134.2; DB 10; Length 1663;
 Best Local Similarity 97.8%; Pred. No. 2.7e-10;
 RESULT 1133
 ID AAS45477 standard; DNA; 7657 BP.
 DE Chemically pretreated complementary DNA associated with cell cycle #91.
 PN WO200168911-A2.
 PD 20-SEP-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.7%; Score 134.2; DB 4; Length 7657;
 Best Local Similarity 97.8%; Pred. No. 2.5e-10;
 RESULT 1134
 ID ABL34022 standard; DNA; 7657 BP.
 DE Human immune system associated gene SEQ ID NO: 1995.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.7%; Score 134.2; DB 6; Length 7657;
 Best Local Similarity 97.8%; Pred. No. 2.5e-10;
 RESULT 1135
 ID ABK31429 standard; DNA; 9814 BP.
 DE Signal transduction associated gene modified complementary DNA #136.
 PN WO200200926-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.7%; Score 134.2; DB 6; Length 9814;
 Best Local Similarity 97.8%; Pred. No. 2.5e-10;
 RESULT 1136
 ID ABL34196 standard; DNA; 37973 BP.
 DE Human immune system associated gene SEQ ID NO: 2169.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.7%; Score 134.2; DB 6; Length 37973;

Best Local Similarity 97.8%; Pred. No. 2.3e-10;
 RESULT 1137
 ID ABX38052 standard; cDNA; 242 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #3217.
 PN US2002437139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 4.7%; Score 134; DB 8; Length 242;
 Best Local Similarity 96.5%; Pred. No. 3.1e-10;
 RESULT 1138
 ID ADL35477 standard; DNA; 305 BP.
 DE Human filamin A alpha-related functional screen hit DNA 3.
 PN WO2004019893-A2.
 PD 11-MAR-2004.
 PA (RIGE-) RIGEL PHARM INC.
 Query Match 4.7%; Score 134; DB 12; Length 305;
 Best Local Similarity 96.5%; Pred. No. 3.1e-10;
 RESULT 1139
 ID ACN55002 standard; cDNA; 342 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-K6-A9, SEQ:9783.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.7%; Score 134; DB 13; Length 342;
 Best Local Similarity 85.6%; Pred. No. 3.1e-10;
 RESULT 1140
 ID ABV57020 standard; cDNA; 472 BP.
 DE Human prostate expression marker cDNA 57011.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 134; DB 5; Length 472;
 Best Local Similarity 90.5%; Pred. No. 3e-10;
 RESULT 1141
 ID ACN49504 standard; cDNA; 593 BP.
 DE Cotton primed seed EST Clone ID: LIB3825-034-Q6-K6-G11, SEQ:4285.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.7%; Score 134; DB 13; Length 593;
 Best Local Similarity 96.5%; Pred. No. 3e-10;
 RESULT 1142
 ID ACN56642 standard; cDNA; 598 BP.
 DE Cotton gynoeceum tissue EST Clone ID: LIB3829-001-Q1-N6-H1, SEQ:11423.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.7%; Score 134; DB 13; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1143
 ID ADI73484 standard; DNA; 756 BP.
 DE Human ovarian cancer DNA marker #6226.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 134; DB 5; Length 756;
 Best Local Similarity 82.5%; Pred. No. 3e-10;
 RESULT 1144
 ID ADL38614 standard; DNA; 756 BP.
 DE Human ovarian cancer DNA marker #12504.
 PN WO200170979-A2.

PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 134; DB 5; Length 756;
 Best Local Similarity 82.5%; Pred. No. 3e-10;
 RESULT 1145
 ID ADOQ22074 standard; DNA; 980 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4894.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 4.7%; Score 134; DB 12; Length 980;
 Best Local Similarity 85.6%; Pred. No. 2.9e-10;
 RESULT 1146
 ID ADF94940 standard; cDNA; 1311 BP.
 DE Human gene 8-derived ACP30-like cDNA, SEQ ID NO:36.
 PN WO2003031586-A2.
 PD 17-APR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (BLON/) BLONDEL O.
 PA (RUBE/) RUBEN S M.
 Query Match 4.7%; Score 134; DB 10; Length 1311;
 Best Local Similarity 98.5%; Pred. No. 2.9e-10;
 RESULT 1147
 ID ABL49347 standard; DNA; 5152 BP.
 DE Human polynucleotide associated with DNA replication SEQ ID NO 47.
 PN WO200177377-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.7%; Score 134; DB 6; Length 5152;
 Best Local Similarity 95.8%; Pred. No. 2.7e-10;
 RESULT 1148
 ID ABK40074 standard; DNA; 8899 BP.
 DE Human chemically pretreated gene sequence #78 strand 2.
 PN WO200202806-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.7%; Score 134; DB 6; Length 8899;
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;
 RESULT 1149
 ID ABL32837 standard; DNA; 8899 BP.
 DE Human immune system associated gene SEQ ID NO: 810.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.7%; Score 134; DB 6; Length 8899;
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;
 RESULT 1150
 ID ABX43930 standard; cDNA; 283 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #9095.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 4.7%; Score 133.8; DB 8; Length 283;
 Best Local Similarity 97.1%; Pred. No. 3.3e-10;
 RESULT 1151
 ID ABX37058 standard; cDNA; 415 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #2223.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 4.7%; Score 133.8; DB 8; Length 415;
 Best Local Similarity 92.2%; Pred. No. 3.2e-10;
 RESULT 1152
 ID ABV54238 standard; cDNA; 474 BP.
 DE Human prostate expression marker cDNA 54229.
 PN WO200160860-A2.
 PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 133.8; DB 5; Length 474;
 Best Local Similarity 83.3%; Pred. No. 3.2e-10;
 RESULT 1153
 ID AAL16112 standard; cDNA; 817 BP.
 DE Human breast cancer expressed polynucleotide 8569.
 PN WO200151628-A2.
 PD 19-JUL-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 133.8; DB 4; Length 817;
 Best Local Similarity 73.2%; Pred. No. 3.1e-10;
 RESULT 1154
 ID ACN86064 standard; DNA; 861 BP.
 DE Breast cancer related marker, seq id 7214.
 PN US2003099974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 4.7%; Score 133.8; DB 11; Length 861;
 Best Local Similarity 73.2%; Pred. No. 3.1e-10;
 RESULT 1155
 ID ADL63529 standard; DNA; 874 BP.
 DE Human ovarian cancer DNA marker #21741.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 133.8; DB 5; Length 874;
 Best Local Similarity 89.4%; Pred. No. 3.1e-10;
 RESULT 1156
 ID ADQ29621 standard; DNA; 2566 BP.
 DE Human colorectal cancer-associated protein coding sequence #43.
 PN EP1439393-A2.
 PD 21-JUL-2004.
 PA (FARB) BAYER HEALTHCARE LLC.
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 Query Match 4.7%; Score 133.8; DB 12; Length 2566;
 Best Local Similarity 98.5%; Pred. No. 3e-10;
 RESULT 1157
 ID ABL33801 standard; DNA; 6115 BP.
 DE Human immune system associated gene SEQ ID NO: 1774.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.7%; Score 133.8; DB 6; Length 6115;
 Best Local Similarity 87.0%; Pred. No. 2.9e-10;
 RESULT 1158
 ID ABN80102 standard; DNA; 8712 BP.
 DE Human chemically modified disease associated gene SEQ ID NO 119.
 PN WO200200927-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.7%; Score 133.8; DB 6; Length 8712;
 Best Local Similarity 95.2%; Pred. No. 2.8e-10;
 RESULT 1159
 ID ABX42068 standard; cDNA; 259 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #7233.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 4.7%; Score 133.6; DB 8; Length 259;
 Best Local Similarity 86.0%; Pred. No. 3.5e-10;
 RESULT 1160
 ID ACH28630 standard; cDNA; 477 BP.
 DE Human adult ovary cDNA #7010.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.

Query Match 4.7%; Score 133.6; DB 9; Length 477;
Best Local Similarity 86.0%; Pred. No. 3.4e-10;
RESULT 1161
ID ADP04748 standard; cDNA; 1352 BP.
DE Sea squirt cDNA with tissue specific expression in development Seq 343.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 4.7%; Score 133.6; DB 12; Length 1352;
Best Local Similarity 88.4%; Pred. No. 3.3e-10;
RESULT 1162
ID AAF98380 standard; cDNA; 2178 BP.
DE Human cDNA clone BL187_4 sequence SEQ ID 10.
PN WO200119988-A1.
PD 22-MAR-2001.
PA (GENY) GENETICS INST INC.
Query Match 4.7%; Score 133.6; DB 5; Length 2178;
Best Local Similarity 91.0%; Pred. No. 3.2e-10;
RESULT 1163
ID AAS45339 standard; DNA; 6025 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #22.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133.6; DB 4; Length 6025;
Best Local Similarity 88.4%; Pred. No. 3.1e-10;
RESULT 1164
ID AAS46794 standard; DNA; 56153 BP.
DE Tumour suppressor gene derived chemically modified sequence #520.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133.6; DB 4; Length 56153;
Best Local Similarity 83.9%; Pred. No. 2.8e-10;
RESULT 1165
ID AAS35937 standard; DNA; 148 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1437.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 4; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1166
ID AAK89970 standard; DNA; 148 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3546.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 4; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1167
ID AAI62624 standard; DNA; 148 BP.
DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 274.
PN WO200155324-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 4; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1168
ID AAK78753 standard; DNA; 148 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33565.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 4; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1169
ID AAK81310 standard; DNA; 148 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36122.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 4; Length 148;

Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1170
ID AAK73937 standard; DNA; 148 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28749.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 4; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1171
ID AAK79569 standard; DNA; 148 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34381.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 4; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1172
ID AAL04801 standard; DNA; 148 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7489.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 4; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1173
ID AAL06718 standard; DNA; 148 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9406.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 4; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1174
ID AAL07121 standard; DNA; 148 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9809.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 4; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1175
ID AAL05015 standard; DNA; 148 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7703.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 4; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1176
ID ABA08155 standard; DNA; 148 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 950.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 4; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1177
ID ABL97695 standard; DNA; 148 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2347.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 4; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1178
ID ABL97908 standard; DNA; 148 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2560.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 4; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;

RESULT 1179
 ID AAS29186 standard; DNA; 148 BP.
 DE Genomic sequence #29 encoding novel human DNA-binding protein.
 PN WO200155162-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 133.4; DB 5; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1180
 ID AAS29163 standard; DNA; 148 BP.
 DE Genomic sequence #6 encoding novel human DNA-binding protein.
 PN WO200155162-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 133.4; DB 5; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1181
 ID AAS29228 standard; DNA; 148 BP.
 DE Genomic sequence #71 encoding novel human DNA-binding protein.
 PN WO200155162-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 133.4; DB 5; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1182
 ID AAS29176 standard; DNA; 148 BP.
 DE Genomic sequence #19 encoding novel human DNA-binding protein.
 PN WO200155162-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 133.4; DB 5; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1183
 ID ABAL7037 standard; DNA; 148 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 9368.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 133.4; DB 5; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1184
 ID AAD16668 standard; DNA; 148 BP.
 DE Human pancreatic related protein-encoding exon, SEQ ID NO:32.
 PN WO200155327-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 133.4; DB 5; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1185
 ID ABS68316 standard; DNA; 148 BP.
 DE Human DNA-binding protein genomic DNA sequence #19.
 PN US2002102638-A1.
 PD 01-AUG-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 4.7%; Score 133.4; DB 6; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1186
 ID ABS68303 standard; DNA; 148 BP.
 DE Human DNA-binding protein genomic DNA sequence #6.
 PN US2002102638-A1.
 PD 01-AUG-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 4.7%; Score 133.4; DB 6; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1187
 ID ABS68326 standard; DNA; 148 BP.
 DE Human DNA-binding protein genomic DNA sequence #29.
 PN US2002102638-A1.
 PD 01-AUG-2002.

PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 4.7%; Score 133.4; DB 6; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1188
 ID ABS68368 standard; DNA; 148 BP.
 DE Human DNA-binding protein genomic DNA sequence #71.
 PN US2002102638-A1.
 PD 01-AUG-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 4.7%; Score 133.4; DB 6; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1189
 ID ADA41651 standard; DNA; 148 BP.
 DE Human secreted protein related DNA.
 PN WO2002102993-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 133.4; DB 8; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1190
 ID ADC25448 standard; cDNA; 148 BP.
 DE Human cDNA from extracellular matrix gene 53 #4.
 PN US2003049650-A1.
 PD 13-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 133.4; DB 10; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1191
 ID ADC25490 standard; cDNA; 148 BP.
 DE Human cDNA from extracellular matrix gene 80 #2.
 PN US2003049650-A1.
 PD 13-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 133.4; DB 10; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1192
 ID ADC25425 standard; cDNA; 148 BP.
 DE Human cDNA from extracellular matrix gene 14 #3.
 PN US2003049650-A1.
 PD 13-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 133.4; DB 10; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1193
 ID ADC25438 standard; cDNA; 148 BP.
 DE Human cDNA from extracellular matrix gene 25 #2.
 PN US2003049650-A1.
 PD 13-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 133.4; DB 10; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1194
 ID ADC74709 standard; DNA; 148 BP.
 DE Human secreted protein-related DNA - SEQ ID 1342.
 PN WO2003038063-A2.
 PD 08-MAY-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 133.4; DB 10; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1195
 ID ADE46631 standard; DNA; 148 BP.
 DE Human cardiovascular system related genomic DNA #197.
 PN US2003059908-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 133.4; DB 10; Length 148;
 Best Local Similarity 99.3%; Pred. No. 3.9e-10;
 RESULT 1196
 ID ADA57783 standard; DNA; 148 BP.

DE BAC fragment containing human secreted protein gene #537.
PN WO2002102994-A2.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 10; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1197
ID ADNA1714 standard; DNA; 148 BP.
DE Novel human secreted protein polynucleotide seqid 836.
PN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYV/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAPL/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 4.7%; Score 133.4; DB 12; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1198
ID ADJ08049 standard; DNA; 148 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1437.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133.4; DB 13; Length 148;
Best Local Similarity 99.3%; Pred. No. 3.9e-10;
RESULT 1199
ID AAF24365 standard; DNA; 172 BP.
DE Retroviral recombination assay coding sequence fragment #10.
PN WO200104360-A2.
PD 18-JAN-2001.
PA (UABR-) UAB RES FOUND.
PA (TRAN-) TRANZYME INC.
Query Match 4.7%; Score 133.4; DB 5; Length 172;
Best Local Similarity 99.3%; Pred. No. 3.8e-10;
RESULT 1200
ID AAV41451 standard; cDNA; 202 BP.
DE Nucleotide sequence of the 3' portion of the BL229_22 clone.
PN WO9821332-A2.
PD 22-MAY-1998.
PA (GENY) GENETICS INST INC.
Query Match 4.7%; Score 133.4; DB 2; Length 202;
Best Local Similarity 99.3%; Pred. No. 3.8e-10;
RESULT 1201
ID AAF98423 standard; cDNA; 202 BP.
DE Human cDNA clone BL229_22 3' sequence SEQ ID 81.
PN WO200119988-A1.
PD 22-MAR-2001.
PA (GENY) GENETICS INST INC.
Query Match 4.7%; Score 133.4; DB 5; Length 202;
Best Local Similarity 99.3%; Pred. No. 3.8e-10;
RESULT 1202
ID AAI82950 standard; cDNA; 402 BP.
DE Human polynucleotide SEQ ID NO 3010.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 133.4; DB 4; Length 402;
Best Local Similarity 95.8%; Pred. No. 3.7e-10;
RESULT 1203
ID AAI85952 standard; cDNA; 420 BP.
DE Human polynucleotide SEQ ID NO 6012.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.

Query Match 4.7%; Score 133.4; DB 4; Length 420;
Best Local Similarity 96.4%; Pred. No. 3.7e-10;
RESULT 1204
ID ABV57899 standard; cDNA; 565 BP.
DE Human prostate expression marker cDNA 57890.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 133.4; DB 5; Length 565;
Best Local Similarity 99.3%; Pred. No. 3.6e-10;
RESULT 1205
ID AAH71472 standard; cDNA; 597 BP.
DE Human cervical cancer marker nucleic acid 2746.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 133.4; DB 4; Length 597;
Best Local Similarity 89.9%; Pred. No. 3.6e-10;
RESULT 1206
ID ACN87353 standard; DNA; 611 BP.
DE Breast cancer related marker, seq id 8503.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.7%; Score 133.4; DB 11; Length 611;
Best Local Similarity 78.6%; Pred. No. 3.6e-10;
RESULT 1207
ID ACN87667 standard; DNA; 617 BP.
DE Breast cancer related marker, seq id 8817.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.7%; Score 133.4; DB 11; Length 617;
Best Local Similarity 78.0%; Pred. No. 3.6e-10;
RESULT 1208
ID AAH71551 standard; cDNA; 621 BP.
DE Human cervical cancer marker nucleic acid 2825.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 133.4; DB 4; Length 621;
Best Local Similarity 79.4%; Pred. No. 3.6e-10;
RESULT 1209
ID ABX49378 standard; cDNA; 237 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #14543.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.7%; Score 133.2; DB 8; Length 237;
Best Local Similarity 86.5%; Pred. No. 4e-10;
RESULT 1210
ID ACN48457 standard; cDNA; 424 BP.
DE Cotton primed seed EST Clone ID: LIB3825-025-Q6-K6-E6, SEQ:3238.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133.2; DB 13; Length 424;
Best Local Similarity 88.9%; Pred. No. 3.9e-10;
RESULT 1211
ID ACN55951 standard; cDNA; 543 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-030-Q6-N6-F11, SEQ:10732.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.

Query Match 4.7%; Score 133.2; DB 13; Length 543;
Best Local Similarity 91.6%; Pred. No. 3.9e-10;
RESULT 1212
ID ADG33178 standard; DNA; 1381 BP.
DE Human DNA differentially expressed in patients with SLE SeqID502.
PD WO2003090694-A2.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 4.7%; Score 133.2; DB 10; Length 1381;
Best Local Similarity 97.8%; Pred. No. 3.7e-10;
RESULT 1213
ID ABN80090 standard; DNA; 8186 BP.
DE Human chemically modified disease associated gene SEQ ID NO 107.
PD WO200200927-A2.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133.2; DB 6; Length 8186;
Best Local Similarity 88.9%; Pred. No. 3.5e-10;
RESULT 1214
ID ABK40075 standard; DNA; 9021 BP.
DE Human chemically pretreated gene sequence #79 strand 1.
PD WO200202806-A2.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133.2; DB 6; Length 9021;
Best Local Similarity 86.5%; Pred. No. 3.4e-10;
RESULT 1215
ID ABL34232 standard; DNA; 9021 BP.
DE Human immune system associated gene SEQ ID NO: 2205.
PD WO200200928-A2.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133.2; DB 6; Length 9021;
Best Local Similarity 86.5%; Pred. No. 3.4e-10;
RESULT 1216
ID ABK33988 standard; DNA; 9021 BP.
DE Human DNA for staging of Astrocytomas #37.
PD WO200202808-A2.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133.2; DB 6; Length 9021;
Best Local Similarity 86.5%; Pred. No. 3.4e-10;
RESULT 1217
ID ADA20388 standard; DNA; 9021 BP.
DE Prostate tumour related genomic DNA sample #27.
PD WO2002103042-A2.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133.2; DB 8; Length 9021;
Best Local Similarity 86.5%; Pred. No. 3.4e-10;
RESULT 1218
ID ADA84195 standard; DNA; 9021 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:53.
PD WO2002103041-A2.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133.2; DB 8; Length 9021;
Best Local Similarity 86.5%; Pred. No. 3.4e-10;
RESULT 1219
ID ABX43106 standard; cDNA; 365 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #8271.
PD US2002137139-A1.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.7%; Score 133; DB 8; Length 365;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
RESULT 1220
ID ABV38062 standard; cDNA; 425 BP.
DE Human prostate expression marker cDNA 38053.
PD WO200160860-A2.

PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 133; DB 5; Length 425;
Best Local Similarity 90.4%; Pred. No. 4.2e-10;
RESULT 1221
ID ACN49708 standard; cDNA; 554 BP.
DE Cotton primed seed EST Clone ID: LIB3825-025-Q6-N6-F6, SEQ:4489.
PD US2004123340-A1.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 554;
Best Local Similarity 100.0%; Pred. No. 4.1e-10;
RESULT 1222
ID ABV16074 standard; cDNA; 843 BP.
DE Human prostate expression marker cDNA 16065.
PD WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 133; DB 5; Length 843;
Best Local Similarity 79.2%; Pred. No. 4.1e-10;
RESULT 1223
ID ABQ54211 standard; cDNA; 970 BP.
DE Human ovarian antigen HHFBY53 cDNA, SEQ ID NO:91.
PD WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 6; Length 970;
Best Local Similarity 90.4%; Pred. No. 4e-10;
RESULT 1224
ID ABZ71397 standard; cDNA; 1687 BP.
DE Secreted protein-encoding gene 41 cDNA clone HDP5H53, SEQ ID NO:218.
PD WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 8; Length 1687;
Best Local Similarity 88.2%; Pred. No. 4e-10;
RESULT 1225
ID ADM67116 standard; DNA; 2090 BP.
DE Human homologue of murine adipocyte specific DNA SeqID 252.
PD WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGE INC.
Query Match 4.7%; Score 133; DB 12; Length 2090;
Best Local Similarity 90.4%; Pred. No. 3.9e-10;
RESULT 1226
ID ABK31264 standard; DNA; 6794 BP.
DE Signal transduction associated gene modified DNA #54.
PD WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 6794;
Best Local Similarity 79.7%; Pred. No. 3.7e-10;
RESULT 1227
ID ABL70219 standard; DNA; 6794 BP.
DE Chemically treated cell signalling DNA sequence#55.
PD WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 6794;
Best Local Similarity 79.7%; Pred. No. 3.7e-10;
RESULT 1228
ID AAS61174 standard; DNA; 6794 BP.
DE Human gene regulation-associated gene oligonucleotide #129.
PD WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 6794;
Best Local Similarity 79.7%; Pred. No. 3.7e-10;
RESULT 1229
ID ABL32230 standard; DNA; 14568 BP.

DE Human immune system associated gene SEQ ID NO: 203.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIC-) EPIGENOMICS AG.
 Query Match 4.7%; Score 133; DB 6; Length 14568;
 Best Local Similarity 85.5%; Pred. No. 3.6e-10;
 RESULT 1230
 ID ABV08830 standard; cDNA; 420 BP.
 DE Human prostate expression marker cDNA 8821.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 132.8; DB 5; Length 420;
 Best Local Similarity 72.7%; Pred. No. 4.5e-10;
 RESULT 1231
 ID AAI87434 standard; cDNA; 454 BP.
 DE Human polynucleotide SEQ ID NO 7494.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.7%; Score 132.8; DB 4; Length 454;
 Best Local Similarity 89.4%; Pred. No. 4.5e-10;
 RESULT 1232
 ID ACN59858 standard; cDNA; 531 BP.
 DE CotCon gynoecium tissue EST Clone ID: LIB3829-035-Q1-K6-D8, SEQ:14639.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.7%; Score 132.8; DB 13; Length 531;
 Best Local Similarity 98.5%; Pred. No. 4.4e-10;
 RESULT 1233
 ID AAF72410 standard; cDNA; 1985 BP.
 DE Human PRO271 cDNA.
 PN WO200104311-A1.
 PD 18-JAN-2001.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 4; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1234
 ID AAS45938 standard; cDNA; 1985 BP.
 DE Human DNA encoding PRO polypeptide sequence #14.
 PN WO200168848-A2.
 PD 20-SEP-2001.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 4; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1235
 ID ACA60174 standard; cDNA; 1985 BP.
 DE Human cDNA for secreted/transmembrane protein PRO271.
 PN US2003003530-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1236
 ID ACA9398 standard; cDNA; 1985 BP.
 DE cDNA encoding human PRO polypeptide #14.
 PN US2003036141-A1.
 PD 20-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1237
 ID ACA73398 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003036146-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1238
 ID ACA05713 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003036162-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1239
 ID ACA66547 standard; cDNA; 1985 BP.
 DE cDNA encoding human PRO protein #14.
 PN US2003036137-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1240
 ID ACD07574 standard; cDNA; 1985 BP.
 DE Novel human secreted and transmembrane protein PRO271 cDNA.
 PN US2002197671-A1.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1241
 ID ACF20122 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003040063-A1.
 PD 27-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1242
 ID ACF19508 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003040064-A1.
 PD 27-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1243
 ID ACD21796 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003027267-A1.
 PD 06-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1244
 ID ACF12961 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003036160-A1.
 PD 20-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1245
 ID ACD25064 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003044925-A1.
 PD 06-MAR-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1246
 ID ACF00113 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003054474-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1247
 ID ACA72170 standard; cDNA; 1985 BP.
 DE Novel human secreted and transmembrane protein PRO271 cDNA.
 PN US2003032114-A1.
 PD 13-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;

RESULT 1248
ID ACD04694 standard; cDNA; 1985 BP.
DE Human secreted and transmembrane protein PRO271 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1249
ID ACD18155 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1250
ID ACD08162 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1251
ID ABX71622 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO271.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1252
ID ACA88596 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1253
ID ACA70038 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1254
ID ACD12260 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1255
ID AC74175 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1256
ID ACD15803 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1257
ID ACD25371 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1258

ID ACD17848 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1259
ID ACC88135 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1260
ID ACD21489 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1261
ID ACD18556 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1262
ID ACH06954 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane polypeptide PRO271 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1263
ID ABX98166 standard; cDNA; 1985 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 27.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1264
ID ACD13917 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1265
ID ACD09697 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1266
ID ACC88442 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1267
ID ACD21182 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1268
ID ABX75554 standard; cDNA; 1985 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO271.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1269
ID ABX97757 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1270
ID ACA97233 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1271
ID ACA57696 standard; cDNA; 1985 BP.
DE Human PRO271 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1272
ID ACD14224 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1273
ID ACC91007 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1274
ID ACC88749 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1275
ID ACD06946 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1276
ID ACA67397 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1277
ID ACC81452 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1278
ID ACC89056 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1279
ID ACC86412 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1280
ID ACC89670 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1281
ID ACC92849 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1282
ID ACA72477 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1283
ID ACA88995 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1284
ID ACA69731 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1285
ID ACA96874 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1286
ID ACA90870 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1287
ID ACA70652 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1288
ID ACA95162 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1289
 ID ACA86105 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003027263-A1.
 PD 06-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1290
 ID ACC89977 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003027271-A1.
 PD 06-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1291
 ID ACD12585 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US20030316125-A1.
 PD 20-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1292
 ID ACF19815 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003040068-A1.
 PD 27-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1293
 ID ABX76759 standard; cDNA; 1985 BP.
 DE Human PRO polynucleotide #14.
 PN US2003027280-A1.
 PD 06-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1294
 ID ABX96191 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein cDNA, #40.
 PN US2002160374-A1.
 PD 31-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1295
 ID ACA73091 standard; cDNA; 1985 BP.
 DE Novel human secreted and transmembrane protein PRO271 cDNA.
 PN US2003022300-A1.
 PD 30-JAN-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1296
 ID ACA05512 standard; cDNA; 1985 BP.
 DE cDNA encoding human secreted protein PRO271.
 PN US2003023054-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1297
 ID ACA68634 standard; cDNA; 1985 BP.
 DE Novel human secreted and transmembrane protein PRO271 cDNA.
 PN US20030316136-A1.
 PD 20-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1298
 ID ACA74478 standard; cDNA; 1985 BP.
 DE cDNA encoding human PRO polypeptide #14.
 PN US20030316138-A1.
 PD 20-FEB-2003.

Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1299
 ID ACA70345 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003032109-A1.
 PD 13-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1300
 ID ACD14531 standard; cDNA; 1985 BP.
 DE Human PRO polynucleotide #14.
 PN US2003040066-A1.
 PD 27-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1301
 ID ACD20179 standard; cDNA; 1985 BP.
 DE Human secreted / transmembrane polypeptide PRO271 cDNA.
 PN US20030316060-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1302
 ID ACA68203 standard; cDNA; 1985 BP.
 DE Novel human secreted and transmembrane protein PRO271 cDNA.
 PN US2003032104-A1.
 PD 13-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1303
 ID ABX98668 standard; cDNA; 1985 BP.
 DE Novel human secreted and transmembrane protein PRO271 cDNA.
 PN US20030316157-A1.
 PD 20-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1304
 ID ACC81145 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003032120-A1.
 PD 13-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1305
 ID ACA95469 standard; cDNA; 1985 BP.
 DE Novel human secreted and transmembrane protein PRO271 cDNA.
 PN US20030316155-A1.
 PD 20-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1306
 ID ACD04387 standard; cDNA; 1985 BP.
 DE Novel human secreted and transmembrane protein PRO271 cDNA.
 PN US2003022296-A1.
 PD 30-JAN-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1307
 ID ACC87828 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003027281-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1308
 ID ACF12490 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003040058-A1.
 PD 27-FEB-2003.
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;

Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1309
ID ACA96205 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1310
ID ACA64979 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1311
ID ACA73705 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1312
ID ACA74117 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1313
ID ACA96512 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1314
ID ACD10618 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1315
ID ACC91314 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1316
ID ACD02649 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US20030322301-A1.
PD 30-JAN-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1317
ID ACC87214 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1318
ID ACC85798 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1319

ID ACA5286 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1320
ID ACA94103 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1321
ID ACA97847 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1322
ID ACA91349 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1323
ID ACA90563 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1324
ID ACD16110 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1325
ID ACD17271 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1326
ID ACC91928 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1327
ID ACA74785 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1328
ID ACA91656 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1329
ID ACA71300 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032116-A1.

PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1330
ID ACC90700 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1331
ID ACA65710 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO protein #14.
PN US20030316139-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1332
ID ACA54982 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1333
ID ACA94855 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1334
ID ACD16417 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1335
ID ACD15496 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US200303152-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1336
ID ABX16599 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 8; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1337
ID ACA97540 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1338
ID ACA98989 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1339
ID ACC91621 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040076-A1.
PD 27-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1340
ID ACD11032 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US200308352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1341
ID ACD14882 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1342
ID ACD19817 standard; cDNA; 1985 BP.
DE Human secreted / transmembrane polypeptide PRO271 cDNA.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1343
ID ACD11646 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1344
ID ACC95775 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1345
ID ACF16338 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1346
ID ACF02456 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1347
ID ACF02763 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1348
ID ACF21350 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1349

ID ACF10034 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1350
ID ACF77927 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1351
ID ACD4632 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1352
ID ACD49395 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1353
ID ACF28162 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1354
ID ACD8852 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1355
ID ACD84247 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1356
ID ACD99021 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1357
ID ADA77779 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1358
ID ACF48763 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1359
ID ADB29417 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1360
ID ACD09083 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1361
ID ACF11876 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1362
ID ACF41110 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1363
ID ACF15724 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1364
ID ACF16031 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1365
ID ACD31858 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1366
ID ACF18666 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1367
ID ACF09113 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;

Best Local Similarity 86.9%; Pred. No. 4.2e-10;
ID ACF78234 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1369
ID ACF51833 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1370
ID ACF26320 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1371
ID ACF24113 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1372
ID ACF63424 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1373
ID ACF50298 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1374
ID ACH07769 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1375
ID ACF13575 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1376
ID ACD41501 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1377

ID ACF31914 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1378
ID ACF23192 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1379
ID ACF39882 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1380
ID ACD45404 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1381
ID ACF53061 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1382
ID ACF27241 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1383
ID ACF45079 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1384
ID ACF29697 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1385
ID ACD89773 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1386
ID ACD84554 standard; cDNA; 1985 BP.

DE Human PRO polynucleotide #14.
 PN US2003068703-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1387
 ID ACD98714 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003068732-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1388
 ID ACF77006 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003082717-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1389
 ID ACF76699 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003104548-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1390
 ID ACF49684 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003104542-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1391
 ID ACF49991 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003104543-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1392
 ID ACD09390 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003036127-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1393
 ID ACD08469 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003040061-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1394
 ID ACF12193 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003036130-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1395
 ID ACC94691 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003054468-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1396

ID ACD22410 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003054470-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1397
 ID ACF15110 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003044917-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1398
 ID ACC97205 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003044929-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1399
 ID ADA18273 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein cDNA, #42.
 PN US2003039971-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1400
 ID ACD66964 standard; cDNA; 1985 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO271.
 PN US2003045693-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1401
 ID ACC92235 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003059880-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1402
 ID ACF13882 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003064465-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1403
 ID ACF14189 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003054478-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1404
 ID ACF09420 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003068718-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1405
 ID ACD45711 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003064454-A1.

PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1406
 ID ACD47860 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003064461-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1407
 ID ACD67591 standard; cDNA; 1985 BP.
 DE cDNA encoding human PRO polypeptide #14.
 PN US2003068724-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1408
 ID ACF25399 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003068727-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1409
 ID ACF29083 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003068772-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1410
 ID ACD84861 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003068714-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1411
 ID ACF83940 standard; cDNA; 1985 BP.
 DE Human PRO polynucleotide #14.
 PN US2003068758-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1412
 ID ACD87931 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003068776-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1413
 ID ACF30618 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003069407-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1414
 ID ACF32221 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003104555-A1.
 PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1415
 ID ACH11881 standard; cDNA; 1985 BP.
 DE cDNA encoding human PRO polypeptide #14.
 PN US2003049768-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1416
 ID ACH12188 standard; cDNA; 1985 BP.
 DE cDNA encoding human PRO polypeptide #14.
 PN US2003049771-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1417
 ID ACD40580 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003032134-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1418
 ID ACF18052 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003054481-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1419
 ID ACF08499 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003049778-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1420
 ID ACF311300 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003049782-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1421
 ID ACF52140 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003054476-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1422
 ID ACD50009 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003068733-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1423
 ID ACF38712 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003068592-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;
 RESULT 1424
 ID ACF38712 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003068592-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;

```
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1424
ID ACF26627 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1425
ID ACF24727 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1426
ID ACF46307 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1427
ID ACF27855 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1428
ID ACD89159 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1429
ID ACF63731 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1430
ID ACF60371 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1431
ID ACHI2495 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1432
ID ACH09918 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1433
ID ACD03773 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1434
ID ACD10311 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1435
ID ACD11953 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1436
ID ACD83125 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1437
ID ACF42338 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1438
ID ADA16248 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1439
ID ACF18359 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1440
ID ACF02149 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1441
ID ACF21657 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1442
ID ACF10341 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073169-A1.
PD 17-APR-2003.
```

Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1443
ID ACF37393 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1444
ID ACF44755 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1445
ID ACD90387 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1446
ID ACD91000 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1447
ID ACF30311 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1448
ID ACD87010 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1449
ID ACF60064 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1450
ID ACF46614 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1451
ID ACF75471 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1452

ID ADA79571 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1453
ID ACF17131 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1454
ID ACF22885 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1455
ID ACF07885 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1456
ID ACF08192 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1457
ID ACF40496 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1458
ID ACF53675 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1459
ID ACD46939 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1460
ID ACF47842 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;
RESULT 1461
ID ACF47228 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068753-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1462
ID ACF46000 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1463
ID ACD86089 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1464
ID ACF52447 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1465
ID ACF52754 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1466
ID ACF64747 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1467
ID ACF76392 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1468
ID ACF61292 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1469
ID ACF61599 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1470
ID ACD30630 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;

RESULT 1471
ID ACD31551 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1472
ID ACD32472 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1473
ID ACF17438 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1474
ID ACF07271 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1475
ID ACF20429 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1476
ID ACF21043 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1477
ID ACF20736 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1478
ID ACD47553 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1479
ID ACF47535 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1480
ID ACF53368 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068679-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1481
ID ACD86703 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1482
ID ACH04951 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1483
ID ACF44448 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1484
ID ADA42393 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1485
ID ADA81298 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1486
ID ACD22103 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1487
ID ACD24450 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1488
ID ACD39653 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1489
ID ACD3960 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1490
ID ACF13268 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1491
ID ACF03070 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1492
ID ACD23303 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1493
ID ACF78541 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1494
ID ACF11262 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1495
ID ACF50605 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1496
ID ACF34100 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1497
ID ACD46325 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1498
ID ACD48167 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;
Query Match
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1499
ID ACF27548 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;
RESULT 1500
ID ACP24420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 132.8; DB 9; Length 1985;
Best Local Similarity 86.9%; Pred. No. 4.2e-10;

This Page Blank (uspto)

OM protein - protein search, using sw model
Run on: May 8, 2005, 15:55:03 ; Search time 77 Seconds
(without alignments)
3616.461 Million cell updates/sec

Title: US-10-063-692-38
Perfect score: 3945
Sequence: 1 MELGCTWQLGLTFLQLLLIS.....LSTAFKVLFPKDWIERNMK 720
Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%

Database : A_Geneseq_16Dec04:*
Listing first 1500 summaries
Maximum Match 100%

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AA66695	standard; protein; 720 AA.				
DE	Membrane-bound protein PRO1344.					
PN	WO9963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 3;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 2						
ID	AAU29108	standard; protein; 720 AA.				
DE	Human PRO polypeptide sequence #85.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 4;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 3						
ID	AAB87544	standard; protein; 720 AA.				
DE	Human PRO1344.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 4;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 4						
ID	AAB65218	standard; protein; 720 AA.				
DE	Human PRO1344 (UNQ699) protein sequence SEQ ID NO:231.					
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 4;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 5						
ID	ABG95869	standard; protein; 720 AA.				
DE	Human secreted/transmembrane protein PRO1344.					
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 5;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 6						
ID	ABU58484	standard; protein; 720 AA.				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description

RESULT 1

ID AAY6695 standard; protein; 720 AA.

DE Membrane-bound protein PRO1344.

PN WO9963088-A2.

PD 09-DEC-1999.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 3; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 2

ID AAU29108 standard; protein; 720 AA.

DE Human PRO polypeptide sequence #85.

PN WO200168848-A2.

PD 20-SEP-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 4; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 3

ID AAB87544 standard; protein; 720 AA.

DE Human PRO1344.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 4; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 4

ID AAB65218 standard; protein; 720 AA.

DE Human PRO1344 (UNQ699) protein sequence SEQ ID NO:231.

PN WO200073454-A1.

PD 07-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 4; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 5

ID ABG95869 standard; protein; 720 AA.

DE Human secreted/transmembrane protein PRO1344.

PN US2002119130-A1.

PD 29-AUG-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 5; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 6

ID ABU58484 standard; protein; 720 AA.

DE Human PRO polypeptide #85.

PN US2003027272-A1.

PD 06-FEB-2003.

Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 7

ID ABU89032 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.

PN US2003032127-A1.

PD 13-FEB-2003.

Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 8

ID ABU84347 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.

PN US2003032112-A1.

PD 13-FEB-2003.

Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 9

ID ABR66221 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003027278-A1.

PD 06-FEB-2003.

Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 10

ID ABR65611 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003036159-A1.

PD 20-FEB-2003.

Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 11

ID ABU99551 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.

PN US2003040070-A1.

PD 27-FEB-2003.

Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 12

ID ABUS8033 standard; protein; 720 AA.

DE Human PRO polypeptide #65.

PN US2003027163-A1.

PD 06-FEB-2003.

Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 13

ID ABUS9111 standard; protein; 720 AA.

DE Novel human secreted or transmembrane protein PRO1344.

PN US2002132252-A1.

PD 19-SEP-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 14

ID ABU82623 standard; protein; 720 AA.

DE Human secreted/transmembrane protein PRO1344.

PN US2003032023-A1.

PD 13-FEB-2003.

Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 15

ID ABU82790 standard; protein; 720 AA.

DE Human PRO polypeptide #85.

PN US2003032113-A1.

PD 13-FEB-2003.

Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 16

ID ABU89911 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.

PN US2003036147-A1.

PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 17
ID ABR68160 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 18
ID ABU60542 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 19
ID ABU96213 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 20
ID ABU92644 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 21
ID ABO08721 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 22
ID ABO02773 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 23
ID ABR74927 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 24
ID ABR94689 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 25
ID ABU13924 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 26
ID ABU85662 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036140-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 27
ID ABU98822 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 28
ID ABU98037 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 29
ID ABU91743 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 30
ID ABU9436 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 31
ID ABU86277 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 32
ID ABU67490 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 33
ID ABU80518 standard; protein; 720 AA.
DE Human PRO protein #85.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 34
ID ABU72509 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 35
ID ABU90894 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 36
ID ABO33953 standard; protein; 720 AA.

DE Human secreted/transmembrane protein PRO1344.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 37
ID ABR99436 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 38
ID ABR98826 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 39
ID ABO16349 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 40
ID ABR92249 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 41
ID ABO18890 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 42
ID ABR78311 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 43
ID ABU71970 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 44
ID ABU85047 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 45
ID ABO00186 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 46
ID ABO11518 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 47
ID ABO02163 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 48
ID ABU89737 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 49
ID ABU83432 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 50
ID ABO06233 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 51
ID ABR59269 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 52
ID ABO09331 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 53
ID ABO19195 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 54
ID ABO11213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 55
ID ABR66831 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 56
ID ABO16044 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040060-A1.

PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 57
ID ABO13750 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 58
ID ABU71524 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 59
ID ABU65653 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, SEQ ID 170.
PN US200303156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 60
ID ABO07501 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 61
ID ABO03688 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 62
ID ABR67136 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 63
ID ABO15739 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 64
ID ABU56020 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, PRO1344.
PN US200302298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 65
ID ABU72305 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 66
ID ABU65348 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032102-A1.

PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 67
ID ABU95293 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 68
ID ABU71196 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 69
ID ABO07806 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 70
ID ABR70047 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 71
ID ABR69380 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 72
ID ABO01521 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 73
ID ABU81323 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 74
ID ABR60120 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 75
ID ABU90978 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 76
ID ABR67855 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027269-A1.

PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 77
ID ABR65243 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 78
ID ABR68465 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 79
ID ABR71877 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 80
ID ABUS9258 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 81
ID ABUS5357 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 82
ID ABUS9047 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 83
ID ABUS3127 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 84
ID ABUS4983 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 85
ID ABUS0531 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 86
ID ABUS4042 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 87
ID ABUS3693 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 88
ID ABO25955 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 89
ID ABR64938 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 90
ID ABO27299 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 91
ID ABR68770 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 92
ID ABO06586 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 93
ID ABR99131 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 94
ID ABUS7015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 95
ID ABUS5967 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 96
ID ABUS2254 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;

```
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 97
ID ABR66526 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027281-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 98
ID ABR90944 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 99
ID ABO08111 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 100
ID ABU92494 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 101
ID ABU1822 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 102
ID ABU65986 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 103
ID ABU8164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 104
ID ABR59815 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 105
ID ABU94003 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 106
ID ABU99856 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 107
ID ABR66526 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 108
ID ABR90944 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 109
ID ABO53279 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 110
ID ABUS8964 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 111
ID ABU94371 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 112
ID ABU79253 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 113
ID ABU86582 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 114
ID ABU86887 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 115
ID ABU94676 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 116
ID ABO04603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
```

RESULT 117
ID ABR70352 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 118
ID ABR92342 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 119
ID ABR98517 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 120
ID ABR65916 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 121
ID ABR64633 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 122
ID ABR59407 standard; protein; 720 AA.
DE Novel human secreted or transmembrane protein PRO1109.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 123
ID ABR79558 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 124
ID ABR92949 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 125
ID ABR95908 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 126
ID ABR91128 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 127
ID ABR90221 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 128
ID ABO09636 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 129
ID ABO10908 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 130
ID ABR70962 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 131
ID ABR98281 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 132
ID ABR7570 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 133
ID ABR91438 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 134
ID ABR9286 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 135
ID ABR84652 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 136
ID ABR69742 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 137
ID ABR80119 standard; protein; 720 AA.
DE Human PRO protein #85.

PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 138
ID ABU82493 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 139
ID ABU92173 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 140
ID ABU93388 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017541-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 141
ID ABO09941 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003017543-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 142
ID ABO09026 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036152-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 143
ID ABU96457 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 144
ID ABU10879 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 145
ID ABU10594 standard; protein; 720 AA.
DE Human secreted/transmembrane protein #85.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 146
ID ABU81631 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 147

ID ABU72127 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 148
ID ABU95603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032115-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 149
ID ABU96812 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032140-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 150
ID ABR70657 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 151
ID ABO05008 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 152
ID ABO08416 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 153
ID ABU88570 standard; protein; 720 AA.
DE Human secreted and transmembrane polypeptide PRO1344.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 154
ID ABO34084 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 155
ID ABO05623 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 156
ID ABR74012 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 157
ID ABR95604 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 158
ID ABR80901 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 159
ID ABR81206 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 160
ID ABM00902 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 161
ID ABR88504 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003058743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 162
ID ABM77325 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 163
ID ABO28809 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 164
ID ABO31554 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 165
ID ABM07971 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 166

ID ABO40451 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 167
ID ABO35876 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 168
ID ABO44015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 169
ID ADA77922 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 170
ID ABM24810 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 171
ID ABO03078 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 172
ID ABR90334 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 173
ID ABM17248 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 174
ID ABR94994 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 175
ID ABR95299 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

ID ABM29080 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 195
ID ABM07056 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 196
ID ABM21150 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 197
ID ABM09496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 198
ID ABO41366 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 199
ID ABO36181 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 200
ID ABO43710 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 201
ID ABM76410 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 202
ID ABM76106 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 203
ID ABM25725 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 204
ID ABM26030 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 205
ID ADA21428 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 206
ID ABO03383 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 207
ID ABO02468 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 208
ID ABO44257 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 209
ID ABR90639 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 210
ID ABR73707 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 211
ID ABO16959 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 212
ID ABR94384 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 213
ID ABR75891 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 214
ID ABR71267 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 215
ID ABR93164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 216
ID ABR93469 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 217
ID ADA10215 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, PRO1344.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 218
ID ABR87894 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 219
ID ABO27894 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 220
ID ABO30029 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 221
ID ABO33238 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 222
ID ABO4926 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 223
ID ABO8886 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 224
ID ABO36486 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 225
ID ABO35571 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 226
ID ABO39536 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 227
ID ABM10411 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 228
ID ABM11936 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 229
ID ABO52082 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 230
ID ABO52387 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 231
ID ADA19900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 232
ID ABO23705 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 233
ID ADB17283 standard; protein; 720 AA.
DE Human transmembrane PRO polypeptide (SeqID 38).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 234
ID ADA17759 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 235
ID ABR97191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 236
ID ABR86979 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 237
ID ABM11021 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 238
ID ABM28165 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 239
ID ABO32164 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 240
ID ABM15291 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 241
ID ABM06446 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 242
ID ABM04257 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 243
ID ABM22370 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 244
ID ABM07666 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 245
ID ABO40756 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 246
ID ABM35403 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 247
ID ABM33166 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 248
ID ABO52692 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 249
ID ABO50252 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 250
ID ABU99246 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040055-A1.

PD, 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 251
ID ABO04298 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US20030316164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 252
ID ABO05928 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 253
ID ABM18468 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 254
ID ADA27867 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 255
ID ABR97496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 256
ID ABR80596 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 257
ID ABM01207 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 258
ID ABR88809 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 259
ID ABM13461 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 260
ID ABM20845 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 261
ID ABO41976 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 262
ID ABO42586 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 263
ID ABM10106 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 264
ID ABO38621 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 265
ID ABM32861 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 266
ID ABM22675 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 267
ID ABM74886 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 268
ID ADA79714 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 269
ID ABR96276 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 270
ID ABM02427 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 271
ID ABR86369 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 272
ID ABR86674 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 273
ID ABM16638 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 274
ID ABM29690 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 275
ID ABO29114 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 276
ID ABM23895 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 277
ID ABM23285 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 278
ID ABM22065 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 279
ID ABO37706 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 280
ID ABM28470 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 281
ID ABM28775 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 282
ID ABM66419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 283
ID ABM75801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 284
ID ABM34081 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 285
ID ABM34386 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 286
ID ABO20317 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 287
ID ABO21232 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 288
ID ABO22147 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054477-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 289
ID ADA20072 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 290
ID ABO34185 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 291
ID ABR36581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 292
ID ADA94447 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 293
ID ABR85759 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 294
ID ABR99741 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 295
ID ABM00597 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 296
ID ABM00292 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 297
ID ABO29724 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 298

ID ABM23590 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 299
ID ABM29385 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 300
ID ABO38316 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 301
ID ABO45616 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 302
ID ABM20540 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 303
ID ADA81441 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 304
ID ABO16654 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 305
ID ABO18280 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 306
ID ABO22707 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 307
ID ABO23012 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054461-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 308
ID ABR92554 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 309
ID ABR81511 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 310
ID ABR77935 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 311
ID ABR89724 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 312
ID ABM26640 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 313
ID ABM13766 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 314
ID ABO28504 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 315
ID ABO30334 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 316
ID ABM07361 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 317
ID ABM03952 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 318
ID ABO37096 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 319
ID ABO41671 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 320
ID ABO35266 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 321
ID ABM25115 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 322
ID ABO47507 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 323
ID ABO47812 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 324
ID ABO48422 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 325
ID ABO51472 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 326
ID ABO51777 standard; protein; 720 AA.

DE Human PRO polypeptide #85.
PN US2003049767-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 327
ID ABO50557 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 328
ID ABR79681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 329
ID ABM16943 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 330
ID ABO17975 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 331
ID ABO20927 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 332
ID ABR9686 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 333
ID ADA38672 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 334
ID ABM12241 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 335
ID ABM16333 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 336
ID ABO24200 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 337
ID ABM14681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 338
ID ABM04562 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 339
ID ABM06751 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 340
ID ABM09191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 341
ID ABO39231 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 342
ID ABM75496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 343
ID ABM25420 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 344
ID ABM19930 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 345
ID ABO46836 standard; protein; 720 AA.
DE Human PRO polypeptide #85.

PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 346
ID ABO47141 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 347
ID ADA83239 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 348
ID ABR71572 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 349
ID ABR72182 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 350
ID ABR98521 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 351
ID ABO6891 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 352
ID ABR94844 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 353
ID ABR73402 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 354
ID ABR76496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200304932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 355
ID ABR73097 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 356
ID ABM18163 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 357
ID ABO20622 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 358
ID ABO25365 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 359
ID ABO25670 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 360
ID ABR94079 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 361
ID ADA92793 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 362
ID ABR79986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 363
ID ABM1326 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 364
ID ABO32933 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 365
ID ABR73097 standard; protein; 720 AA.

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 365
ID ABO30639 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 366
ID ABO30944 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 367
ID ABM27250 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 368
ID ABM29995 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 369
ID ABM05531 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 370
ID ABM15596 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 371
ID ABM08581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 372
ID ABO42281 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 373
ID ABO38011 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 374
ID ABO45921 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 375
ID ABM66724 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 376
ID ADB20282 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 377
ID ABM19625 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 378
ID ABO49337 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 379
ID ABO49642 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 380
ID ADA78534 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 381
ID ABR88199 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 382
ID ADA00369 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 383
ID ABM26945 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068739-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 384
ID ABM03342 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068763-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 385
ID ABO39841 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068689-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 386
ID ABO49947 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049776-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 387
ID ABO50862 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049780-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 388
ID ABO05318 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036126-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 389
ID ABR74622 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044924-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 390
ID ABR77101 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044927-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 391
ID ABM17858 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040072-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 392
ID ABR95909 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040073-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 393
ID ABO21842 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054475-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 394
ID ABO20012 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032124-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 395
ID ABO24315 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003084467-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 396
ID ABR86064 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049759-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 397
ID ABM10716 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064455-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 398
ID ABM76715 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054465-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 399
ID ABR89419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073170-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 400
ID ABM12546 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073176-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 401
ID ABM05836 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068717-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 402
ID ABO34961 standard; protein; 720 AA.
DE Human PRO polypeptide #85.

[illegible]

ID ABO31249 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 422
ID ABO14376 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 423
ID ABO09801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 424
ID ABO38926 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 425
ID ABO34691 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 426
ID ABO51167 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 427
ID ABO03993 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 428
ID ABO10463 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 429
ID ABO53170 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 430
ID ABR77706 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 431
ID ABR78916 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 432
ID ABO24010 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 433
ID ABR93774 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 434
ID ABO01817 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 435
ID ABO78240 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049784-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 436
ID ABR90029 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 437
ID ADA22354 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 438
ID ABO27555 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 439
ID ABO31356 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 440
ID ABO31859 standard; protein; 720 AA.

Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 460
ID ABM22980 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 461
ID ABM30300 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 462
ID ABM21760 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 463
ID ABM21455 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 464
ID ABM14986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 465
ID ABO41061 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 466
ID ABO36791 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 467
ID ABO37401 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 468
ID ABM75191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 469
ID ABM33471 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 470
ID ABO46226 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 471
ID ADA82605 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 472
ID ADB85611 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 473
ID ADB96239 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 474
ID ABM31825 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 475
ID ABM31215 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 476
ID ADB85913 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 477
ID ABM32130 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 478
ID ABM32435 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 479
ID ADB68290 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 480
ID ADB68097 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 481
ID ABM31520 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 482
ID ABM30910 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 483
ID ADB90914 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 484
ID ADC57711 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 485
ID ADC55075 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 486
ID ADC11942 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 487
ID ADC06994 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 488
ID ADC56364 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 489
ID ADC17173 standard; protein; 720 AA.
DE Mammalian PRO polypeptide (seqID 38).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 490
ID ADC07419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 491
ID ADC11409 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 492
ID ADC14871 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 493
ID ADC52366 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 494
ID ADC14531 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 495
ID ADD08063 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 496
ID ADC81888 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 497
ID ADD07530 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002193299-A1.
PD 19-DEC-2002.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 498
ID ADC82421 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 499
ID ADD05643 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 500
ID ADD08601 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 501
ID ADD06850 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 502
ID ADC83097 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 503
ID ADD55204 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 504
ID ADD36042 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 505
ID ADD56162 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 506
ID ADD54600 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 507
ID ADE26754 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.

PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 508
ID ADE26221 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 509
ID ADF67158 standard; protein; 720 AA.
DE Human PRO1344 amino acid sequence SEQ ID NO:231.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 510
ID ADG01043 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 511
ID ADG08596 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 512
ID ADG02638 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 513
ID ADG01345 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 514
ID ADF95520 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 515
ID ADF95217 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 516
ID ADG12335 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;

```
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 517
ID ADH24070 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 518
ID ADH34096 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 519
ID ADH29929 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 520
ID ADH23900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 521
ID ADH08995 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 522
ID ADG85304 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 523
ID ADH24580 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 524
ID ADH37436 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 525
ID ADH02025 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 526
ID ADH37606 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 527
ID ADG85644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 528
ID ADH24240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 529
ID ADH38534 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 530
ID ADG83655 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 531
ID ADH29463 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 532
ID ADH27579 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 533
ID ADH37776 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 534
ID ADH37953 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 535
ID ADH29463 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
```

ID ADH57373 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 536
ID ADH53515 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 537
ID ADH53685 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 538
ID ADH52021 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 539
ID ADH49876 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 540
ID ADI25386 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 541
ID ADH90179 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 542
ID ADI25556 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 543
ID ADH97730 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 544
ID ADI35412 standard; protein; 720 AA.

DE Human PRO polypeptide #65.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 545
ID ADI03578 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 546
ID ADI11935 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 547
ID ADH90009 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 548
ID ADH99904 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 549
ID ADH98410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 550
ID ADI11085 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 551
ID ADI11595 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 552
ID ADH98240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 553
ID ADH98580 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181708-A1.
PD 25-SEP-2003.

```
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 554
ID ADH98070 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 555
ID ADI05058 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 556
ID ADI03408 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 557
ID ADI04803 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 558
ID ADH78257 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 559
ID ADI19601 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 560
ID ADH90349 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 561
ID ADI03068 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 562
ID ADH77917 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 563
ID ADH97900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 564
ID ADI01285 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 565
ID ADI01980 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 566
ID ADI03238 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 567
ID ADI11425 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 568
ID ADI02327 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 569
ID ADI11765 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 570
ID ADI05402 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 571
ID ADH79474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
```

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 572
ID ADI19431 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 573
ID ADI05232 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 574
ID ADH79644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 575
ID ADI01470 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 576
ID ADI01640 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 577
ID ADI01810 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 578
ID ADH79814 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 579
ID ADI04632 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 580
ID ADI02768 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 581
ID ADH78087 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 582
ID ADI25726 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 583
ID ADI25896 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 584
ID ADK65408 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 585
ID ADH98750 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 586
ID ADH79991 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 587
ID ADL32776 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 588
ID ADM30310 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 589
ID ADL93722 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 590
ID ADL93722 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

ID ADC52176 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 591
ID ADE74307 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 592
ID ADE74919 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 593
ID ADF35357 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003194750-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 594
ID ADG11607 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 595
ID ADF96132 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 596
ID ADG04403 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 597
ID ADG00563 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 598
ID ADH06608 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 599
ID ADH06438 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 600
ID ADG68859 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 601
ID ADH27749 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 602
ID ADH25090 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 603
ID ADH33722 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 604
ID ADG82819 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 605
ID ADH02365 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 606
ID ADH07972 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 607
ID ADG69369 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 608
ID ADH39190 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 609
ID ADH26100 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 610
ID ADG83930 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 611
ID ADH19477 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 612
ID ADG85474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 613
ID ADH06268 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 614
ID ADH30098 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 615
ID ADH24410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 616
ID ADH33069 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 617
ID ADG69539 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 618
ID ADH07802 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 619
ID ADG85814 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 620
ID ADH39360 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 621
ID ADH33552 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 622
ID ADH33892 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 623
ID ADH01102 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 624
ID ADG69709 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 625
ID ADH20970 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 626
ID ADH02195 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 627
ID ADG69199 standard; protein; 720 AA.

PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 646
 ID ADH90689 standard; protein; 720 AA.
 DE Novel human secreted and transmembrane protein PRO1344.
 PN US2003181701-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 647
 ID ADJ54808 standard; protein; 720 AA.
 DE Human PRO polypeptide #85.
 PN US2004023321-A1.
 PD 05-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 648
 ID ADJ98564 standard; protein; 720 AA.
 DE Novel human secreted and transmembrane protein PRO1344.
 PN US2003187137-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 649
 ID ADJ98734 standard; protein; 720 AA.
 DE Novel human secreted and transmembrane protein PRO1344.
 PN US2003187228-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 650
 ID ADH78893 standard; protein; 720 AA.
 DE Novel human secreted and transmembrane protein PRO1344.
 PN US2003181703-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 651
 ID ADJ99127 standard; protein; 720 AA.
 DE Novel human secreted and transmembrane protein PRO1344.
 PN US2003186408-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 652
 ID ADJ99297 standard; protein; 720 AA.
 DE Novel human secreted and transmembrane protein PRO1344.
 PN US2003187196-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 653
 ID ADJ98915 standard; protein; 720 AA.
 DE Novel human secreted and transmembrane protein PRO1344.
 PN US2003187242-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 654
 ID ADH79063 standard; protein; 720 AA.
 DE Novel human secreted and transmembrane protein PRO1344.
 PN US2003181702-A1.
 PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 655
 ID ADK00923 standard; protein; 720 AA.
 DE Human PRO polypeptide #19.
 PN US2003186407-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 656
 ID ADK14444 standard; protein; 720 AA.
 DE Novel human secreted and transmembrane protein PRO1344.
 PN US2003187229-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 657
 ID ADJ64579 standard; protein; 720 AA.
 DE Human PRO polypeptide #85.
 PN US2004038337-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 658
 ID ADM31475 standard; protein; 720 AA.
 DE Novel human secreted and transmembrane protein PRO1344.
 PN US2004048334-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 659
 ID ADM36522 standard; protein; 720 AA.
 DE Novel human secreted and transmembrane protein PRO1344.
 PN US2004053358-A1.
 PD 18-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 660
 ID ADM40327 standard; protein; 720 AA.
 DE Novel human secreted and transmembrane protein PRO1344.
 PN US2004048335-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 661
 ID ADM80893 standard; protein; 720 AA.
 DE Human PRO polypeptide #19.
 PN US2004058411-A1.
 PD 25-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 662
 ID ADN37935 standard; protein; 720 AA.
 DE Novel human secreted and transmembrane protein PRO1344.
 PN US2004091959-A1.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3945; DB 8; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;
 RESULT 663
 ID AAB70532 standard; protein; 720 AA.
 DE Human PRO2 protein sequence SEQ ID NO:4.
 PN WO200110902-A2.
 PD 15-FEB-2001.
 PA (CURA-) CURAGEN CORP.

Query Match 99.8%; Score 3939; DB 4; Length 720;
Best Local Similarity 99.7%; Pred. No. 3.1e-204;
RESULT 664
ID AAU00401 standard; protein; 720 AA.
DE Human secreted protein, POLY13.
PN WO200119856-A2.
PD 22-MAR-2001.
PA (CURA-) CURAGEN CORP.
Query Match 99.8%; Score 3939; DB 4; Length 720;
Best Local Similarity 99.7%; Pred. No. 3.1e-204;
RESULT 665
ID ADH89028 standard; protein; 720 AA.
DE Human polypeptide #13.
PN US2003198958-A1.
PD 23-OCT-2003.
PA (SHIM/) SHIMKETS R A.
PA (FERN/) FERNANDES E.
PA (HERR/) HERRMANN J L.
PA (LIUK/) LIU X.
PA (YANG/) YANG M.
PA (BOLD/) BOLDOG F L.
PA (SMIT/) SMITHSON G.
PA (RAST/) RASTELLI L.
Query Match 99.8%; Score 3939; DB 8; Length 720;
Best Local Similarity 99.7%; Pred. No. 3.1e-204;
RESULT 666
ID AAF8280 standard; protein; 720 AA.
DE Human TANGO 215 protein.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 99.8%; Score 3936; DB 3; Length 720;
Best Local Similarity 99.7%; Pred. No. 4.5e-204;
RESULT 667
ID AAB85891 standard; protein; 737 AA.
DE Human serine protease-like protein (hc-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 737;
Best Local Similarity 97.6%; Pred. No. 2.8e-203;
RESULT 668
ID AAB93670 standard; protein; 737 AA.
DE Human protein sequence SEQ ID NO:13202.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 737;
Best Local Similarity 97.6%; Pred. No. 2.8e-203;
RESULT 669
ID ADJ89990 standard; protein; 737 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1796.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 99.4%; Score 3921.5; DB 7; Length 737;
Best Local Similarity 97.6%; Pred. No. 2.8e-203;
RESULT 670
ID ADN04640 standard; protein; 737 AA.
DE Antipsoriatic protein sequence #505.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
Best Local Similarity 97.6%; Pred. No. 2.8e-203;
RESULT 671
ID ADS85034 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SeqID36.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.

Query Match 99.4%; Score 3921.5; DB 8; Length 737;
Best Local Similarity 97.6%; Pred. No. 2.8e-203;
RESULT 672
ID ADS85022 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SeqID24.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
Best Local Similarity 97.6%; Pred. No. 2.8e-203;
RESULT 673
ID AAB85893 standard; protein; 762 AA.
DE Human serine protease-like protein (hc-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 762;
Best Local Similarity 97.6%; Pred. No. 2.9e-203;
RESULT 674
ID AAB85892 standard; protein; 720 AA.
DE Mouse serine protease-like protein (mc-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 91.6%; Score 3612; DB 4; Length 720;
Best Local Similarity 90.1%; Pred. No. 1.3e-186;
RESULT 675
ID AAB09927 standard; protein; 719 AA.
DE Murine TANGO 215 protein.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 91.3%; Score 3602.5; DB 3; Length 719;
Best Local Similarity 90.1%; Pred. No. 4.1e-186;
RESULT 676
ID AAE19180 standard; protein; 649 AA.
DE Human protease, PRTS-17 protein.
PN WO200208396-A2.
PD 31-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 88.7%; Score 3500.5; DB 5; Length 649;
Best Local Similarity 90.0%; Pred. No. 1.2e-180;
RESULT 677
ID AAB70531 standard; protein; 567 AA.
DE Human Prol protein sequence SEQ ID NO:2.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 78.3%; Score 3089.5; DB 4; Length 567;
Best Local Similarity 99.5%; Pred. No. 1.4e-158;
RESULT 678
ID AAB49533 standard; protein; 570 AA.
DE Clone HPPEY75.
PN WO200061774-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.7%; Score 2946.5; DB 3; Length 570;
Best Local Similarity 96.8%; Pred. No. 7.2e-151;
RESULT 679
ID ADR41485 standard; protein; 551 AA.
DE Human CD-like molecule HSXDF41, SEQ ID NO:284.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.6%; Score 2944; DB 5; Length 551;
Best Local Similarity 99.3%; Pred. No. 9.5e-151;
RESULT 680
ID AAM41706 standard; protein; 499 AA.
DE Human polypeptide SEQ ID NO 6637.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.

Query Match 65.3%; Score 2577.5; DB 4; Length 499;
 Best Local Similarity 96.6%; Pred. No. 4.8e-131;
 RESULT 681
 ID AAE20817 standard; protein; 455 AA.
 DE Human gene 5 encoded secreted protein HSLGU75, SEQ ID NO:79.
 PN WO200218435-A1.
 PD 07-MAR-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 61.2%; Score 2413; DB 5; Length 455;
 Best Local Similarity 99.3%; Pred. No. 3.2e-122;
 RESULT 682
 ID ABG64652 standard; protein; 455 AA.
 DE Human albumin fusion protein #1327.
 PN WO20017137-A1.
 PD 18-OCT-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 61.2%; Score 2413; DB 5; Length 455;
 Best Local Similarity 99.3%; Pred. No. 3.2e-122;
 RESULT 683
 ID ADL77919 standard; protein; 455 AA.
 DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1401.
 PN US2004010134-A1.
 PD 15-JAN-2004.
 PA (ROSE/) ROSEN C A.
 PA (HASE/) HASELTINE W A.
 Query Match 61.2%; Score 2413; DB 8; Length 455;
 Best Local Similarity 99.3%; Pred. No. 3.2e-122;
 RESULT 684
 ID ADL06662 standard; protein; 417 AA.
 DE Human 373 cell conversion promoter FP938.
 PN CN1403477-A.
 PD 19-MAR-2003.
 PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
 Query Match 52.2%; Score 2059; DB 7; Length 417;
 Best Local Similarity 95.6%; Pred. No. 3.4e-103;
 RESULT 685
 ID AAM39920 standard; protein; 359 AA.
 DE Human polypeptide SEQ ID NO 3065.
 PN WO20015312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 48.4%; Score 1909; DB 4; Length 359;
 Best Local Similarity 100.0%; Pred. No. 3.6e-95;
 RESULT 686
 ID AAM39957 standard; protein; 359 AA.
 DE Human polypeptide SEQ ID NO 3102.
 PN WO20015312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 48.4%; Score 1909; DB 4; Length 359;
 Best Local Similarity 100.0%; Pred. No. 3.6e-95;
 RESULT 687
 ID AAE20797 standard; protein; 323 AA.
 DE Human gene 5 encoded secreted protein HSLGU75, SEQ ID NO:59.
 PN WO200218435-A1.
 PD 07-MAR-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 43.3%; Score 1708.5; DB 5; Length 323;
 Best Local Similarity 94.1%; Pred. No. 2.1e-84;
 RESULT 688
 ID ABG64653 standard; protein; 323 AA.
 DE Human albumin fusion protein #1328.
 PN WO20017137-A1.
 PD 18-OCT-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 43.3%; Score 1708.5; DB 5; Length 323;
 Best Local Similarity 94.1%; Pred. No. 2.1e-84;
 RESULT 689
 ID ADL77920 standard; protein; 323 AA.
 DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1402.
 PN US2004010134-A1.
 PD 15-JAN-2004.
 PA (ROSE/) ROSEN C A.

PA (HASE/) HASELTINE W A.
 Query Match 43.3%; Score 1708.5; DB 8; Length 323;
 Best Local Similarity 94.1%; Pred. No. 2.1e-84;
 RESULT 690
 ID AAM24485 standard; protein; 234 AA.
 DE Human EST encoded protein SEQ ID NO: 2010.
 PN WO200154477-A2.
 PD 02-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 29.8%; Score 1175.5; DB 4; Length 234;
 Best Local Similarity 91.4%; Pred. No. 7.8e-56;
 RESULT 691
 ID ABP72332 standard; protein; 1019 AA.
 DE Horseshoe crab Factor C.
 PN WO2003002976-A2.
 PD 09-JAN-2003.
 PA (WHIK) BIOWHITTAKER INC.
 Query Match 17.0%; Score 672; DB 6; Length 1019;
 Best Local Similarity 25.6%; Pred. No. 4.1e-28;
 RESULT 692
 ID AAM43394 standard; protein; 1019 AA.
 DE Singapore horseshoe crab factor C proenzyme (CrFC 21).
 PN SG42456-A1.
 PD 15-AUG-1997.
 PA (UYSI-) UNIV SINGAPORE NAT.
 Query Match 16.9%; Score 665; DB 2; Length 1019;
 Best Local Similarity 25.4%; Pred. No. 9.7e-28;
 RESULT 693
 ID AAY05750 standard; protein; 1019 AA.
 DE Horseshoe crab Factor C.
 PN WO9915676-A1.
 PD 01-APR-1999.
 PA (UYSI-) UNIV SINGAPORE NAT.
 Query Match 16.9%; Score 665; DB 2; Length 1019;
 Best Local Similarity 25.4%; Pred. No. 9.7e-28;
 RESULT 694
 ID AAM94302 standard; protein; 1019 AA.
 DE Horseshoe crab Factor C protein #2.
 PN US5858706-A.
 PD 12-JAN-1999.
 PA (UYSI-) UNIV SINGAPORE NAT.
 Query Match 16.9%; Score 665; DB 2; Length 1019;
 Best Local Similarity 25.4%; Pred. No. 9.7e-28;
 RESULT 695
 ID AAY42490 standard; protein; 1019 AA.
 DE Recombinant N-terminally truncated Horseshoe crab Factor C protein.
 PN US5985590-A.
 PD 16-NOV-1999.
 PA (UYSI-) UNIV SINGAPORE NAT.
 Query Match 16.9%; Score 665; DB 3; Length 1019;
 Best Local Similarity 25.4%; Pred. No. 9.7e-28;
 RESULT 696
 ID AAB60935 standard; protein; 1019 AA.
 DE Horseshoe crab recombinant Factor C #2.
 PN WO200127289-A2.
 PD 19-APR-2001.
 PA (UYSI-) UNIV SINGAPORE NAT.
 Query Match 16.9%; Score 665; DB 4; Length 1019;
 Best Local Similarity 25.4%; Pred. No. 9.7e-28;
 RESULT 697
 ID ABP72334 standard; protein; 1019 AA.
 DE Horseshoe crab Factor C.
 PN WO2003002976-A2.
 PD 09-JAN-2003.
 PA (WHIK) BIOWHITTAKER INC.
 Query Match 16.9%; Score 665; DB 6; Length 1019;
 Best Local Similarity 25.4%; Pred. No. 9.7e-28;
 RESULT 698
 ID AAM43393 standard; protein; 1083 AA.
 DE Singapore horseshoe crab factor C proenzyme (CrFC 26).
 PN SG42456-A1.
 PD 15-AUG-1997.
 PA (UYSI-) UNIV SINGAPORE NAT.

Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1e-27;
RESULT 699
ID AAY05749 standard; protein; 1083 AA.
DE Horseshoe crab Factor C.
PN, WO9915676-A1.
PD 01-APR-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1e-27;
RESULT 700
ID AAW94301 standard; protein; 1083 AA.
DE Horseshoe crab Factor C protein #1.
PN US5858706-A.
PD 12-JAN-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1e-27;
RESULT 701
ID AAY42489 standard; protein; 1083 AA.
DE Horseshoe crab recombinant Factor C protein.
PN US5985590-A.
PD 16-NOV-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 3; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1e-27;
RESULT 702
ID AAB60934 standard; protein; 1083 AA.
DE Horseshoe crab recombinant Factor C #1.
PN WO200127289-A2.
PD 19-APR-2001.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 4; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1e-27;
RESULT 703
ID ABP72333 standard; protein; 1083 AA.
DE Horseshoe crab Factor C.
PN WO2003002976-A2.
PD 09-JAN-2003.
PA (WHIK) B10WHITAKER INC.
Query Match 16.9%; Score 665; DB 6; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1e-27;
RESULT 704
ID AAM41743 standard; protein; 146 AA.
DE Human polypeptide SEQ ID NO 6674.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 16.8%; Score 662; DB 4; Length 146;
Best Local Similarity 85.4%; Pred. No. 2.3e-28;
RESULT 705
ID AAY11743 standard; protein; 103 AA.
DE Human 5' EST secreted protein SEQ ID No: 343.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 14.7%; Score 580; DB 2; Length 103;
Best Local Similarity 97.1%; Pred. No. 4.3e-24;
RESULT 706
ID ADE87459 standard; protein; 699 AA.
DE Human MBL-associated serine protease-1 protein.
PN EP1344533-A1.
PD 17-SEP-2003.
PA (NATL-) NATIMMUNE AS.
Query Match 12.1%; Score 476; DB 7; Length 699;
Best Local Similarity 24.6%; Pred. No. 1e-17;
RESULT 707
ID ADL91028 standard; protein; 699 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:14.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATI-) NATIMMUNE AS.
Query Match 12.0%; Score 475; DB 8; Length 699;

Best Local Similarity 24.6%; Pred. No. 1.2e-17;
RESULT 708
ID ABM83722 standard; protein; 698 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3971.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.0%; Score 474.5; DB 8; Length 698;
Best Local Similarity 24.4%; Pred. No. 1.2e-17;
RESULT 709
ID AAB85060 standard; protein; 728 AA.
DE Human serine protease MASP-3 polypeptide.
PN WO200140451-A2.
PD 07-JUN-2001.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 11.9%; Score 471; DB 4; Length 728;
Best Local Similarity 25.0%; Pred. No. 2e-17;
RESULT 710
ID ADE87461 standard; protein; 728 AA.
DE Human MBL-associated serine protease-4 protein.
PN EP1344533-A1.
PD 17-SEP-2003.
PA (NATI-) NATIMMUNE AS.
Query Match 11.9%; Score 468; DB 7; Length 728;
Best Local Similarity 25.0%; Pred. No. 2.9e-17;
RESULT 711
ID ADL91027 standard; protein; 728 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:13.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATI-) NATIMMUNE AS.
Query Match 11.9%; Score 468; DB 8; Length 728;
Best Local Similarity 25.0%; Pred. No. 2.9e-17;
RESULT 712
ID AAB47559 standard; protein; 728 AA.
DE Protease PRS-1.
PN WO200171004-A2.
PD 27-SEP-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.7%; Score 461; DB 4; Length 728;
Best Local Similarity 24.9%; Pred. No. 6.9e-17;
RESULT 713
ID AAG80756 standard; protein; 707 AA.
DE Murine Clr protein.
PN KR2001077614-A.
PD 20-AUG-2001.
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.
PA (KIMT/) KIM T Y.
Query Match 10.9%; Score 429; DB 5; Length 707;
Best Local Similarity 22.3%; Pred. No. 3.6e-15;
RESULT 714
ID ABB50288 standard; protein; 705 AA.
DE Complement component 1 r ovarian tumour marker protein, SEQ ID NO:66.
PN WO200175177-A2.
PD 11-OCT-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 10.2%; Score 403.5; DB 4; Length 705;
Best Local Similarity 22.9%; Pred. No. 8.4e-14;
RESULT 715
ID AAG80757 standard; protein; 705 AA.
DE Human Clr protein.
PN KR2001077614-A.
PD 20-AUG-2001.
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.
PA (KIMT/) KIM T Y.
Query Match 10.2%; Score 403.5; DB 5; Length 705;
Best Local Similarity 22.9%; Pred. No. 8.4e-14;
RESULT 716
ID ADP65211 standard; protein; 705 AA.
DE Human complement component 1, r subcomponent.
PN WO2003072827-A1.
PD 04-SEP-2003.

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 10.2%; Score 403.5; DB 7; Length 705;
 Best Local Similarity 22.6%; Pred. No. 8.4e-14;
 RESULT 717
 ID ABG31619 standard; protein; 686 AA.
 DE Human mannan-binding lectin associated serine protease-2 protein.
 PN US2002082208-A1.
 PD 27-JUN-2002.
 PA (JENS/) JENSENIUS J C.
 PA (THIE/) THIEL S.
 Query Match 10.2%; Score 401.5; DB 5; Length 686;
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;
 RESULT 718
 ID AAE14564 standard; protein; 686 AA.
 DE Human MASP-2 protein.
 PN WO200206460-A2.
 PD 24-JAN-2002.
 PA (JENS/) JENSENIUS J C.
 PA (THIE/) THIEL S.
 Query Match 10.2%; Score 401.5; DB 5; Length 686;
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;
 RESULT 719
 ID ABG32115 standard; protein; 686 AA.
 DE Mannan-binding lectin associated serine protease-2 (MASP-2).
 PN US2002082209-A1.
 PD 27-JUN-2002.
 PA (JENS/) JENSENIUS J C.
 PA (THIE/) THIEL S.
 Query Match 10.2%; Score 401.5; DB 5; Length 686;
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;
 RESULT 720
 ID ADL91025 standard; protein; 686 AA.
 DE Human mannose binding lectin amino acid sequence SEQ ID NO:11.
 PN WO2004024925-A2.
 PD 25-MAR-2004.
 PA (NATI-) NATIMUNE AS.
 Query Match 10.2%; Score 401.5; DB 8; Length 686;
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;
 RESULT 721
 ID AAE14568 standard; protein; 686 AA.
 DE Human MASP-2 protein, alternative version.
 PN WO200206460-A2.
 PD 24-JAN-2002.
 PA (JENS/) JENSENIUS J C.
 PA (THIE/) THIEL S.
 Query Match 10.2%; Score 400.5; DB 5; Length 686;
 Best Local Similarity 22.7%; Pred. No. 1.2e-13;
 RESULT 722
 ID ADE87460 standard; protein; 686 AA.
 DE Human MBL-associated serine protease-2 protein.
 PN EP1344533-A1.
 PD 17-SEP-2003.
 PA (NATI-) NATIMUNE AS.
 Query Match 10.2%; Score 400.5; DB 7; Length 686;
 Best Local Similarity 22.7%; Pred. No. 1.2e-13;
 RESULT 723
 ID ADQ27010 standard; protein; 671 AA.
 DE Human MASP-2 mature polypeptide.
 PN WO2004050907-A2.
 PD 17-JUN-2004.
 PA (UYAA-) UNIV.AARHUS.
 PA (AARH) AARHUS AMT.
 Query Match 10.1%; Score 399.5; DB 8; Length 671;
 Best Local Similarity 22.8%; Pred. No. 1.3e-13;
 RESULT 724
 ID AAE14565 standard; peptide; 671 AA.
 DE Human mature MASP-2 protein.
 PN WO200206460-A2.
 PD 24-JAN-2002.
 PA (JENS/) JENSENIUS J C.
 PA (THIE/) THIEL S.
 Query Match 10.1%; Score 398.5; DB 5; Length 671;
 Best Local Similarity 22.8%; Pred. No. 1.5e-13;

RESULT 725
 ID ADE56422 standard; protein; 694 AA.
 DE Rat Protein BAA25797, SEQ ID NO 2275.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 8.6%; Score 340.5; DB 7; Length 694;
 Best Local Similarity 21.2%; Pred. No. 2e-10;
 RESULT 726
 ID ADE83526 standard; protein; 694 AA.
 DE Rat Protein BAA25797, SEQ ID NO 11123.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 8.6%; Score 340.5; DB 7; Length 694;
 Best Local Similarity 21.2%; Pred. No. 2e-10;
 RESULT 727
 ID ADE56418 standard; protein; 695 AA.
 DE Rat Protein D88250, SEQ ID NO 2271.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 8.6%; Score 340.5; DB 7; Length 695;
 Best Local Similarity 21.2%; Pred. No. 2.1e-10;
 RESULT 728
 ID ADD45338 standard; protein; 695 AA.
 DE Rat Protein D88250, SEQ ID NO 10771.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 8.6%; Score 340.5; DB 7; Length 695;
 Best Local Similarity 21.2%; Pred. No. 2.1e-10;
 RESULT 729
 ID AAB43579 standard; protein; 760 AA.
 DE Human cancer associated protein sequence SEQ ID NO:1024.
 PN WO200055350-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 8.5%; Score 336; DB 3; Length 760;
 Best Local Similarity 21.7%; Pred. No. 3.9e-10;
 RESULT 730
 ID ADD45340 standard; protein; 688 AA.
 DE Human Protein Q9UCV3, SEQ ID NO 10773.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 8.5%; Score 334; DB 7; Length 688;
 Best Local Similarity 21.7%; Pred. No. 4.6e-10;
 RESULT 731
 ID ADE56420 standard; protein; 688 AA.
 DE Human Protein Q9UCV3, SEQ ID NO 2273.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 8.5%; Score 334; DB 7; Length 688;
 Best Local Similarity 21.7%; Pred. No. 4.6e-10;
 RESULT 732
 ID ADP65315 standard; protein; 688 AA.
 DE Human complement c1s component precursor (c1 esterase).
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 8.5%; Score 334; DB 7; Length 688;
 Best Local Similarity 21.7%; Pred. No. 4.6e-10;
 RESULT 733
 ID ADJ75392 standard; protein; 688 AA.
 DE Marker gene related amino acid sequence SEQ ID NO:644.

PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 8.5%; Score 334; DB 8; Length 688;
Best Local Similarity 21.7%; Pred. No. 4.6e-10;
RESULT 734
ID ADL91020 standard; protein; 688 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:6.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATI-) NATIMUNE AS.
Query Match 8.5%; Score 334; DB 8; Length 688;
Best Local Similarity 21.7%; Pred. No. 4.6e-10;
RESULT 735
ID ABM1337 standard; protein; 688 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2660, SEQ:3453.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 334; DB 8; Length 688;
Best Local Similarity 21.7%; Pred. No. 4.6e-10;
RESULT 736
ID ADI16884 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 420.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.4%; Score 332; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 7.1e-10;
RESULT 737
ID ADI16818 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 354.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.4%; Score 332; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 7.1e-10;
RESULT 738
ID AAE06940 standard; protein; 1019 AA.
DE Human enterokinase protein.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match 8.4%; Score 331.5; DB 4; Length 1019;
Best Local Similarity 22.9%; Pred. No. 9e-10;
RESULT 739
ID ADA83985 standard; protein; 1019 AA.
DE Human PRSS7 protein.
PN WO2002103028-A2.
PD 27-DEC-2002.
PA (BIOM-) BIOMEDICAL CENT.
Query Match 8.4%; Score 331.5; DB 6; Length 1019;
Best Local Similarity 22.9%; Pred. No. 9e-10;
RESULT 740
ID ADI10400 standard; protein; 1019 AA.
DE Human cell surface protease #16.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.4%; Score 331.5; DB 7; Length 1019;
Best Local Similarity 22.9%; Pred. No. 9e-10;
RESULT 741
ID ADJ46924 standard; protein; 1019 AA.
DE Human transmembrane serine protease (MTSP)-related polypeptide #6.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 8.4%; Score 331.5; DB 8; Length 1019;
Best Local Similarity 22.9%; Pred. No. 9e-10;
RESULT 742
ID ADJ70437 standard; protein; 1019 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2243.
PN WO2003087768-A2.

PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 8.4%; Score 330.5; DB 7; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1e-09;
RESULT 743
ID ADJ70480 standard; protein; 3389 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2286.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 8.4%; Score 329.5; DB 7; Length 3389;
Best Local Similarity 20.8%; Pred. No. 3.5e-09;
RESULT 744
ID ADH72216 standard; protein; 3567 AA.
DE Human protein of the invention NOV54b SEQ ID NO:1112.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.4%; Score 329.5; DB 8; Length 3567;
Best Local Similarity 20.8%; Pred. No. 3.7e-09;
RESULT 745
ID AARI3623 standard; protein; 460 AA.
DE Human Protein C zymogen SC.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 8.3%; Score 329; DB 2; Length 460;
Best Local Similarity 25.5%; Pred. No. 5.8e-10;
RESULT 746
ID ABG76507 standard; protein; 1274 AA.
DE DNA encoding protein modification and maintenance molecule #11.
PN WO200260942-A2.
PD 08-AUG-2002.
PA (INCY) INCYTE GENOMICS INC.
Query Match 8.3%; Score 328.5; DB 5; Length 1274;
Best Local Similarity 20.8%; Pred. No. 1.6e-09;
RESULT 747
ID AAU11815 standard; protein; 1783 AA.
DE Cancer and neurogenesis associated gene, variant 5G-3V3.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 1783;
Best Local Similarity 20.8%; Pred. No. 2.2e-09;
RESULT 748
ID AAU11813 standard; protein; 1800 AA.
DE Cancer and neurogenesis associated gene, variant 5G-3V1.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 1800;
Best Local Similarity 20.8%; Pred. No. 2.2e-09;
RESULT 749
ID AAU11812 standard; protein; 1826 AA.
DE Cancer and neurogenesis associated gene.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 1826;
Best Local Similarity 20.8%; Pred. No. 2.2e-09;
RESULT 750
ID AAU11814 standard; protein; 2008 AA.
DE Cancer and neurogenesis associated gene, variant 5G-3V2.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 2008;
Best Local Similarity 20.8%; Pred. No. 2.4e-09;
RESULT 751
ID AAU11817 standard; protein; 2306 AA.
DE Cancer and neurogenesis associated gene, variant 5R23V2.

PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 2306;
Best Local Similarity 20.8%; Pred. No. 2.8e-09;
RESULT 752
ID RAU11816 standard; protein; 2352 AA.
DE Cancer and neurogenesis associated gene, variant 5R-3V2.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 2352;
Best Local Similarity 20.8%; Pred. No. 2.8e-09;
RESULT 753
ID AAB19551 standard; protein; 683 AA.
DE Human matrix protease (truncated form).
PN WO200053232-A1.
PD 14-SEP-2000.
PA (GEOU) UNIV GEORGETOWN.
Query Match 8.3%; Score 328; DB 3; Length 683;
Best Local Similarity 21.4%; Pred. No. 9.5e-10;
RESULT 754
ID AAY90284 standard; protein; 762 AA.
DE Human peptidase, HPEP-1 protein sequence.
PN WO200042201-A2.
PD 20-JUL-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 8.3%; Score 328; DB 3; Length 762;
Best Local Similarity 21.4%; Pred. No. 1.1e-09;
RESULT 755
ID RAM25628 standard; protein; 851 AA.
DE Human protein sequence SEQ ID NO:1143.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 328; DB 4; Length 851;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 756
ID ABB11428 standard; peptide; 851 AA.
DE Human membrane-type Ser kinase homologue, SEQ ID NO:1798.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 328; DB 4; Length 851;
Best Local Similarity 21.6%; Pred. No. 1.2e-09;
RESULT 757
ID ADO55145 standard; protein; 853 AA.
DE Protein #47 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 8.3%; Score 328; DB 8; Length 853;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 758
ID AAB19552 standard; protein; 855 AA.
DE Human matrix protease.
PN WO200053232-A1.
PD 14-SEP-2000.
PA (GEOU) UNIV GEORGETOWN.
Query Match 8.3%; Score 328; DB 3; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 759
ID AAB35465 standard; protein; 855 AA.
DE Human membrane-type serine protease MT-SPI.
PN WO200123524-A2.
PD 05-APR-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 8.3%; Score 328; DB 4; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 760
ID ADI16817 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 353.
PN WO200268649-A2.

PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 328; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 761
ID ADI16883 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 419.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 328; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 762
ID ADI16876 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 412.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 328; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 763
ID ADN39867 standard; protein; 855 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C237.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.3%; Score 328; DB 7; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 764
ID ADN04754 standard; protein; 855 AA.
DE Antipsoriatic protein sequence #558.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 8.3%; Score 328; DB 8; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 765
ID ADP23334 standard; protein; 855 AA.
DE PRO polypeptide SEQ ID NO:428.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 8.3%; Score 328; DB 8; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 766
ID ADR66721 standard; protein; 863 AA.
DE Human prostatic carcinoma derived protein SEQ ID 233 #3.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 8.3%; Score 328; DB 8; Length 863;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 767
ID ADR66379 standard; protein; 863 AA.
DE Human prostatic carcinoma derived protein SEQ ID 233 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 8.3%; Score 328; DB 8; Length 863;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 768
ID AAB58274 standard; protein; 449 AA.
DE Lung cancer associated polypeptide sequence SEQ ID 612.
PN WO200055180-A2.
PD 21-SEP-2000.

PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A. 8.3%; Score 327.5; DB 3; Length 449;
Query Match 23.3%; Pred. No. 6.8e-10;
Best Local Similarity 23.3%; Pred. No. 6.8e-10;
RESULT 769
ID ADL64961 standard; protein; 688 AA.
DE Human complement component 1 protein, CIS.
PN US2004033582-A1.
PD 19-FEB-2004.
PA (EDMO/) EDMONDS M.
PA (HUIL/) HUI L.
PA (PERR/) PERRONE M.
PA (POWE/) POWELL J R.
PA (RAMA/) RAMANATHAN C S.
PA (SWAN/) SWANSON B.
PA (TSUC/) TSUCHIHASHI Z.
PA (ZERB/) ZERBA K.
Query Match 8.3%; Score 327; DB 8; Length 689;
Best Local Similarity 21.7%; Pred. No. 1.1e-09;
RESULT 770
ID ADL16508 standard; protein; 757 AA.
DE Human NOVX protein to treat human pathological conditions SeqID44.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 327; DB 5; Length 757;
Best Local Similarity 21.8%; Pred. No. 1.2e-09;
RESULT 771
ID AAY06671 standard; protein; 855 AA.
DE Tumour antigen derived gene-15 (TAGD-15) protein.
PN WO9942120-A1.
PD 26-AUG-1999.
PA (UYAR-) UNIV ARKANSAS.
Query Match 8.3%; Score 327; DB 2; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 772
ID AAB98500 standard; protein; 855 AA.
DE Human TAGD-15.
PN WO200129056-A1.
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Query Match 8.3%; Score 327; DB 4; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 773
ID AAE06930 standard; protein; 855 AA.
DE Human membrane-type serine protease (MTSP) 1.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 4; Length 855;
Best Local Similarity 21.8%; Pred. No. 1.3e-09;
RESULT 774
ID AAO22929 standard; protein; 855 AA.
DE Type II transmembrane serine protease 1 protein SEQ ID No 2.
PN WO200272786-A2.
PD 19-SEP-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 775
ID ADL16816 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 352.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 776
ID ADL16882 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 418.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 327; DB 8; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 777
ID ADL16975 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 411.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 778
ID ABP56619 standard; protein; 855 AA.
DE Human membrane-type serine protease MTSP1 protein SEQ ID NO:2.
PN WO200292841-A2.
PD 21-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 779
ID AAO30146 standard; protein; 855 AA.
DE Human membrane-type serine protease MTSP1 protein.
PN WO2003044179-A2.
PD 30-MAY-2003.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 780
ID AAE29820 standard; protein; 855 AA.
DE Human membrane-type serine protease 1 (MTSP1).
PN WO200277267-A2.
PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 781
ID AAE29791 standard; protein; 855 AA.
DE Human membrane-type serine protease, MTSP1.
PN WO200277263-A2.
PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 782
ID ABP72376 standard; protein; 855 AA.
DE Transmembrane serine protease 1 (MTSP1).
PN WO2003004681-A2.
PD 16-JAN-2003.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 783
ID ADB97551 standard; protein; 855 AA.
DE Human MTSP1, SEQ ID NO:2.
PN WO2003031585-A2.
PD 17-APR-2003.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 7; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 784
ID ADI10371 standard; protein; 855 AA.
DE Human cell surface protease #1.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 7; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 785
ID ADG65326 standard; protein; 855 AA.
DE Human MTSP1.
PN WO2003104394-A2.
PD 18-DEC-2003.
PA (DEND-) DENDREON SAN DIEGO LLC.
Query Match 8.3%; Score 327; DB 8; Length 855;

Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 786
ID AD128861 standard; protein; 855 AA.
DE Human matrixcase (MTSP1) serine protease.
PN WO2004005471-A2.
PD 15-JAN-2004.
PA (DEND-) DENDREON SAN DIEGO LLC.
Query Match 8.3%; Score 327; DB 8; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 787
ID ADJ46895 standard; protein; 855 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #1.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 8; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 788
ID AAE20788 standard; protein; 3095 AA.
DE Rat C3b/C4b complement receptor like protein.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.2%; Score 324; DB 5; Length 3095;
Best Local Similarity 20.1%; Pred. No. 6.4e-09;
RESULT 789
ID ADN42162 standard; protein; 757 AA.
DE Human novel protein NOV 8.
PN US2004033493-A1.
PD 19-FEB-2004.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (GANG/) GANGOLLI E A.
PA (PADL/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUFIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENNA C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C B.
Query Match 8.2%; Score 323; DB 8; Length 757;
Best Local Similarity 21.8%; Pred. No. 1.9e-09;
RESULT 790
ID ADH71146 standard; protein; 3130 AA.
DE Human protein of the invention NOV4f SEQ ID NO:42.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 321; DB 8; Length 3130;
Best Local Similarity 22.6%; Pred. No. 9.4e-09;
RESULT 791
ID ADH71144 standard; protein; 3483 AA.
DE Human protein of the invention NOV4e SEQ ID NO:40.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 321; DB 8; Length 3483;
Best Local Similarity 22.6%; Pred. No. 1e-08;
RESULT 792
ID ADH71136 standard; protein; 3546 AA.

DE Human protein of the invention NOV4a SEQ ID NO:32.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 321; DB 8; Length 3546;
Best Local Similarity 22.6%; Pred. No. 1.1e-08;
RESULT 793
ID AAE20787 standard; protein; 3069 AA.
DE Human C3b/C4b complement receptor like protein #1.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.1%; Score 320.5; DB 5; Length 3069;
Best Local Similarity 20.7%; Pred. No. 9.8e-09;
RESULT 794
ID AAE20789 standard; protein; 3100 AA.
DE Human C3b/C4b complement receptor like protein #2.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.1%; Score 320.5; DB 5; Length 3100;
Best Local Similarity 20.7%; Pred. No. 9.9e-09;
RESULT 795
ID AAU99088 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant G383N/G385T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.1%; Score 319.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 1.7e-09;
RESULT 796
ID AAU99080 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L349N/D351T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.1%; Score 319.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 1.7e-09;
RESULT 797
ID ADG83836 standard; protein; 455 AA.
DE Rough scale snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYQU) UNIV QUEENSLAND.
Query Match 8.1%; Score 319.5; DB 8; Length 455;
Best Local Similarity 23.4%; Pred. No. 1.9e-09;
RESULT 798
ID AAU99078 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant I348N/G350T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.1%; Score 318.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 2e-09;
RESULT 799
ID ADH71142 standard; protein; 2612 AA.
DE Human protein of the invention NOV4d SEQ ID NO:38.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 2612;
Best Local Similarity 22.6%; Pred. No. 1.2e-08;
RESULT 800
ID ABG79169 standard; protein; 2669 AA.
DE Human cub and sushi domain containing protein #2.
PN WO200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 5; Length 2669;
Best Local Similarity 22.6%; Pred. No. 1.2e-08;

RESULT 801
ID ADH7L140 standard; protein; 2669 AA.
DE Human protein of the invention NOV4c SEQ ID NO:36.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 2669;
Best Local Similarity 22.6%; Pred. No. 1.2e-08;
RESULT 802
ID ABG79168 standard; protein; 3104 AA.
DE Human cub and sushi domain containing protein #1.
PN WO200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 5; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.4e-08;
RESULT 803
ID ADH7L168 standard; protein; 3104 AA.
DE Human protein of the invention NOV4q SEQ ID NO:64.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.4e-08;
RESULT 804
ID ADH7L166 standard; protein; 3104 AA.
DE Human protein of the invention NOV4p SEQ ID NO:62.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.4e-08;
RESULT 805
ID ADH7L138 standard; protein; 3104 AA.
DE Human protein of the invention NOV4b SEQ ID NO:34.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.4e-08;
RESULT 806
ID AAU99006 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D189N/K191T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 317.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 2.2e-09;
RESULT 807
ID AAU99066 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T315N/V317T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 317.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.2e-09;
RESULT 808
ID AAR57283 standard; protein; 798 AA.
DE Bovine enterokinase.
PN WO9416083-A1.
PD 21-JUL-1994.
PA (GEMY) GENETICS INST INC.
Query Match 8.0%; Score 317.5; DB 2; Length 798;
Best Local Similarity 24.6%; Pred. No. 4e-09;
RESULT 809
ID AAE20900 standard; protein; 3069 AA.
DE Human C3b/C4b complement receptor like protein #1, alternative version.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.0%; Score 317.5; DB 5; Length 3069;

Best Local Similarity 20.7%; Pred. No. 1.4e-08;
RESULT 810
ID AAE20901 standard; protein; 3100 AA.
DE Human C3b/C4b complement receptor like protein #2, alternative version.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.0%; Score 317.5; DB 5; Length 3100;
Best Local Similarity 20.7%; Pred. No. 1.4e-08;
RESULT 811
ID AAU99076 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant W338N/S340T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 316.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 2.5e-09;
RESULT 812
ID AAU99022 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K217N/L219T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 316.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.5e-09;
RESULT 813
ID AAU99026 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L220N/R222T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.8e-09;
RESULT 814
ID AAU99081 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D351N/Q353S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 2.8e-09;
RESULT 815
ID AAU99071 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S336N/M338S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 2.8e-09;
RESULT 816
ID AAU99087 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant G383N/G385S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.8e-09;
RESULT 817
ID AAU99079 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L349N/D351S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.8e-09;
RESULT 818
ID AAU99089 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L349N/D351S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.8e-09;

ID AAR62653 standard; protein; 461 AA.
 DE Human protein C.
 PN US5358932-A.
 PD 25-OCT-1994.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 8.0%; Score 315.5; DB 2; Length 461;
 Best Local Similarity 24.5%; Pred. No. 3.1e-09;
 RESULT 819
 ID AAR35760 standard; protein; 419 AA.
 DE Protein C (PC).
 PN WO9309804-A1.
 PD 27-MAY-1993.
 PA (SCRI) SCRIPPS RES INST.
 Query Match 8.0%; Score 314.5; DB 2; Length 419;
 Best Local Similarity 23.3%; Pred. No. 3.2e-09;
 RESULT 820
 ID AAU99053 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant R306N/K308S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 8.0%; Score 314.5; DB 5; Length 419;
 Best Local Similarity 24.7%; Pred. No. 3.2e-09;
 RESULT 821
 ID AAU99007 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant S190N/K192S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 8.0%; Score 314.5; DB 5; Length 419;
 Best Local Similarity 24.4%; Pred. No. 3.2e-09;
 RESULT 822
 ID AAU99077 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant I348N/G350S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 8.0%; Score 314.5; DB 5; Length 419;
 Best Local Similarity 24.5%; Pred. No. 3.2e-09;
 RESULT 823
 ID AAU99043 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant L296N.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 8.0%; Score 314.5; DB 5; Length 419;
 Best Local Similarity 24.5%; Pred. No. 3.2e-09;
 RESULT 824
 ID ADG83832 standard; protein; 454 AA.
 DE Red belly black snake venom protease.
 PN WO2003082914-A1.
 PD 09-OCT-2003.
 PA (UYUQ) UNIV QUEENSLAND.
 Query Match 8.0%; Score 314.5; DB 8; Length 454;
 Best Local Similarity 23.0%; Pred. No. 3.5e-09;
 RESULT 825
 ID ADM77504 standard; protein; 461 AA.
 DE Human protein C variant #2 amino acid sequence.
 PN WO2003106666-A2.
 PD 24-DEC-2003.
 PA (MAXY-) MAXYGEN APS.
 Query Match 8.0%; Score 314.5; DB 8; Length 461;
 Best Local Similarity 24.5%; Pred. No. 3.5e-09;
 RESULT 826
 ID AAE23083 standard; protein; 855 AA.
 DE Epithin protein.
 PN WO200203787-A2.
 PD 17-JAN-2002.

PA (DELT-) DELTAGEN INC.
 Query Match 8.0%; Score 314; DB 5; Length 855;
 Best Local Similarity 21.4%; Pred. No. 6.7e-09;
 RESULT 827
 ID ADI16819 standard; protein; 855 AA.
 DE Murine NOVX protein homologue SeqID 355.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 8.0%; Score 314; DB 5; Length 855;
 Best Local Similarity 21.4%; Pred. No. 6.7e-09;
 RESULT 828
 ID ADI16877 standard; protein; 855 AA.
 DE Murine NOVX protein homologue SeqID 413.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 8.0%; Score 314; DB 5; Length 855;
 Best Local Similarity 21.4%; Pred. No. 6.7e-09;
 RESULT 829
 ID AAW72753 standard; protein; 419 AA.
 DE Primary structure of activated human protein C.
 PN EP875563-A2.
 PD 04-NOV-1998.
 PA (ELIL) LILLY & CO ELI.
 Query Match 7.9%; Score 313.5; DB 2; Length 419;
 Best Local Similarity 23.3%; Pred. No. 3.6e-09;
 RESULT 830
 ID AAU99005 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant D189N/K191S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 7.9%; Score 313.5; DB 5; Length 419;
 Best Local Similarity 24.2%; Pred. No. 3.6e-09;
 RESULT 831
 ID AAU99025 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant L220N/R222S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 7.9%; Score 313.5; DB 5; Length 419;
 Best Local Similarity 24.5%; Pred. No. 3.6e-09;
 RESULT 832
 ID AAU99065 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant T315N/V317S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 7.9%; Score 313.5; DB 5; Length 419;
 Best Local Similarity 24.3%; Pred. No. 3.6e-09;
 RESULT 833
 ID AAU99016 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant D214N/S216T.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 7.9%; Score 313.5; DB 5; Length 419;
 Best Local Similarity 24.7%; Pred. No. 3.6e-09;
 RESULT 834
 ID AAU99023 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant K218N/L220S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 7.9%; Score 313.5; DB 5; Length 419;
 Best Local Similarity 24.5%; Pred. No. 3.6e-09;
 RESULT 835

ID AAR13083 standard; protein; 509 AA.
DE PAP-I-protein C fusion construct.
PN WO9109953-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 313; DB 2; Length 509;
Best Local Similarity 23.5%; Pred. No. 4.6e-09;
RESULT 836
ID ADI16820 standard; protein; 855 AA.
DE Rat NOVX protein homologue SeqID 356.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 7.5e-09;
RESULT 837
ID ADI16881 standard; protein; 855 AA.
DE Rat NOVX protein homologue SeqID 417.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 7.5e-09;
RESULT 838
ID ADI16878 standard; protein; 855 AA.
DE Rat NOVX protein homologue SeqID 414.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 7.5e-09;
RESULT 839
ID AAU99072 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S336N/M338T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 840
ID AAU99097 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant DI89N/K191N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 4.1e-09;
RESULT 841
ID AAU99009 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K191N/K193S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 4.1e-09;
RESULT 842
ID AAU99064 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R312N/R314T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 4.1e-09;
RESULT 843
ID AAU99069 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V334N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 844
ID AAU99082 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D351N/Q353T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 845
ID AAU99096 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant M338A.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 846
ID AAU99091 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L387N/N389S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 847
ID AAU99024 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K218N/L220T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 848
ID AAU99048 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H303N/S305T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 849
ID AAU99067 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant F316N/L318S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.3%; Pred. No. 4.1e-09;
RESULT 850
ID AAU99075 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant M338N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 851
ID AAU99092 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L387N/N389T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.

Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 852
ID AAU99011 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K192N/L194S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 853
ID AAU99032 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S250N/S252T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 854
ID ADM77507 standard; protein; 461 AA.
DE Human protein C variant #5 amino acid sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 8; Length 461;
Best Local Similarity 24.3%; Pred. No. 4.5e-09;
RESULT 855
ID ADM77505 standard; protein; 461 AA.
DE Human protein C variant #3 amino acid sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 4.5e-09;
RESULT 856
ID AAB82677 standard; protein; 419 AA.
DE Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 312; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.4e-09;
RESULT 857
ID AAR13537 standard; protein; 460 AA.
DE Human Protein C zymogen N.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 312; DB 2; Length 460;
Best Local Similarity 24.7%; Pred. No. 4.8e-09;
RESULT 858
ID ADG83830 standard; protein; 467 AA.
DE Coastal taipan venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYQU) UNIV QUEENSLAND.
Query Match 7.9%; Score 312; DB 8; Length 467;
Best Local Similarity 23.0%; Pred. No. 4.9e-09;
RESULT 859
ID ABP60993 standard; protein; 1031 AA.
DE Novel human protein. SEQ ID 80.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 7.9%; Score 312; DB 5; Length 1031;
Best Local Similarity 22.6%; Pred. No. 1e-08;
RESULT 860

ID AAU99008 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S190N/K192T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 4.7e-09;
RESULT 861
ID AAU99039 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T254N/N256S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 862
ID AAU99047 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H303N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.3%; Pred. No. 4.7e-09;
RESULT 863
ID AAU99070 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V334N/S336T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 864
ID AAU99017 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E215N/K217S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 865
ID AAU99044 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L296N/T298S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 866
ID AAU99014 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K193N/A195T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 867
ID AAU99031 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S250N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 4.7e-09;
RESULT 868
ID AAU99057 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant K308N/A310S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 869
ID AAU99054 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R306N/K308T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 870
ID AAU99095 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D214A.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 871
ID AAU99015 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D214N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 872
ID AAP81205 standard; protein; 461 AA.
DE Human protein C.
PN EP266190-A.
PD 04-MAY-1988.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 311.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.1e-09;
RESULT 873
ID AAR13539 standard; protein; 461 AA.
DE Human Protein C zymogen LIN.
PN EP43875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.1e-09;
RESULT 874
ID AAR13997 standard; protein; 461 AA.
DE Human protein C zymogen Q329.
PN EP43874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.1e-09;
RESULT 875
ID ADM77503 standard; protein; 461 AA.
DE Human protein C variant #1 amino acid sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.1e-09;
RESULT 876
ID AAB82678 standard; protein; 419 AA.
DE Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S/T254S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.

Query Match 7.9%; Score 311; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 877
ID AAB82675 standard; protein; 419 AA.
DE Human protein C derivative (S11G/Q32E/N33D/L194S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 878
ID ADC40013 standard; protein; 409 AA.
DE Human activated protein C-related protein #2.
PN WO2003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 409;
Best Local Similarity 24.5%; Pred. No. 5.2e-09;
RESULT 879
ID ADC40012 standard; protein; 410 AA.
DE Human activated protein C-related protein #1.
PN WO2003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 410;
Best Local Similarity 24.5%; Pred. No. 5.2e-09;
RESULT 880
ID AAY56803 standard; protein; 415 AA.
DE Truncated human protein C polypeptide.
PN WO9963070-A1.
PD 09-DEC-1999.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 3; Length 415;
Best Local Similarity 24.5%; Pred. No. 5.2e-09;
RESULT 881
ID AAB82673 standard; protein; 419 AA.
DE Wild-type human protein C.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 882
ID AAB36896 standard; protein; 419 AA.
DE Human protein C derivative 3.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 883
ID AAB36894 standard; protein; 419 AA.
DE Human protein C derivative 1.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 884
ID AAE08625 standard; protein; 419 AA.
DE Human mature wild type protein C.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 885
ID AAU99063 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R312N/R314S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.

Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 886
ID AAU99012 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K192N/L194T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 887
ID AAU99050 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S304N/R306T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 888
ID AAU99010 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K191N/K193T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 5.3e-09;
RESULT 889
ID AAU99040 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T254N/N256T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 890
ID AAU99060 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E309N/K311T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 891
ID AAU99055 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E307N/E309S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 892
ID AAU99056 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E307N/E309T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 893
ID AAU99059 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E309N/K311S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 894
ID AAU99002 standard; protein; 419 AA.
DE Human Protein C zymogen protein.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 895
ID AAU99051 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 896
ID AAU99052 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 897
ID ABR55547 standard; protein; 419 AA.
DE Amino acid sequence of mature human protein C (PC).
PN FR2831170-A1.
PD 25-APR-2003.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 7.9%; Score 310.5; DB 6; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 898
ID ADC40014 standard; protein; 419 AA.
DE Human activated protein C-related protein #3.
PN WO2003075834-A2.
PD 18-SEP-2003.
PA (ELLIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 899
ID ADO18786 standard; protein; 419 AA.
DE Mature human zymogen-like protein C.
PN WO2004044130-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 8; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 900
ID ADG3834 standard; protein; 453 AA.
DE Mainland tiger snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYQU) UNIV QUEENSLAND.
Query Match 7.9%; Score 310.5; DB 8; Length 453;
Best Local Similarity 22.8%; Pred. No. 5.7e-09;
RESULT 901
ID AAP81104 standard; protein; 460 AA.
DE Sequence of human protein C.
PN JP63263083-A.
PD 31-OCT-1988.
PA (FARH) HOECHST JAPAN LTD.
Query Match 7.9%; Score 310.5; DB 1; Length 460;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 902
ID AAW25086 standard; protein; 460 AA.
DE Human protein C.
PN WO9720043-A1.

Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 894
ID AAU99002 standard; protein; 419 AA.
DE Human Protein C zymogen protein.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 895
ID AAU99051 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 896
ID AAU99052 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 897
ID ABR55547 standard; protein; 419 AA.
DE Amino acid sequence of mature human protein C (PC).
PN FR2831170-A1.
PD 25-APR-2003.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 7.9%; Score 310.5; DB 6; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 898
ID ADC40014 standard; protein; 419 AA.
DE Human activated protein C-related protein #3.
PN WO2003075834-A2.
PD 18-SEP-2003.
PA (ELLIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 899
ID ADO18786 standard; protein; 419 AA.
DE Mature human zymogen-like protein C.
PN WO2004044130-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 8; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 900
ID ADG3834 standard; protein; 453 AA.
DE Mainland tiger snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYQU) UNIV QUEENSLAND.
Query Match 7.9%; Score 310.5; DB 8; Length 453;
Best Local Similarity 22.8%; Pred. No. 5.7e-09;
RESULT 901
ID AAP81104 standard; protein; 460 AA.
DE Sequence of human protein C.
PN JP63263083-A.
PD 31-OCT-1988.
PA (FARH) HOECHST JAPAN LTD.
Query Match 7.9%; Score 310.5; DB 1; Length 460;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 902
ID AAW25086 standard; protein; 460 AA.
DE Human protein C.
PN WO9720043-A1.

ID 05-JUN-1997.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 310.5; DB 2; Length 460;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 903
ID AAP60001 standard; protein; 461 AA.
DE Sequence of polypeptide with human protein C activity.
PN EP191606-A.
PD 20-AUG-1986.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 904
ID AAP70855 standard; protein; 461 AA.
DE Human protein C.
PN EP215548-A.
PD 25-MAR-1987.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 7.9%; Score 310.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 905
ID AAP90401 standard; protein; 461 AA.
DE Zymogen form of human protein C.
PN EP323149-A.
PD 05-JUL-1989.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 906
ID AAR13622 standard; protein; 461 AA.
DE Human protein C.
PN WO9112320-A.
PD 22-AUG-1991.
PA (ZYMO) ZYMOGENETICS INC.
PA (TEIJ) TEIJIN LTD.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 907
ID AAR13081 standard; protein; 461 AA.
DE Human protein C.
PN WO9109953-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 908
ID AAR13074 standard; protein; 461 AA.
DE Protein C precursor.
PN WO9109951-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
PA (TEIJ) TEIJIN LTD.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 909
ID AAR34295 standard; protein; 461 AA.
DE Protein C.
PN JP05064588-A.
PD 19-MAR-1993.
PA (TEIJ) TEIJIN LTD.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 910
ID AAW02600 standard; protein; 461 AA.
DE Human protein C.
PN US5516650-A.
PD 14-MAY-1996.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 911

ID AAY49561 standard; protein; 461 AA.
DE Human lecithin cholesterol acyltransferase protein sequence.
PN WO950454-A2.
PD 07-OCT-1999.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 912
ID AAB82674 standard; protein; 461 AA.
DE Wild-type human protein C.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 913
ID AAB36895 standard; protein; 461 AA.
DE Human protein C derivative 2.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 914
ID AAE08626 standard; protein; 461 AA.
DE Human wild type protein C.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 915
ID AAU99001 standard; protein; 461 AA.
DE Human Protein C precursor protein.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 916
ID ADM77502 standard; protein; 461 AA.
DE Human protein C wild-type amino acid sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 917
ID ADO18787 standard; protein; 461 AA.
DE Human zymogen-like protein C.
PN WO2004044190-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 918
ID AAB82676 standard; protein; 419 AA.
DE Human protein C derivative (S11G/Q32E/N33D/L194S/T254S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 919
ID AAE08630 standard; protein; 419 AA.
DE Human protein C derivative #4.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310; DB 4; Length 419;

Best Local Similarity 24.5%; Pred. No. 5.6e-09;
 RESULT 920
 ID AAR13538 standard; protein; 460 AA.
 DE Human Protein C zymogen FN.
 PN EP443875-A.
 PD 28-AUG-1991.
 PA (ELIL) LILLY & CO ELI.
 Query Match 7.9%; Score 310; DB 2; Length 460;
 Best Local Similarity 24.7%; Pred. No. 6.1e-09;
 RESULT 921
 ID AAB36897 standard; protein; 419 AA.
 DE Human protein C derivative 4.
 PN WO200066754-A1.
 PD 09-NOV-2000.
 PA (ELIL) LILLY & CO ELI.
 Query Match 7.8%; Score 309.5; DB 4; Length 419;
 Best Local Similarity 24.5%; Pred. No. 6e-09;
 RESULT 922
 ID AAB36898 standard; protein; 419 AA.
 DE Human protein C derivative 5.
 PN WO200066754-A1.
 PD 09-NOV-2000.
 PA (ELIL) LILLY & CO ELI.
 Query Match 7.8%; Score 309.5; DB 4; Length 419;
 Best Local Similarity 24.5%; Pred. No. 6e-09;
 RESULT 923
 ID AAU99018 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant E215N/K217T.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 Query Match 7.8%; Score 309.5; DB 5; Length 419;
 Best Local Similarity 24.4%; Pred. No. 6e-09;
 RESULT 924
 ID AAU99033 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant K251N.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 Query Match 7.8%; Score 309.5; DB 5; Length 419;
 Best Local Similarity 24.5%; Pred. No. 6e-09;
 RESULT 925
 ID AAU99013 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant K193N/A195S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 Query Match 7.8%; Score 309.5; DB 5; Length 419;
 Best Local Similarity 24.2%; Pred. No. 6e-09;
 RESULT 926
 ID AAU99068 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant F316N/L318T.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 Query Match 7.8%; Score 309.5; DB 5; Length 419;
 Best Local Similarity 24.4%; Pred. No. 6e-09;
 RESULT 927
 ID AAU99062 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant A310N/R312T.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 Query Match 7.8%; Score 309.5; DB 5; Length 419;
 Best Local Similarity 24.8%; Pred. No. 6e-09;
 RESULT 928
 ID AAU99020 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant S216N/K218T.

PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 Query Match 7.8%; Score 309.5; DB 5; Length 419;
 Best Local Similarity 24.4%; Pred. No. 6e-09;
 RESULT 929
 ID AAU99035 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant S252N.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 Query Match 7.8%; Score 309.5; DB 5; Length 419;
 Best Local Similarity 24.5%; Pred. No. 6e-09;
 RESULT 930
 ID AAU99085 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant E357N/D359S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 Query Match 7.8%; Score 309.5; DB 5; Length 419;
 Best Local Similarity 24.5%; Pred. No. 6e-09;
 RESULT 931
 ID AAU99058 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant K308N/A310T.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 Query Match 7.8%; Score 309.5; DB 5; Length 419;
 Best Local Similarity 24.5%; Pred. No. 6e-09;
 RESULT 932
 ID AAU99019 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant S216N/K218S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 Query Match 7.8%; Score 309.5; DB 5; Length 419;
 Best Local Similarity 24.5%; Pred. No. 6e-09;
 RESULT 933
 ID AAU99094 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant H388N/Y390T.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 Query Match 7.8%; Score 309.5; DB 5; Length 419;
 Best Local Similarity 24.7%; Pred. No. 6e-09;
 RESULT 934
 ID AAU99089 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant L386N/H388S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 Query Match 7.8%; Score 309.5; DB 5; Length 419;
 Best Local Similarity 24.8%; Pred. No. 6e-09;
 RESULT 935
 ID AAP90070 standard; protein; 461 AA.
 DE Human protein C.
 PN EP319312-A.
 PD 07-JUN-1989.
 PA (ELIL) LILLY & CO ELI.
 Query Match 7.8%; Score 309.5; DB 1; Length 461;
 Best Local Similarity 24.5%; Pred. No. 6.5e-09;
 RESULT 936
 ID AAR13540 standard; protein; 461 AA.
 DE Human Protein C zymogen FLIN.
 PN EP443875-A.
 PD 28-AUG-1991.

PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.5e-09;
RESULT 937
ID ADI16874 standard; protein; 799 AA.
DE Murine NOVX protein homologue SeqID 410.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 309.5; DB 5; Length 799;
Best Local Similarity 21.6%; Pred. No. 1.1e-08;
RESULT 938
ID ADI16880 standard; protein; 799 AA.
DE Murine NOVX protein homologue SeqID 416.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 309.5; DB 5; Length 799;
Best Local Similarity 21.6%; Pred. No. 1.1e-08;
RESULT 939
ID AAE08627 standard; protein; 419 AA.
DE Human protein C derivative #1.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 940
ID AAE08629 standard; protein; 419 AA.
DE Human protein C derivative #3.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 941
ID AAU99049 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S304N/R306S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.8e-09;
RESULT 942
ID AAU99061 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant A310N/R312S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.1%; Pred. No. 6.8e-09;
RESULT 943
ID AAU99090 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L386N/H388T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.8e-09;
RESULT 944
ID AAU99086 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E357N/D359T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.8e-09;
RESULT 945
ID AAU99036 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant S252N/T254S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.8e-09;
RESULT 946
ID AAU99045 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant Y302N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.8e-09;
RESULT 947
ID AAU99034 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K251N/T253S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.8e-09;
RESULT 948
ID ADM77506 standard; protein; 461 AA.
DE Human protein C variant #4 amino acid sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 7.4e-09;
RESULT 949
ID AAE08628 standard; protein; 419 AA.
DE Human protein C derivative #2.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 308; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.2e-09;
RESULT 950
ID AAU99084 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R352N/D354T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.6%; Pred. No. 7.7e-09;
RESULT 951
ID AAU99021 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K217N/L219S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 7.7e-09;
RESULT 952
ID AAU99046 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant Y302N/S304T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.7e-09;
RESULT 953
ID AAU99093 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H388N/Y390S.
PN WO200232461-A2.

PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 7.7e-09;
RESULT 954
ID AAU99083 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R352N/D354S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 306.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.7e-09;
RESULT 955
ID AAU99074 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V339T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 306.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 8.7e-09;
RESULT 956
ID AAU99003 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D172N/K174S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 306.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 8.7e-09;
RESULT 957
ID AAU99027 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V243N/V245S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 301.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 1.6e-08;
RESULT 965
ID AAU99028 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V243N/V245T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.7%; Score 302.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 1.4e-08;
RESULT 966
ID AAU99038 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T253N/D255T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 301.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.6e-08;
RESULT 967
ID AAP93714 standard; protein; 461 AA.
DE Hybrid protein of protein-C and Factor-X.
PN EP296413-A.
PD 28-DEC-1988.
PA (FARH) HOECHST JAPAN LTD.
Query Match 7.6%; Score 301.5; DB 1; Length 461;
Best Local Similarity 24.7%; Pred. No. 1.8e-08;
RESULT 968
ID AAU99041 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D255N/D257S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 299.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 2.1e-08;
RESULT 969
ID AAU99029 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V245N/P247S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.7%; Score 305.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 9.8e-09;
RESULT 960
ID AAU99073 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V339S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.7%; Score 305.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 9.8e-09;
RESULT 961
ID AAU99082 standard; protein; 461 AA.
DE Human protein C zymogen Q097.
PN EP443874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.7%; Score 304.5; DB 2; Length 461;

Best Local Similarity 24.4%; Pred. No. 1.2e-08;
RESULT 962
ID AAR13584 standard; protein; 461 AA.
DE Human protein C zymogen Q248.
PN EP443874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.7%; Score 304.5; DB 2; Length 461;
Best Local Similarity 24.4%; Pred. No. 1.2e-08;
RESULT 963
ID AAU99037 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T253N/D255S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.7%; Score 302.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.4e-08;
RESULT 964
ID AAU99028 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V243N/V245T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.7%; Score 302.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 1.4e-08;
RESULT 965
ID AAU99027 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V243N/V245S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 301.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 1.6e-08;
RESULT 966
ID AAU99038 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T253N/D255T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 301.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.6e-08;
RESULT 967
ID AAP93714 standard; protein; 461 AA.
DE Hybrid protein of protein-C and Factor-X.
PN EP296413-A.
PD 28-DEC-1988.
PA (FARH) HOECHST JAPAN LTD.
Query Match 7.6%; Score 301.5; DB 1; Length 461;
Best Local Similarity 24.7%; Pred. No. 1.8e-08;
RESULT 968
ID AAU99041 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D255N/D257S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 299.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 2.1e-08;
RESULT 969
ID AAU99029 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V245N/P247S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.7%; Score 305.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 9.8e-09;
RESULT 970
ID AAU99030 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant V245N/P247T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.6%; Score 298.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 2.3e-08;
RESULT 971
ID: AAU99042 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D255N/D257T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.6%; Score 298.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 2.3e-08;
RESULT 972
ID ADB65750 standard; protein; 397 AA.
DE Human protein encoded by clone UTERU20087070.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.6%; Score 298; DB 7; Length 397;
Best Local Similarity 24.1%; Pred. No. 2.4e-08;
RESULT 973
ID ADI17268 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 804.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.5%; Score 296; DB 5; Length 230;
Best Local Similarity 32.3%; Pred. No. 1.8e-08;
RESULT 974
ID ADI17276 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 812.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.5%; Score 296; DB 5; Length 230;
Best Local Similarity 32.3%; Pred. No. 1.8e-08;
RESULT 975
ID ADJ83075 standard; protein; 230 AA.
DE Trypsin-like serine protease protein - SEQ ID 66.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHP/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERRHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 7.5%; Score 296; DB 7; Length 230;

Best Local Similarity 32.3%; Pred. No. 1.8e-08;
RESULT 976
ID ABG21442 standard; protein; 932 AA.
DE Novel human diagnostic protein #21433.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.5%; Score 296; DB 4; Length 932;
Best Local Similarity 21.0%; Pred. No. 6.7e-08;
RESULT 977
ID AAR09290 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue GF6 (Leu 66, Asp 67, Thr 68, Gln 117).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match 7.5%; Score 294; DB 2; Length 562;
Best Local Similarity 23.3%; Pred. No. 5.4e-08;
RESULT 978
ID ABU12065 standard; protein; 986 AA.
DE Human NOV12a CG92293-01 protein SEQ ID 50.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.4%; Score 293; DB 6; Length 986;
Best Local Similarity 23.1%; Pred. No. 1e-07;
RESULT 979
ID AAR70903 standard; protein; 527 AA.
DE Human t-PA variant (N103,A432,A434).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 292; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 6.5e-08;
RESULT 980
ID AAR70895 standard; protein; 527 AA.
DE Human t-PA variant (N103,A331,A332).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 292; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 6.5e-08;
RESULT 981
ID ADN03787 standard; protein; 516 AA.
DE Antipsoriatic protein sequence #90.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 291.5; DB 8; Length 516;
Best Local Similarity 23.1%; Pred. No. 6.8e-08;
RESULT 982
ID ABM80985 standard; protein; 516 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81669, SEQ:2539.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 291.5; DB 8; Length 516;
Best Local Similarity 23.1%; Pred. No. 6.8e-08;
RESULT 983
ID ADQ39246 standard; protein; 516 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 909.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.4%; Score 291.5; DB 8; Length 516;
Best Local Similarity 23.1%; Pred. No. 6.8e-08;
RESULT 984
ID AAR13921 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with H432A and R434A substns.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 291.5; DB 2; Length 522;

Best Local Similarity 22.7%; Pred. No. 6.8e-08;
 RESULT 985
 ID AAP70475 standard; protein; 564 AA.
 DE Sequence of tissue plasminogen (TPA) analogue.
 PN WO8703906-A.
 PD 02-JUL-1987.
 PA (UPJO) UPJOHN CO.
 PA (MARO/) MAROTTI K R.
 Query Match 7.4%; Score 291.5; DB 1; Length 564;
 Best Local Similarity 22.9%; Pred. No. 7.4e-08;
 RESULT 986
 ID ADG83838 standard; protein; 376 AA.
 DE Rough scale snake venom prothrombin activator, trocarin.
 PN WO2003082914-A1.
 PD 09-OCT-2003.
 PA (UYQU) UNIV QUEENSLAND.
 Query Match 7.4%; Score 291; DB 8; Length 376;
 Best Local Similarity 22.2%; Pred. No. 5.4e-08;
 RESULT 987
 ID AAP60614 standard; protein; 516 AA.
 DE Plasmid pDAP3 encoded sequence.
 PN JP61139386-A.
 PD 26-JUN-1986.
 PA (TOXJ) TOYO SODA MFG CO LTD.
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 PA (CENG) CENTRAL GLASS CO LTD.
 PA (HODO) HODOGAYA CHEM IND CO LTD.
 Query Match 7.4%; Score 290.5; DB 1; Length 516;
 Best Local Similarity 23.1%; Pred. No. 7.7e-08;
 RESULT 988
 ID AAP70257 standard; protein; 516 AA.
 DE Sequence of human tissue plasminogen activator (TPA) and leader.
 PN EP231883-A.
 PD 12-AUG-1987.
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 PA (NIPS) NIPPON SODA CO.
 PA (CENG) CENTRAL GLASS CO LTD.
 PA (TOXJ) TOYO SODA MFG CO LTD.
 PA (NISC) NISSAN CHEM IND LTD.
 PA (NISC) NISSAN CHEMICAL INDS KK.
 Query Match 7.4%; Score 290.5; DB 1; Length 516;
 Best Local Similarity 23.1%; Pred. No. 7.7e-08;
 RESULT 989
 ID AAR70878 standard; protein; 483 AA.
 DE Human tissue PA variant (deltal-44,N103,D184,E275).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC.
 Query Match 7.4%; Score 290; DB 2; Length 483;
 Best Local Similarity 23.3%; Pred. No. 7.7e-08;
 RESULT 990
 ID AAR70885 standard; protein; 483 AA.
 DE Human tissue PA variant (deltal-44,N103,D184,E275,I277).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC.
 Query Match 7.4%; Score 290; DB 2; Length 483;
 Best Local Similarity 23.3%; Pred. No. 7.7e-08;
 RESULT 991
 ID AAR70894 standard; protein; 527 AA.
 DE Human t-PA variant (N103,A303,A304).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC.
 Query Match 7.4%; Score 290; DB 2; Length 527;
 Best Local Similarity 24.0%; Pred. No. 8.3e-08;
 RESULT 992
 ID ADL00357 standard; protein; 520 AA.
 DE Human tissue type plasminogen activator (h-tPA) mutant polypeptide.
 PN CN1397564-A.
 PD 19-FEB-2003.
 PA (LIBB/) LI B.
 Query Match 7.3%; Score 289.5; DB 7; Length 520;

Best Local Similarity 23.2%; Pred. No. 8.7e-08;
 RESULT 993
 ID AAR12340 standard; protein; 559 AA.
 DE T-PA variant contg. fibrinectin for thrombosis lysis (1).
 PN JP03061482-A.
 PD 18-MAR-1991.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 Query Match 7.3%; Score 289.5; DB 2; Length 559;
 Best Local Similarity 22.2%; Pred. No. 9.4e-08;
 RESULT 994
 ID AAR22664 standard; protein; 564 AA.
 DE tPA analogue K2A.
 PN US5106741-A.
 PD 21-APR-1992.
 PA (UPJO) UPJOHN CO.
 Query Match 7.3%; Score 289.5; DB 2; Length 564;
 Best Local Similarity 23.4%; Pred. No. 9.4e-08;
 RESULT 995
 ID AAB06934 standard; protein; 658 AA.
 DE Human membrane-type serine protease (MTSP) 4-S splice variant.
 PN WO200157194-A2.
 PD 09-AUG-2001.
 PA (CORV-) CORVAS INT INC.
 Query Match 7.3%; Score 289.5; DB 4; Length 658;
 Best Local Similarity 22.7%; Pred. No. 1.1e-07;
 RESULT 996
 ID ADI10379 standard; protein; 658 AA.
 DE Human cell surface protease #5.
 PN WO200295007-A2.
 PD 28-NOV-2002.
 PA (CORV-) CORVAS INT INC.
 Query Match 7.3%; Score 289.5; DB 7; Length 658;
 Best Local Similarity 22.7%; Pred. No. 1.1e-07;
 RESULT 997
 ID ADJ46903 standard; protein; 658 AA.
 DE Human transmembrane serine protease (MTSP) polypeptide #5.
 PN US2004001801-A1.
 PD 01-JAN-2004.
 PA (CORV-) CORVAS INT INC.
 Query Match 7.3%; Score 289.5; DB 8; Length 658;
 Best Local Similarity 22.7%; Pred. No. 1.1e-07;
 RESULT 998
 ID AAB06933 standard; protein; 802 AA.
 DE Human membrane-type serine protease (MTSP) 4-L splice variant.
 PN WO200157194-A2.
 PD 09-AUG-2001.
 PA (CORV-) CORVAS INT INC.
 Query Match 7.3%; Score 289.5; DB 4; Length 802;
 Best Local Similarity 22.7%; Pred. No. 1.3e-07;
 RESULT 999
 ID ADI10377 standard; protein; 802 AA.
 DE Human cell surface protease #4.
 PN WO200295007-A2.
 PD 28-NOV-2002.
 PA (CORV-) CORVAS INT INC.
 Query Match 7.3%; Score 289.5; DB 7; Length 802;
 Best Local Similarity 22.7%; Pred. No. 1.3e-07;
 RESULT 1000
 ID ADJ46901 standard; protein; 802 AA.
 DE Human transmembrane serine protease (MTSP) polypeptide #4.
 PN US2004001801-A1.
 PD 01-JAN-2004.
 PA (CORV-) CORVAS INT INC.
 Query Match 7.3%; Score 289.5; DB 8; Length 802;
 Best Local Similarity 22.7%; Pred. No. 1.3e-07;
 RESULT 1001
 ID AAR21598 standard; protein; 527 AA.
 DE tPA variant - T103N, D236A, D238A, K240A.
 PN WO20202612-A.
 PD 20-FEB-1992.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 289; DB 2; Length 527;
 Best Local Similarity 23.4%; Pred. No. 9.4e-08;

```
RESULT 1002
ID AAR09217 standard; protein; 529 AA.
DE t-PA insertion variant I304 HH.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 289; DB 2; Length 529;
Best Local Similarity 23.4%; Pred. No. 9.5e-08;
RESULT 1003
ID AAB85076 standard; peptide; 296 AA.
DE Amino acid sequence of WASP-1 polypeptide.
PN WO200140451-A2.
PD 07-JUN-2001.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 7.3%; Score 288.5; DB 4; Length 296;
Best Local Similarity 29.3%; Pred. No. 5.9e-08;
RESULT 1004
ID AAY41710 standard; protein; 802 AA.
DE Human PRO618 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 2; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1005
ID AAB44266 standard; protein; 802 AA.
DE Human PRO618 (UNQ354) protein sequence SEQ ID NO:169.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 3; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1006
ID AAB24052 standard; protein; 802 AA.
DE Human PRO618 protein sequence SEQ ID NO:24.
PN WO200053754-A1.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 3; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1007
ID AAU82755 standard; protein; 802 AA.
DE Amino acid sequence of novel human protease #54.
PN WO200200860-A2.
PD 03-JAN-2002.
PA (SUG-) SUGEN INC.
Query Match 7.3%; Score 288.5; DB 5; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1008
ID ABO25212 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1009
ID ABU72218 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1010
ID ABO48498 standard; protein; 802 AA.
DE Human secreted and transmembrane polypeptide PRO618.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1011
ID ABU61096 standard; protein; 802 AA.
DE Human PRO618 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1012
ID ABU80365 standard; protein; 802 AA.
DE Human secreted/transmembrane protein PRO618.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1013
ID ADA24708 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1014
ID ABO19667 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1015
ID ADA12369 standard; protein; 802 AA.
DE Human secreted/transmembrane polypeptide PRO618.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1016
ID ABO19558 standard; protein; 802 AA.
DE Novel human secreted and transmembrane polypeptide #26.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1017
ID ADB73675 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003045482-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1018
ID ADB76391 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1019
ID ADC43817 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1020
ID ADC61577 standard; protein; 802 AA.
```


DE Human secreted/transmembrane protein, PRO618.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1021
ID ADC63541 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1022
ID ADC66641 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1023
ID ADC68765 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1024
ID ADC62825 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1025
ID ADC67890 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1026
ID ADC41210 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1027
ID ADC67265 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1028
ID ADC62201 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1029
ID ADC41834 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.

PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1030
ID ADE49203 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1031
ID ADE35257 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1032
ID ADE16371 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1033
ID ADD72986 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1034
ID ADD72344 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1035
ID ADE16995 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1036
ID ADF47009 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1037
ID ADG52766 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1038
ID ADG60086 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003206915-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match 22.7%; Pred. No. 1.5e-07;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1039
ID ADI60846 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match 22.7%; Pred. No. 1.5e-07;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1040
ID ADE48503 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match 22.7%; Pred. No. 1.5e-07;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1041
ID ADE89604 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATC/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1042
ID ADF61244 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match 22.7%; Pred. No. 1.5e-07;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1043
ID ADF39936 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match 22.7%; Pred. No. 1.5e-07;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1044
ID ADF45732 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003211092-A1.

PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match 22.7%; Pred. No. 1.5e-07;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1045
ID ADF24128 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match 22.7%; Pred. No. 1.5e-07;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1046
ID ADF40560 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match 22.7%; Pred. No. 1.5e-07;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1047
ID ADF23504 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match 22.7%; Pred. No. 1.5e-07;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1048
ID ADF33487 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match 22.7%; Pred. No. 1.5e-07;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1049
ID ADF26954 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match 22.7%; Pred. No. 1.5e-07;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1050
ID ADF27590 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match 22.7%; Pred. No. 1.5e-07;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1051
ID ADF41184 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match 22.7%; Pred. No. 1.5e-07;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1052
ID ADF32863 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match 22.7%; Pred. No. 1.5e-07;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1053
ID ADF25229 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003211092-A1.

PD 13-NOV-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1054
ID ADF26330 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1055
ID ADF34119 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1056
ID ADF46356 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1057
ID ADG50342 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1058
ID ADG49718 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1059
ID ADG51590 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1060
ID ADG49094 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1061
ID ADG48470 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1062
ID ADG50966 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004005312-A1.
PD 08-JAN-2004.

PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1063
ID ADG58910 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1064
ID ADG62366 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1065
ID ADH25391 standard; protein; 802 AA.
DE Human neurotrophin homologue related protein sequence SEQ ID NO:169.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1066
ID ADH17168 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1067
ID ADL07002 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1068
ID ADT91615 standard; protein; 802 AA.
DE Human PRO618 protein sequence.
PN AU2002317529-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1069
ID AAB98507 standard; protein; 902 AA.
DE Murine epithin.
PN WO200129056-A1.
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS. 7.3%; Score 288.5; DB 4; Length 902;
Query Match
Best Local Similarity 21.4%; Pred. No. 1.7e-07;
RESULT 1070
ID AAU80517 standard; protein; 902 AA.
DE Mouse epithilin-like serine protease.
PN WO200196378-A2.
PD 20-DEC-2001.
PA (FARB) BAYER AG. 7.3%; Score 288.5; DB 5; Length 902;
Query Match
Best Local Similarity 21.4%; Pred. No. 1.7e-07;
RESULT 1071
ID AAU77549 standard; protein; 902 AA.
DE Murine type II membrane serine protease, epithin.
PN WO20022461-A2.
PD 14-FEB-2002.
PA (FARB) BAYER AG.

```
Query Match
Best Local Similarity 7.3%; Score 288.5; DB 5; Length 902;
RESULT 1072
ID AAR05489 standard; protein; 527 AA.
DE tPA024 precursor protein.
PN EP373896-A.
PD 20-JUN-1990.
PA (YAMA ) YAMANOUCHI PHARM CO LTD.
PA (YAMA ) NIPPON STEEL CORP.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.6%; Pred. No. 1.1e-07;
RESULT 1073
ID AAR21599 standard; protein; 527 AA.
DE tPA variant - N117Q, D236A, D238A, K240A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1074
ID AAR20220 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-012.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.1e-07;
RESULT 1075
ID AAR20219 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-011.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.1e-07;
RESULT 1076
ID AAR20217 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-009.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.1e-07;
RESULT 1077
ID AAR20218 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-010.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.1e-07;
RESULT 1078
ID AAR70901 standard; protein; 527 AA.
DE Human t-PA variant (N103,A416,A417,A418) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 1.1e-07;
RESULT 1079
ID AAR70904 standard; protein; 527 AA.
DE Human t-PA variant (N103,A440) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1080
ID AAY49558 standard; protein; 356 AA.
DE Human protein C protein sequence.
PN WO9950454-A2.
PD 07-OCT-1999.
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
Query Match
Best Local Similarity 7.3%; Score 287.5; DB 2; Length 356;
RESULT 1081
ID AAM52187 standard; protein; 406 AA.
DE Human FVII mutant K143N/N145T/R315N/V317T.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match
Best Local Similarity 7.3%; Score 287.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 8.9e-08;
RESULT 1082
ID ADJ56078 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K143N/ N145T/ R290N/ A292T.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO ) NOVO NORDISK AS.
Query Match
Best Local Similarity 7.3%; Score 287.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 8.9e-08;
RESULT 1083
ID AAR13918 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with K416A, H417A and E418A substns.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 287.5; DB 2; Length 522;
Best Local Similarity 22.9%; Pred. No. 1.1e-07;
RESULT 1084
ID ABP43952 standard; protein; 795 AA.
DE Human PRO618.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 7.3%; Score 287.5; DB 5; Length 795;
Best Local Similarity 22.7%; Pred. No. 1.7e-07;
RESULT 1085
ID ADG83828 standard; protein; 467 AA.
DE Coastal taipan venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYQU ) UNIV QUEENSLAND.
Query Match
Best Local Similarity 7.3%; Score 287; DB 8; Length 467;
Best Local Similarity 22.5%; Pred. No. 1.1e-07;
RESULT 1086
ID AAR70879 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,S184,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1087
ID AAR70883 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,K210,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1088
ID AAR70884 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1089
ID AAR70886 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,S184,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1090
ID AAY49558 standard; protein; 356 AA.
DE Human protein C protein sequence.
PN WO9950454-A2.
PD 07-OCT-1999.
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
```

```
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1090
ID AAR70877 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1091
ID AAR70887 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,K213,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1092
ID AAR70881 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,R210,A211,R212,R213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1093
ID AAR70882 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,R252,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1094
ID AAR70889 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,R252,E275,O277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1095
ID AAR70888 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,R210,A211,R212,R213,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1096
ID AAR70890 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,K210,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1097
ID AAR70880 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,K213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1098
ID AAR70907 standard; protein; 527 AA.
DE Human t-PA variant (N103,A460,A462).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.2e-07;
RESULT 1099
ID AAR70874 standard; protein; 527 AA.
DE Human t-PA variant (N67,N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.2e-07;
RESULT 1100
ID AAR70892 standard; protein; 527 AA.
DE Human t-PA variant (N103,A283,A287).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.2e-07;
RESULT 1101
ID AAM52182 standard; protein; 406 AA.
DE Human FVII mutant K143N/N145T.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.3%; Score 286.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 1e-07;
RESULT 1102
ID ADJ56073 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K143N/ N145T.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1e-07;
RESULT 1103
ID ADO10589 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #25.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1e-07;
RESULT 1104
ID ADG83826 standard; protein; 467 AA.
DE Brown snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYQU ) UNIV QUEENSLAND.
Query Match 7.3%; Score 286.5; DB 8; Length 467;
Best Local Similarity 22.2%; Pred. No. 1.1e-07;
RESULT 1105
ID AAR14486 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with Y67N substitution.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 286.5; DB 2; Length 522;
Best Local Similarity 22.7%; Pred. No. 1.3e-07;
RESULT 1106
ID AAR44816 standard; protein; 527 AA.
DE Human tPA variant (N67,N103).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
RESULT 1107
ID AAR44812 standard; protein; 527 AA.
DE Human tPA variant N103.
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
```

RESULT 1108
ID AAR70868 standard; protein; 527 AA.
DE Human t-PA variant (N67,A432,A434).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
RESULT 1109
ID AAR70860 standard; protein; 527 AA.
DE Human t-PA variant (N67,A331,A332).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1110
ID AAR70900 standard; protein; 527 AA.
DE Human t-PA variant (N103,A410).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 1.4e-07;
RESULT 1111
ID AAR9220 standard; protein; 529 AA.
DE t-PA insertion variant 1304H, 1305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 529;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
RESULT 1112
ID AAP70449 standard; protein; 530 AA.
DE Sequence encoded by of synthetic gene for mature human tissue plasminogen activator (tPA).
PN WO8705934-A.
PD 08-OCT-1987.
PA (CREA/) CREA R.
Query Match 7.2%; Score 286; DB 1; Length 530;
Best Local Similarity 22.9%; Pred. No. 1.4e-07;
RESULT 1113
ID AAR12342 standard; protein; 561 AA.
DE T-PA with -ve charged finger and/or kringle domain (1).
PN JF03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 286; DB 2; Length 561;
Best Local Similarity 22.1%; Pred. No. 1.4e-07;
RESULT 1114
ID AAR9289 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BENT12 (Asp 67, Thr 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBT-) BRIT BIO-TECHN LTD.
Query Match 7.2%; Score 286; DB 2; Length 562;
Best Local Similarity 23.3%; Pred. No. 1.5e-07;
RESULT 1115
ID AAP70880 standard; protein; 527 AA.
DE Thrombolytic proteins 1-9-1-11 having t-PA activity and R275 is deleted or replaced and containing a modified N-linked glycosylation site.
PN WO8704722-A.
PD 13-AUG-1987.
PA (GEMY) GENETICS INST INC.
PA (LARS/) LARSEN G R.
Query Match 7.2%; Score 285.5; DB 1; Length 527;
Best Local Similarity 23.1%; Pred. No. 1.5e-07;
RESULT 1116
ID AAP91683 standard; protein; 527 AA.
DE Sequence of tissue plasminogen activator (tPA).
PN WO8911531-A.
PD 30-NOV-1989.

PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 1; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.5e-07;
RESULT 1117
ID AAR9270 standard; protein; 527 AA.
DE t-PA variant H331A, H332A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.5e-07;
RESULT 1118
ID AAR9278 standard; protein; 527 AA.
DE t-PA variant H432A, R434A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 1.5e-07;
RESULT 1119
ID AAP71449 standard; protein; 528 AA.
DE Modified human tissue plasminogen activator.
PN EP238304-A.
PD 23-SEP-1987.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 1; Length 528;
Best Local Similarity 23.4%; Pred. No. 1.6e-07;
RESULT 1120
ID AAR13148 standard; protein; 556 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (2).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 285; DB 2; Length 556;
Best Local Similarity 21.9%; Pred. No. 1.6e-07;
RESULT 1121
ID AAB11710 standard; protein; 264 AA.
DE Human serine protease BSSP5 (hbSSP5) SEQ ID NO:2.
PN WO200031243-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 7.2%; Score 284.5; DB 3; Length 264;
Best Local Similarity 28.0%; Pred. No. 8.6e-08;
RESULT 1122
ID AAP91961 standard; protein; 518 AA.
DE Sequence of des 1-44E275 t-PA mutant.
PN WO8909266-A.
PD 05-OCT-1989.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284.5; DB 1; Length 518;
Best Local Similarity 22.9%; Pred. No. 1.6e-07;
RESULT 1123
ID ABM84749 standard; protein; 629 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4998.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.2%; Score 284.5; DB 8; Length 629;
Best Local Similarity 19.5%; Pred. No. 1.9e-07;
RESULT 1124
ID ABM82817 standard; protein; 629 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3066.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.2%; Score 284.5; DB 8; Length 629;
Best Local Similarity 19.5%; Pred. No. 1.9e-07;
RESULT 1125
ID AAR70851 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,D184,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.

Query Match 7.2%; Score 284; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 1.8e-07;
RESULT 1126
ID AAR70844 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,D184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 1.6e-07;
RESULT 1127
ID AAR44809 standard; protein; 527 AA.
DE Human tPA variant (N65, 567).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 1.8e-07;
RESULT 1128
ID AAR70859 standard; protein; 527 AA.
DE Human t-PA variant (N103,A477).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.8e-07;
RESULT 1129
ID AAR70859 standard; protein; 527 AA.
DE Human t-PA variant (N67,A303,A304).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.8%; Pred. No. 1.8e-07;
RESULT 1130
ID AAR70893 standard; protein; 527 AA.
DE Human t-PA variant (N103,A296,A297,A298,A299).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 1.8e-07;
RESULT 1131
ID AAR70891 standard; protein; 527 AA.
DE Human t-PA variant (N103,A267).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.7%; Pred. No. 1.8e-07;
RESULT 1132
ID AAP70474 standard; protein; 562 AA.
DE Sequence of tissue plasminogen (TPA) analogue.
PN WO8703906-A.
PD 02-JUL-1987.
PA (UPJO) UPJOHN CO.
PA (MARO/) MAROTTI K R.
Query Match 7.2%; Score 284; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 1.9e-07;
RESULT 1133
ID AAR09286 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT5 (Ser 67, Ser 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match 7.2%; Score 284; DB 2; Length 562;
Best Local Similarity 23.1%; Pred. No. 1.9e-07;
RESULT 1134
ID AAR23807 standard; protein; 562 AA.
DE t-PA (Tyr 297) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.

Query Match 7.2%; Score 284; DB 2; Length 562;
Best Local Similarity 23.2%; Pred. No. 1.9e-07;
RESULT 1135
ID ABB80068 standard; protein; 406 AA.
DE Human coagulation factor VII mutant L305V/M306D/D309S.
PN WO200183725-A1.
PD 08-NOV-2001.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 5; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1136
ID ABG73125 standard; protein; 406 AA.
DE Human coagulation factor VII mutant polypeptide L305V/M306D/D309S.
PN WO200277218-A1.
PD 03-OCT-2002.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 6; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1137
ID ADJ5852 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant L305V/ M306D/ D309S.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 8; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1138
ID ADE83543 standard; protein; 482 AA.
DE Rat Protein NP 058839, SEQ ID NO 11161.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.2%; Score 283.5; DB 7; Length 482;
Best Local Similarity 22.8%; Pred. No. 1.7e-07;
RESULT 1139
ID AAR13917 standard; peptide; 522 AA.
DE Delta (466-470) tPA variant with K296A, H297A, R298A and R299A
DE substitutions.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283.5; DB 2; Length 522;
Best Local Similarity 22.8%; Pred. No. 1.8e-07;
RESULT 1140
ID AAP90169 standard; peptide; 571 AA.
DE Tissue plasminogen activator mutant 2G.
PN WO8907146-A.
PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Query Match 7.2%; Score 283.5; DB 1; Length 571;
Best Local Similarity 22.4%; Pred. No. 2e-07;
RESULT 1141
ID AAR09257 standard; protein; 483 AA.
DE t-PA variant d1-44, N184D, I210R, G211A, K212R, V213R, T252R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 1.8e-07;
RESULT 1142
ID AAR09269 standard; protein; 527 AA.
DE t-PA variant E303A, R304A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.7%; Pred. No. 2e-07;
RESULT 1143
ID AAR44810 standard; protein; 527 AA.
DE Human tPA variant (N65, T67).
PN US5270198-A.
PD 14-DEC-1993.

PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 2e-07;
RESULT 1144
ID AAR44817 standard; protein; 527 AA.
DE Human tPA variant (N67,A296,A297,A298,A299).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2e-07;
RESULT 1145
ID AAR44814 standard; protein; 527 AA.
DE Human tPA variant (N105, T107).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.6%; Pred. No. 2e-07;
RESULT 1146
ID AAR70899 standard; protein; 527 AA.
DE Human tPA variant (N103,A408).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 22.9%; Pred. No. 2e-07;
RESULT 1147
ID AAR12341 standard; protein; 560 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (3).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 283; DB 2; Length 560;
Best Local Similarity 22.1%; Pred. No. 2.1e-07;
RESULT 1148
ID AAR12367 standard; protein; 561 AA.
DE T-PA with -ve charged finger and/or kringle domain (7).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 283; DB 2; Length 561;
Best Local Similarity 22.1%; Pred. No. 2.1e-07;
RESULT 1149
ID AAR09231 standard; protein; 524 AA.
DE T-PA deletion variant d297-299.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 282.5; DB 2; Length 524;
Best Local Similarity 22.8%; Pred. No. 2.1e-07;
RESULT 1150
ID AAR09246 standard; protein; 483 AA.
DE t-PA variant dl-44, N184D, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 2.1e-07;
RESULT 1151
ID AAR09254 standard; protein; 483 AA.
DE t-PA variant dl-44, I210R, G211H, K212Q, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 483;
Best Local Similarity 22.8%; Pred. No. 2.1e-07;
RESULT 1152
ID AAR09230 standard; protein; 525 AA.
DE t-PA deletion variant d297-298.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.

Query Match 7.1%; Score 282; DB 2; Length 525;
Best Local Similarity 23.4%; Pred. No. 2.2e-07;
RESULT 1153
ID AAR09255 standard; protein; 527 AA.
DE t-PA variant I210R, G211H, K212Q, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 22.8%; Pred. No. 2.2e-07;
RESULT 1154
ID AAR21600 standard; protein; 527 AA.
DE tPA variant - E94A, D95A, T103N.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.2e-07;
RESULT 1155
ID AAR70866 standard; protein; 527 AA.
DE Human t-PA variant (N67,A416,A417,A418).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.2e-07;
RESULT 1156
ID AAR70902 standard; protein; 527 AA.
DE Human t-PA variant (N103,A426,A427,A429,A430).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.2e-07;
RESULT 1157
ID AAR70869 standard; protein; 527 AA.
DE Human t-PA variant (N67,A440).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.2e-07;
RESULT 1158
ID AAR2582 standard; protein; 562 AA.
DE Tissue plasminogen activator with S-119 substd for M and QG196-98 substd for NGT.
PN JP63230083-A.
PD 26-SEP-1988.
PA (EISA) EISAI CO LTD.
Query Match 7.1%; Score 282; DB 1; Length 562;
Best Local Similarity 23.2%; Pred. No. 2.4e-07;
RESULT 1159
ID AAR09287 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT6 (Thr 67, Asp 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match 7.1%; Score 282; DB 2; Length 562;
Best Local Similarity 23.1%; Pred. No. 2.4e-07;
RESULT 1160
ID AAR23808 standard; protein; 562 AA.
DE t-PA (Glu 298) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 282; DB 2; Length 562;
Best Local Similarity 23.5%; Pred. No. 2.4e-07;
RESULT 1161
ID AAR23810 standard; protein; 562 AA.
DE t-PA (Gly 301) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.

Query Match 7.1%; Score 282; DB 2; Length 562;
Best Local Similarity 23.6%; Pred. No. 2.4e-07;
RESULT 1162
ID AAB84869 standard; protein; 406 AA.
DE Mutant blood coagulant factor VII (FVII-30).
PN JP2001061479-A.
PD 13-MAR-2001.
PA (KAGA) ZH KAGAKU & KESSHI RYOHO KENKYUSHO.
Query Match 7.1%; Score 281.5; DB 4; Length 406;
Best Local Similarity 22.8%; Pred. No. 1.9e-07;
RESULT 1163
ID AAM52185 standard; protein; 406 AA.
DE Human FVII mutant G291N.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 281.5; DB 4; Length 406;
Best Local Similarity 22.8%; Pred. No. 1.9e-07;
RESULT 1164
ID AAO30584 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158D/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1165
ID AAO30626 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1166
ID AAO30582 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1167
ID AAO30616 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1168
ID AAO30572 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1169
ID AAO30628 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158D/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1170
ID ADJ55926 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;

Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1171
ID ADJ55927 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1172
ID ADJ55915 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1173
ID ADJ55970 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1174
ID ADJ56063 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158D/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1175
ID ADJ55959 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1176
ID ADJ56067 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158T/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1177
ID ADJ55971 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1178
ID ADJ56033 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1179
ID ADJ56076 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant G291N.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1180
ID ADJ56076 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant G291N.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.8%; Pred. No. 1.9e-07;

RESULT 1180
ID ADO10585 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #21.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.8%; Pred. No. 1.9e-07;
RESULT 1181
ID ADO10626 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #62.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 1.9e-07;
RESULT 1182
ID ADS12886 standard; protein; 406 AA.
DE Human factor VII G237L mutant.
PN WO2004083361-A2.
PD 30-SEP-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 1.9e-07;
RESULT 1183
ID AAR09233 standard; protein; 522 AA.
DE t-PA deletion variant d297-301.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 522;
Best Local Similarity 23.4%; Pred. No. 2.4e-07;
RESULT 1184
ID AAR13919 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with E426A, R427A, K429A and E430A
DE substitutions.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 522;
Best Local Similarity 22.7%; Pred. No. 2.4e-07;
RESULT 1185
ID AAR09239 standard; protein; 524 AA.
DE t-PA deletion variant d300-302.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 524;
Best Local Similarity 23.2%; Pred. No. 2.4e-07;
RESULT 1186
ID AAR12366 standard; protein; 562 AA.
DE T-PA with -ve charged finger and/or kringle domain (5).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281.5; DB 2; Length 562;
Best Local Similarity 21.9%; Pred. No. 2.5e-07;
RESULT 1187
ID AAR09249 standard; protein; 483 AA.
DE t-PA variant d1-44, I210R, G211A, K212R, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.3%; Pred. No. 2.3e-07;
RESULT 1188
ID AAR70855 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,K210,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.

PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1189
ID AAR70845 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,S184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1190
ID AAR70848 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,R252,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1191
ID AAR70849 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,K210,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1192
ID AAR70854 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,R252,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1193
ID AAR70843 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1194
ID AAR70846 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,K213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1195
ID AAR79144 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,S184,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1196
ID AAR70850 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1197
ID AAR70852 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,K213,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;

Query Match 7.1%; Score 281; DB 2; Length 483;
 Best Local Similarity 23.2%; Pred. No. 2.3e-07;
 RESULT 1198
 ID AAR70847 standard; protein; 483 AA.
 DE Human tissue PA variant (deltal-44,N67,R210,A211,R212,R213,E275).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 281; DB 2; Length 483;
 Best Local Similarity 23.0%; Pred. No. 2.3e-07;
 RESULT 1199
 ID AAR70853 standard; protein; 483 AA.
 DE Human tissue PA variant (deltal-44,N67,R210,A211,R212,R213,E275,I277).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 281; DB 2; Length 483;
 Best Local Similarity 23.0%; Pred. No. 2.3e-07;
 RESULT 1200
 ID AAR70851 standard; protein; 487 AA.
 DE Cattle Factor Xa.
 PN WO9418227-A2.
 PD 18-AUG-1994.
 PA (DENZ-) DENZYME APS.
 Query Match 7.1%; Score 281; DB 2; Length 487;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1201
 ID AAW76216 standard; protein; 488 AA.
 DE Human Factor X protein.
 PN WO9838317-A1.
 PD 03-SEP-1998.
 PA (IMMO) IMMUNO AG.
 Query Match 7.1%; Score 281; DB 2; Length 488;
 Best Local Similarity 24.0%; Pred. No. 2.4e-07;
 RESULT 1202
 ID AAW76217 standard; protein; 488 AA.
 DE Human Factor X protein analogue.
 PN WO9838317-A1.
 PD 03-SEP-1998.
 PA (IMMO) IMMUNO AG.
 Query Match 7.1%; Score 281; DB 2; Length 488;
 Best Local Similarity 22.6%; Pred. No. 2.4e-07;
 RESULT 1203
 ID AAW76218 standard; protein; 488 AA.
 DE Human Factor X protein.
 PN WO9838318-A1.
 PD 03-SEP-1998.
 PA (IMMO) IMMUNO AG.
 Query Match 7.1%; Score 281; DB 2; Length 489;
 Best Local Similarity 24.0%; Pred. No. 2.4e-07;
 RESULT 1204
 ID AAB70411 standard; protein; 488 AA.
 DE Human factor X protein sequence SEQ ID NO:2.
 PN WO200110896-A2.
 PD 15-FEB-2001.
 PA (BAXT) BAXTER AG.
 Query Match 7.1%; Score 281; DB 4; Length 488;
 Best Local Similarity 24.0%; Pred. No. 2.4e-07;
 RESULT 1205
 ID AAR60502 standard; protein; 492 AA.
 DE Serine protease for fusion protein cleavage.
 PN WO9418227-A2.
 PD 18-AUG-1994.
 PA (DENZ-) DENZYME APS.
 Query Match 7.1%; Score 281; DB 2; Length 492;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1206
 ID AAR09238 standard; protein; 525 AA.
 DE t-PA deletion variant d300-301.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 281; DB 2; Length 525;

Best Local Similarity 22.8%; Pred. No. 2.5e-07;
 RESULT 1207
 ID AAR09276 standard; protein; 527 AA.
 DE t-PA variant K416A, H417A, E418A.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 281; DB 2; Length 527;
 Best Local Similarity 23.2%; Pred. No. 2.5e-07;
 RESULT 1208
 ID AAR09279 standard; protein; 527 AA.
 DE t-PA variant R440A.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 281; DB 2; Length 527;
 Best Local Similarity 23.0%; Pred. No. 2.5e-07;
 RESULT 1209
 ID AAR70875 standard; protein; 527 AA.
 DE Human t-PA variant (N60,N103).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 281; DB 2; Length 527;
 Best Local Similarity 23.2%; Pred. No. 2.5e-07;
 RESULT 1210
 ID AAR70876 standard; protein; 527 AA.
 DE Human t-PA variant (N60,N67,N103).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 281; DB 2; Length 527;
 Best Local Similarity 23.2%; Pred. No. 2.5e-07;
 RESULT 1211
 ID AAR70857 standard; protein; 527 AA.
 DE Human t-PA variant (N67,A283,A287).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 281; DB 2; Length 527;
 Best Local Similarity 23.2%; Pred. No. 2.5e-07;
 RESULT 1212
 ID AAR70898 standard; protein; 527 AA.
 DE Human t-PA variant (N103,A364,A365,A366).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 281; DB 2; Length 527;
 Best Local Similarity 23.2%; Pred. No. 2.5e-07;
 RESULT 1213
 ID AAR70906 standard; protein; 527 AA.
 DE Human t-PA variant (N103,A449,A453).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 281; DB 2; Length 527;
 Best Local Similarity 23.0%; Pred. No. 2.5e-07;
 RESULT 1214
 ID AAR70872 standard; protein; 527 AA.
 DE Human t-PA variant (N67,A460,A462).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 281; DB 2; Length 527;
 Best Local Similarity 23.2%; Pred. No. 2.5e-07;
 RESULT 1215
 ID AAR70842 standard; protein; 527 AA.
 DE Wild type tissue plasminogen activator protein.
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 281; DB 2; Length 527;
 Best Local Similarity 23.2%; Pred. No. 2.5e-07;

RESULT 1216
ID AAR13150 standard; protein; 558 AA.
DE T-PA with -ve charged finger and/or kringle domain (3).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281; DB 2; Length 558;
Best Local Similarity 23.0%; Pred. No. 2.7e-07;
RESULT 1217
ID AAR13152 standard; protein; 559 AA.
DE T-PA with -ve charged finger and/or kringle domain (6).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281; DB 2; Length 559;
Best Local Similarity 23.0%; Pred. No. 2.7e-07;
RESULT 1218
ID AAP80691 standard; protein; 1087 AA.
DE Hybrid plasminogen/t-PA compound 1.
PN EP292326-A.
PD 23-NOV-1988.
PA (BEEC) BEECHAM GROUP PLC.
Query Match 7.1%; Score 281; DB 1; Length 1087;
Best Local Similarity 22.3%; Pred. No. 5e-07;
RESULT 1219
ID ABM81778 standard; protein; 264 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ:4580.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280.5; DB 8; Length 264;
Best Local Similarity 27.2%; Pred. No. 1.4e-07;
RESULT 1220
ID ABM84054 standard; protein; 279 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4303.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.1%; Score 280.5; DB 8; Length 279;
Best Local Similarity 27.2%; Pred. No. 1.5e-07;
RESULT 1221
ID AAO30575 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158D/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1222
ID AAO30604 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1223
ID AAO30577 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1224
ID AAO30594 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1225
ID AAO30595 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158D/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;

ID AAO30569 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1226
ID AAO30606 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158D/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1227
ID AAO30613 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1228
ID AAO30621 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1229
ID AAO30619 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158D/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1230
ID ADJ55876 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant / M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1231
ID ADJ55937 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1232
ID ADJ56047 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158D/ M298Q/ L305V/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1233
ID ADJ55949 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1234
ID ADJ55965 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1235
ID ADJ55965 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;

DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1235
ID ADJ55948 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1236
ID ADJ56057 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y V158T M298Q L305V S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1237
ID ADJ55885 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1238
ID ADJ55921 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1239
ID ADJ55958 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1240
ID ADJ55963 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1241
ID ADJ56016 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/ M298Q/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1242
ID ADJ56046 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158D/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1243
ID ADJ55919 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ S314E.

PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1244
ID ADJ56056 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158T/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1245
ID ADJ55887 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1246
ID ADJ55914 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1247
ID ADJ56004 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305VK337A/ M298Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1248
ID ADO10616 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #52.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.1e-07;
RESULT 1249
ID ADO10607 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #43.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.1e-07;
RESULT 1250
ID AAR09221 standard; protein; 526 AA.
DE t-PA deletion variant d297.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280.5; DB 2; Length 526;
Best Local Similarity 23.1%; Pred. No. 2.7e-07;
RESULT 1251
ID AAP70020 standard; protein; 561 AA.
DE Sequence of tissue plasminogen activator (tPA).
PN EP242836-A.
PD 28-OCT-1987.
PA (BOEF) BOSHRINGER MANNHEIM GMBH.
Query Match 7.1%; Score 280.5; DB 1; Length 561;
Best Local Similarity 21.7%; Pred. No. 2.9e-07;
RESULT 1252
ID ABR62449 standard; protein; 583 AA.

DE Bovine recombinant prothrombin, expressed in Escherichia coli.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.1%; Score 280.5; DB 7; Length 583;
Best Local Similarity 21.9%; Pred. No. 3e-07;
RESULT 1253
ID ABR62451 standard; protein; 635 AA.
DE Bovine recombinant prothrombin, expressed in CHO cells.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.1%; Score 280.5; DB 7; Length 635;
Best Local Similarity 21.9%; Pred. No. 3.2e-07;
RESULT 1254
ID AAR37402 standard; protein; 448 AA.
DE Factor X.
PN WO9309803-A1.
PD 27-MAY-1993.
PA (SCHN/) SCHAFFER S C.
PA (SCRI) SCRIPPS RES INST.
Query Match 7.1%; Score 280; DB 2; Length 448;
Best Local Similarity 24.0%; Pred. No. 2.5e-07;
RESULT 1255
ID AAW66092 standard; peptide; 448 AA.
DE Human factor X variant.
PN WO9839456-A1.
PD 11-SEP-1998.
PA (UNIW) UNIV WASHINGTON.
Query Match 7.1%; Score 280; DB 2; Length 448;
Best Local Similarity 24.0%; Pred. No. 2.5e-07;
RESULT 1256
ID AAR09245 standard; protein; 525 AA.
DE t-PA deletion variant d297, d305.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 525;
Best Local Similarity 23.1%; Pred. No. 2.9e-07;
RESULT 1257
ID AAR05488 standard; protein; 527 AA.
DE t-PA024 precursor protein.
PN EP373896-A.
PD 20-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
PA (YAWA) NIPPON STEEL CORP.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1258
ID AAR09267 standard; protein; 527 AA.
DE t-PA variant D283A, H287A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1259
ID AAR09282 standard; protein; 527 AA.
DE t-PA variant D460A, R462A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1260
ID AAR13911 standard; protein; 527 AA.
DE t-PA deriv. (II).
PN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1261
ID AAR13914 standard; protein; 527 AA.
DE T-PA deriv. (V).
PN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1262
ID AAR13912 standard; protein; 527 AA.
DE T-PA deriv. (III).
PN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1263
ID AAR13910 standard; protein; 527 AA.
DE T-PA deriv. (I).
PN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1264
ID AAR21594 standard; protein; 527 AA.
DE t-PA variant - D95A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1265
ID AAR21593 standard; protein; 527 AA.
DE t-PA analog - E94A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.9e-07;
RESULT 1266
ID AAR20221 standard; protein; 527 AA.
DE t-PA analog expressed by pCDM8-013.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1267
ID AAR20215 standard; protein; 527 AA.
DE R462E t-PA analogue.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1268
ID AAR20216 standard; protein; 527 AA.
DE R462G t-PA analogue.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1269
ID AAR20222 standard; protein; 527 AA.
DE t-PA analog expressed by pCDM8-014.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1270
ID AAR20223 standard; protein; 527 AA.

DE t-PA analogue expressed by pCDM8-018.
PN JF03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIVAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1271
ID AAR44811 standard; protein; 527 AA.
DE Human tPA variant N67.
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1272
ID AAR70865 standard; protein; 527 AA.
DE Human t-PA variant (N67,A410).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 22.9%; Pred. No. 2.9e-07;
RESULT 1273
ID RAM57778 standard; protein; 527 AA.
DE R275E,H417D human tissue-type plasminogen activator protein mutant.
PN WO9821320-A2.
PD 22-MAY-1998.
PA (SCRI) SCRIPPS RES INST.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1274
ID AAM45907 standard; peptide; 527 AA.
DE Single chain form of the intact t-PA molecule.
PN WO9802454-A2.
PD 22-JAN-1998.
PA (ADPR-) ADPROTECH PLC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1275
ID AAE24190 standard; protein; 527 AA.
DE Human tissue plasminogen activator (tPA) protein.
PN WO200240695-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1276
ID AAG79362 standard; protein; 527 AA.
DE Human tissue plasminogen activator.
PN WO200243747-A2.
PD 06-JUN-2002.
PA (ISIS-) ISIS INNOVATION LTD.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1277
ID AAE25044 standard; protein; 527 AA.
DE Human tissue plasminogen activator (tPA) protein.
PN WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1278
ID ADL92126 standard; protein; 527 AA.
DE Altoplase protein sequence.
PN WO2003099862-A1.
PD 04-DEC-2003.
PA (NANO-) APPLIED NANOSYSTEMS BV.
Query Match 7.1%; Score 280; DB 8; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1279
ID ABM82630 standard; protein; 534 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2879.

PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.1%; Score 280; DB 8; Length 534;
Best Local Similarity 22.7%; Pred. No. 2.9e-07;
RESULT 1280
ID ABM82821 standard; protein; 534 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3070.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.1%; Score 280; DB 8; Length 534;
Best Local Similarity 22.7%; Pred. No. 2.9e-07;
RESULT 1281
ID AAR13020 standard; protein; 557 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (4).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 557;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1282
ID AAR13149 standard; protein; 557 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (4).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 557;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1283
ID AAP50219 standard; protein; 561 AA.
DE Tissue plasminogen activator encoded by cDNA clone.
PN EP143081-A.
PD 29-MAY-1985.
PA (CIBA) CIBA GEIGY AG.
Query Match 7.1%; Score 280; DB 1; Length 561;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1284
ID AAP60790 standard; protein; 562 AA.
DE Sequence of human pre-tissue plasminogen activator (pre-t-PA).
PN GB2173804-A.
PD 22-OCT-1986.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1285
ID AAP60810 standard; protein; 562 AA.
DE Sequence of modified human tissue plasminogen activator (t-PA).
PN FR2581652-A.
PD 14-NOV-1986.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1286
ID AAP60214 standard; protein; 562 AA.
DE Sequence of active human uterine tissue plasminogen activator (UTPA).
PN EP178105-A.
PD 16-APR-1986.
PA (INTE-) INTEG GENETICS INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1287
ID AAP81913 standard; protein; 562 AA.
DE Tissue plasminogen activator encoded by pEmpl-tPA.
PN WO8800242-A.
PD 14-JAN-1988.
PA (DAMO-) DAMON BIOTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1288
ID AAP80655 standard; protein; 562 AA.
DE Tissue plasminogen activator analogue.
PN EP293934-A.

PD 07-DEC-1988.
PA (ZYMO) ZYMOGENETICS INC.
PA (NOVO) NOVO IND AS.
PA (EISA) EISA CO LTD.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1289
ID AAP94406 standard; protein; 562 AA.
DE Sequence encoded by native tPA of plasmid pST112.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1290
ID AAP93716 standard; protein; 562 AA.
DE Human melanoma t-PA encoded by plasmid pKG12.
PN EP297066-A.
PD 28-DEC-1988.
PA (KABI) KABIGEN AB.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1291
ID AAP90916 standard; protein; 562 AA.
DE Human tissue plasminogen activator.
PN JP01174388-A.
PD 10-JUL-1989.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1292
ID' AAR09288 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT11 (Ser 67, Leu 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1293
ID AAR06237 standard; protein; 562 AA.
DE Novel tissue plasminogen activator (tPA) encoded by plasmid pST112.
PN EP379890-A.
PD 01-AUG-1990.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1294
ID AAR04700 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA C87S, H420S with altered residues 419 and 420.
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1295
ID AAR04701 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA K419S with altered residue 419.
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1296
ID AAR04699 standard; protein; 562 AA.
DE Native tissue plasminogen activator (t-PA).
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.

PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1297
ID AAR13727 standard; protein; 562 AA.
DE T-PA67+ mutant with supernumerary N-linked oligosaccharide side chain.
PN US5041376-A.
PD 20-AUG-1991.
PA (TEXA) UNIV TEXAS SYSTEM.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1298
ID AAR12847 standard; protein; 562 AA.
DE T-PA Kringie 1 domain substitution mutant.
PN JP03127987-A.
PD 31-MAY-1991.
PA (KANF) KANEGAFUCHI CHEM KK.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1299
ID AAR3811 standard; protein; 562 AA.
DE t-PA (Glu 296, Glu 298, Glu 299) triple mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.5%; Pred. No. 3.1e-07;
RESULT 1300
ID AAR23806 standard; protein; 562 AA.
DE t-PA (Glu 296) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1301
ID AAR23804 standard; protein; 562 AA.
DE t-PA (Glu 304) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1302
ID AAR34426 standard; protein; 562 AA.
DE Sequence of human pre-pro tissue plasminogen activator (t-PA).
PN US5200340-A.
PD 06-APR-1993.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1303
ID AAR96220 standard; protein; 562 AA.
DE Full-length tissue plasminogen activator.
PN US5504001-A.
PD 02-APR-1996.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1304
ID AAY50868 standard; protein; 562 AA.
DE Human tissue plasminogen activator protein fragment.
PN WO957251-A2.
PD 11-NOV-1999.
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
Query Match 7.1%; Score 280; DB 3; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1305
ID AAY43397 standard; protein; 562 AA.
DE Human tissue plasminogen activator protein sequence.
PN US5985607-A.
PD 16-NOV-1999.

PA (CANG-) CANGENE CORP.
 Query Match 7.1%; Score 280; DB 3; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1306
 ID AAY99590 standard; protein; 562 AA.
 DE Human tissue-type plasminogen activator t-PA.
 PN WO200032759-A1.
 PD 08-JUN-2000.
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 Query Match 7.1%; Score 280; DB 3; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1307
 ID RAU97700 standard; protein; 562 AA.
 DE Human tissue plasminogen activator (t-PA) protein sequence.
 PN WO200232446-A2.
 PD 25-APR-2002.
 PA (PFIZ) PFIZER LTD.
 Query Match 7.1%; Score 280; DB 5; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1308
 ID AAE37130 standard; protein; 562 AA.
 DE Human tissue-type plasminogen activator (t-PA) protein.
 PN WO2003033009-A2.
 PD 24-APR-2003.
 PA (OMNI-) OMNIO AB.
 Query Match 7.1%; Score 280; DB 6; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1309
 ID ABR55851 standard; protein; 562 AA.
 DE Human tissue-type plasminogen activator (TPA).
 PN WO2003031464-A2.
 PD 17-APR-2003.
 PA (NEOS-) NEOSE TECHNOLOGIES INC.
 Query Match 7.1%; Score 280; DB 6; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1310
 ID ABUS7646 standard; protein; 562 AA.
 DE Differentially expressed breast cancer associated protein #33.
 PN US002156263-A1.
 PD 24-OCT-2002.
 PA (CHEN/) CHEN H.
 Query Match 7.1%; Score 280; DB 6; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1311
 ID ADN95624 standard; protein; 562 AA.
 DE Human BSC/LEC-related protein sequence SeqID547.
 PN WO2003080640-A1.
 PD 02-OCT-2003.
 PA (LUDW-) LUDWIG INST CANCER RES.
 Query Match 7.1%; Score 280; DB 7; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1312
 ID ADNA9698 standard; protein; 562 AA.
 DE Human tissue type plasminogen activator TPA protein SeqID 26.
 PN WO2004033651-A2.
 PD 22-APR-2004.
 PA (NEOS-) NEOSE TECHNOLOGIES INC.
 Query Match 7.1%; Score 280; DB 8; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1313
 ID ADO28679 standard; protein; 562 AA.
 DE Human tPA protein SEQ ID NO.108.
 PN WO2004044178-A2.
 PD 27-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 280; DB 8; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1314
 ID ABM80983 standard; protein; 562 AA.
 DE Tumour-associated antigenic target (TAT) polypeptide PRO4, SEQ:2535.
 PN WO2004030615-A2.

PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 280; DB 8; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1315
 ID ADQ39248 standard; protein; 562 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 911.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 7.1%; Score 280; DB 8; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1316
 ID AAO30591 standard; protein; 406 AA.
 DE Human coagulation factor VII variant (K316H/L305V/M298Q).
 PN WO2003037932-A2.
 PD 08-MAY-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 279.5; DB 6; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1317
 ID AAO30599 standard; protein; 406 AA.
 DE Human coagulation factor VII variant (K316H/L305V/V158T/M298Q).
 PN WO2003037932-A2.
 PD 08-MAY-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 279.5; DB 6; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1318
 ID AAO30597 standard; protein; 406 AA.
 DE Human coagulation factor VII variant (K316H/L305V/V158D/M298Q).
 PN WO2003037932-A2.
 PD 08-MAY-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 279.5; DB 6; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1319
 ID ADJ55873 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant M298Q/ L305V.
 PN WO2004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 279.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1320
 ID ADJ55985 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant F374Y/ L305V/ M298Q.
 PN WO2004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 279.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1321
 ID ADJ55941 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316H.
 PN WO2004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 279.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1322
 ID ADJ55943 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316H.
 PN WO2004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 279.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1323
 ID ADJ56009 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant F374Y/ L305V/ V158D/ M298Q.
 PN WO2004000366-A1.
 PD 31-DEC-2003.

PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1324
ID ADJ55879 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1325
ID ADJ56014 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/ V158T/ M298Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1326
ID ADJ55881 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1327
ID ADJ55936 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316H.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1328
ID ADO10619 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #55.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.4e-07;
RESULT 1329
ID AAR74689 standard; protein; 520 AA.
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by QRLASQA).
PN CN1082111-A.
PD 16-FEB-1994.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
Query Match 7.1%; Score 279.5; DB 2; Length 520;
Best Local Similarity 23.3%; Pred. No. 3e-07;
RESULT 1330
ID AAR09229 standard; protein; 526 AA.
DE t-PA deletion variant d305.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279.5; DB 2; Length 526;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1331
ID AAR09228 standard; protein; 526 AA.
DE t-PA deletion variant d304.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279.5; DB 2; Length 526;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1332
ID AAR09218 standard; protein; 528 AA.
DE t-PA insertion variant i305 H, T, N, K, R, Q.
PN WO9002798-A.
PD 22-MAR-1990.

PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279.5; DB 2; Length 528;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1333
ID ABG96427 standard; protein; 782 AA.
DE Human ovarian cancer marker OV82.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.1%; Score 279.5; DB 5; Length 782;
Best Local Similarity 20.8%; Pred. No. 4.4e-07;
RESULT 1334
ID AAB84871 standard; protein; 401 AA.
DE Mutant blood coagulant factor VII (FVII-39).
PN JP2001061479-A.
PD 13-MAR-2001.
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
Query Match 7.1%; Score 279; DB 4; Length 401;
Best Local Similarity 22.8%; Pred. No. 2.5e-07;
RESULT 1335
ID AAR09250 standard; protein; 483 AA.
DE t-PA variant dl-44, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1336
ID AAR09248 standard; protein; 483 AA.
DE t-PA variant dl-44, I210R, G211A, K212R, V213R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 483;
Best Local Similarity 22.8%; Pred. No. 3e-07;
RESULT 1337
ID AAR09247 standard; protein; 483 AA.
DE t-PA variant dl-44, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1338
ID AAR09251 standard; protein; 483 AA.
DE t-PA variant dl-44, T252R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1339
ID AAR09263 standard; protein; 483 AA.
DE t-PA variant Y67N, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1340
ID AAR09252 standard; protein; 483 AA.
DE t-PA variant dl-44, V213K, T252R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1341
ID AAR09253 standard; protein; 483 AA.
DE t-PA variant dl-44, I210K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.

```
Query Match          7.1%; Score 279; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 3.e-07;
RESULT 1342
ID AAR09243 standard; protein; 525 AA.
DE t-PA deletion variant d304-305.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.

Query Match          7.1%; Score 279; DB 2; Length 525;
Best Local Similarity 23.0%; Pred. No. 3.2e-07;
RESULT 1343
ID AAR04186 standard; protein; 527 AA.
DE Plasminogen activator.
PN EP365468-A.
PD 25-APR-1990.
PA (CIBA ) CIBA GEIGY AG.
PA (UCPG-) UCP GEN-PHARMA AG.

Query Match          7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 3.3e-07;
RESULT 1344
ID AAR06236 standard; protein; 527 AA.
DE Novel tissue plasminogen activator (tPA) encoding plasmid pTPA102.
PN EP379890-A.
PD 01-AUG-1990.
PA (FUJI ) FUJISAWA PHARM CO LTD.

Query Match          7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1345
ID AAR09256 standard; protein; 527 AA.
DE t-PA variant I210R, G211A, K212R, V213R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.

Query Match          7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 22.8%; Pred. No. 3.3e-07;
RESULT 1346
ID AAR09275 standard; protein; 527 AA.
DE t-PA variant E410A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.

Query Match          7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 22.8%; Pred. No. 3.3e-07;
RESULT 1347
ID AAR09215 standard; protein; 527 AA.
DE t-PA variant F305 H, T, N, K, R, Q.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.

Query Match          7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1348
ID AAR09262 standard; protein; 527 AA.
DE t-PA variant Y67N, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.

Query Match          7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1349
ID AAR21596 standard; protein; 527 AA.
DE t-PA variant - E94A, D95A, N117Q.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH ) GENENTECH INC.

Query Match          7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1350
ID AAR21595 standard; protein; 527 AA.
DE t-PA variant - D95G.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH ) GENENTECH INC.

Query Match          7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1351
ID AAR21597 standard; protein; 527 AA.
DE t-PA variant - E94A, D95A, D236A, K240A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH ) GENENTECH INC.

Query Match          7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1352
ID AAR44813 standard; protein; 527 AA.
DE Human tPA variant (N105, S107).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.

Query Match          7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 3.3e-07;
RESULT 1353
ID AAR70905 standard; protein; 527 AA.
DE Human t-PA variant (N103,A445,A449).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.

Query Match          7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1354
ID AAW57779 standard; protein; 527 AA.
DE R275E,H417E human tissue-type plasminogen activator protein mutant.
PN WO9821320-A2.
PD 22-MAY-1998.
PA (SCRI ) SCRIPPS RES INST.

Query Match          7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1355
ID AAR25435 standard; protein; 528 AA.
DE t-PA variant R299D.
PN WO9211377-A1.
PD 09-JUL-1992.
PA (GETH ) GENENTECH INC.

Query Match          7.1%; Score 279; DB 2; Length 528;
Best Local Similarity 23.5%; Pred. No. 3.3e-07;
RESULT 1356
ID AAR09219 standard; protein; 529 AA.
DE t-PA insertion variant I305 HH.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.

Query Match          7.1%; Score 279; DB 2; Length 529;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1357
ID AAP70882 standard; protein; 530 AA.
DE Thrombolytic protein 1-19-1-21 having t-PA activity, deleted or replaced
DE R275 is and containing a modified N-linked glycosylation site.
PN WO8704722-A.
PD 13-AUG-1987.
PA (GENY ) GENETICS INST INC.
PA (LARS/) LARSEN G R.

Query Match          7.1%; Score 279; DB 1; Length 530;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1358
ID AAP71659 standard; protein; 530 AA.
DE Thrombolytic protein with t-PA activity where R275 is deleted or replaced
DE and containing a modified N-linked glycosylation site.
PN WO8704722-A.
PD 13-AUG-1987.
PA (GENY ) GENETICS INST INC.
PA (LARS/) LARSEN G R.

Query Match          7.1%; Score 279; DB 1; Length 530;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1359
ID AAP70879 standard; protein; 530 AA.
DE Thrombolytic proteins 1-1-1-7 having t-PA activity, where R275 is deleted
```

DE or replaced.
PN WO8704722-A.
PD 13-AUG-1987.
PA (GEMV) GENETICS INST INC.
PA (LARS/) LARSEN G R.
Query Match 7.1%; Score 279; DB 1; Length 530;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1360
ID AAP92277 standard; protein; 530 AA.
DE Sequence of modified tPA-type thrombolytic proteins.
PN WO8810119-A.
PD 29-DEC-1988.
PA (GEMV) GENETICS INST INC.
Query Match 7.1%; Score 279; DB 1; Length 530;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1361
ID AAP30001 standard; protein; 562 AA.
DE Sequence of full length tissue plasminogen activator (t-Pa).
PN EP93619-A.
PD 09-NOV-1983.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 1; Length 562;
Best Local Similarity 22.9%; Pred. No. 3.5e-07;
RESULT 1362
ID AAP94238 standard; protein; 562 AA.
DE Human tissue plasminogen activator (t-Pa) gene.
PN WO8900197-A.
PD 12-JAN-1989.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1363
ID AAR23803 standard; protein; 562 AA.
DE t-PA (Ser 304) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 279; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1364
ID AAR23801 standard; protein; 562 AA.
DE Zymogen-like t-PA (His 305).
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 279; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1365
ID AAW47536 standard; protein; 562 AA.
DE Tissue plasminogen activator variant R275E.
PN US5714372-A.
PD 03-FEB-1998.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1366
ID AAW47537 standard; protein; 562 AA.
DE Tissue plasminogen activator variant I276P.
PN US5714372-A.
PD 03-FEB-1998.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1367
ID AAW47535 standard; protein; 562 AA.
DE Tissue plasminogen activator variant R275G.
PN US5714372-A.
PD 03-FEB-1998.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1368
ID AAW48426 standard; protein; 562 AA.

DE Tissue type plasminogen activator, tPA.
PN KR141262-B1.
PD 15-JUN-1998.
PA (GLDS) LG CHEM LTD.
Query Match 7.1%; Score 279; DB 3; Length 562;
Best Local Similarity 22.9%; Pred. No. 3.5e-07;
RESULT 1369
ID ADR43718 standard; protein; 932 AA.
DE Human protease PRYS-6, SEQ ID 6.
PN WO200220736-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.1%; Score 279; DB 5; Length 932;
Best Local Similarity 23.4%; Pred. No. 5.5e-07;
RESULT 1370
ID AAU82743 standard; protein; 970 AA.
DE Amino acid sequence of novel human protease #42.
PN WO200200860-A2.
PD 03-JAN-2002.
PA (SUGE-) SUGEN INC.
Query Match 7.1%; Score 279; DB 5; Length 970;
Best Local Similarity 23.4%; Pred. No. 5.8e-07;
RESULT 1371
ID ABR39439 standard; protein; 264 AA.
DE Human GENSET polypeptide clone name vCTRL-1.
PN WO2003014151-A2.
PD 20-FEB-2003.
PA (GEST) GENSET SA.
Query Match 7.1%; Score 278.5; DB 6; Length 264;
Best Local Similarity 27.2%; Pred. No. 1.8e-07;
RESULT 1372
ID AAB84867 standard; protein; 406 AA.
DE Mutant blood coagulant factor VII (FVII-5).
PN JP2001061479-A.
PD 13-MAR-2001.
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
Query Match 7.1%; Score 278.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 2.7e-07;
RESULT 1373
ID AAMS2183 standard; protein; 406 AA.
DE Human FVII mutant V253N.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 278.5; DB 4; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.7e-07;
RESULT 1374
ID AAO30631 standard; protein; 406 AA.
DE Human factor VII variant (K316Q/L305V/V158T/E296V/M298Q/K337A).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1375
ID AAO30610 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/K337A).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1376
ID AAO30615 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/K337A/V158T).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1377
ID AAO30587 standard; protein; 406 AA.
DE Human factor VII variant (S314E/L305V/V158T/E296V/M298Q/K337A).

PN WO2003037932-A2.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1378
ID AAO30571 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/K337A/V158T).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1379
ID AAO30630 standard; protein; 406 AA.
DE Human factor VII variant (K316Q/L305V/V158D/E296V/M298Q/K337A).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1380
ID AAO30574 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/K337A/V158D).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1381
ID AAO30618 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/K337A/V158D).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1382
ID AAO30586 standard; protein; 406 AA.
DE Human factor VII variant (S314E/L305V/V158D/E296V/M298Q/K337A).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1383
ID AAO30566 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/K337A).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1384
ID ADJ55962 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1385
ID ADJ56051 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158T/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1386
ID ADJ55918 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ L305V/ S314E/ K337A.
PN WO2004000366-A1.

PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1387
ID ADJ56069 standard; protein; 406 AA.
DE Human factor VII mutein F374Y/ V158T/ E296V/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1388
ID ADJ55917 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1389
ID ADJ55931 standard; protein; 406 AA.
DE Human factor VII protein mutant V158T/ E296V/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1390
ID ADJ55972 standard; protein; 406 AA.
DE Human factor VII protein mutant V158D/ E296V/ M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1391
ID ADJ56005 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/ K337A/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1392
ID ADJ56039 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ V158DK337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1393
ID ADJ56041 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158D/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1394
ID ADJ55928 standard; protein; 406 AA.
DE Human factor VII protein mutant V158D/ E296V/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1395
ID ADJ56064 standard; protein; 406 AA.
DE Human factor VII mutein F374Y/ V158D/ E296V/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.

PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1396
ID ADJ56074 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V253N.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.7e-07;
RESULT 1397
ID ADJ55961 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1398
ID ADJ56017 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ K337A/ S314E/ M298Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.3%; Pred. No. 2.7e-07;
RESULT 1399
ID ADJ55954 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1400
ID ADJ55910 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1401
ID ADJ55975 standard; protein; 406 AA.
DE Human factor VII protein mutant V158T/ E296V/ M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1402
ID ADJ56050 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158T/ M298Q/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1403
ID ADO10592 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #28.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.7e-07;
RESULT 1404
ID ADO10602 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #38.
PN WO2004029091-A2.
PD 08-APR-2004.

PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.7e-07;
RESULT 1405
ID AAP60056 standard; protein; 466 AA.
DE Factor VII peptide encoded by cDNA clone lambda VII2463.
PN EP200421-A.
PD 10-DEC-1986.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.1%; Score 278.5; DB 1; Length 466;
Best Local Similarity 22.0%; Pred. No. 3.1e-07;
RESULT 1406
ID AAR52562 standard; protein; 466 AA.
DE Factor VIII.
PN WO9323074-A1.
PD 25-NOV-1993.
PA (OKLA-) OKLAHOMA MED RES FOUND.
Query Match 7.1%; Score 278.5; DB 2; Length 466;
Best Local Similarity 22.0%; Pred. No. 3.1e-07;
RESULT 1407
ID AAM69606 standard; protein; 466 AA.
DE Human Factor VIIa.
PN WO9831394-A2.
PD 23-JUL-1998.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 278.5; DB 2; Length 466;
Best Local Similarity 22.0%; Pred. No. 3.1e-07;
RESULT 1408
ID ADB36327 standard; protein; 466 AA.
DE Human factor VII (F7) protein reference sequence.
PN US2003087244-A1.
PD 08-MAY-2003.
PA (VITI-) VITIVITY INC.
Query Match 7.1%; Score 278.5; DB 7; Length 466;
Best Local Similarity 22.0%; Pred. No. 3.1e-07;
RESULT 1409
ID AAR74682 standard; protein; 521 AA.
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by ERHSTVQT).
PN CN1082111-A.
PD 16-FEB-1994.
PA (BIOB-) BIOENGINEERING INST ACAD MILITARY.
Query Match 7.1%; Score 278.5; DB 2; Length 521;
Best Local Similarity 22.9%; Pred. No. 3.4e-07;
RESULT 1410
ID AAR09222 standard; protein; 526 AA.
DE t-PA deletion variant d298.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 278.5; DB 2; Length 526;
Best Local Similarity 23.3%; Pred. No. 3.5e-07;
RESULT 1411
ID AAR09224 standard; protein; 526 AA.
DE t-PA deletion variant d300.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 278.5; DB 2; Length 526;
Best Local Similarity 23.3%; Pred. No. 3.5e-07;
RESULT 1412
ID AAR09223 standard; protein; 526 AA.
DE t-PA deletion variant d299.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 278.5; DB 2; Length 526;
Best Local Similarity 23.3%; Pred. No. 3.5e-07;
RESULT 1413
ID AAR09225 standard; protein; 526 AA.
DE t-PA deletion variant d301.
PN WO9002798-A.
PD 22-MAR-1990.

PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 278.5; DB 2; Length 526;
Best Local Similarity 23.1%; Pred. No. 3.5e-07;
RESULT 1414
ID AAR09227 standard; protein; 526 AA.
DE t-PA deletion variant d303.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 278.5; DB 2; Length 526;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1415
ID AAR12343 standard; protein; 562 AA.
DE t-PA with -ve charged finger and/or kringle domain (2).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 278.5; DB 2; Length 562;
Best Local Similarity 21.9%; Pred. No. 3.7e-07;
RESULT 1416
ID AAR12423 standard; protein; 562 AA.
DE T-PA variant having Lys416 substitution (1).
PN JP03061484-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 278.5; DB 2; Length 562;
Best Local Similarity 21.9%; Pred. No. 3.7e-07;
RESULT 1417
ID AAR12424 standard; protein; 562 AA.
DE T-PA variant having Lys416 substitution (3).
PN JP03061484-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 278.5; DB 2; Length 562;
Best Local Similarity 21.9%; Pred. No. 3.7e-07;
RESULT 1418
ID ADJ57511 standard; protein; 701 AA.
DE Human FVII-IgG1 Fc domain fusion protein.
PN WO2004006962-A2.
PD 22-JAN-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 701;
Best Local Similarity 22.0%; Pred. No. 4.5e-07;
RESULT 1419
ID ABB71752 standard; protein; 408 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42048.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.0%; Score 278; DB 4; Length 408;
Best Local Similarity 25.2%; Pred. No. 2.9e-07;
RESULT 1420
ID AAR35762 standard; protein; 448 AA.
DE Factor X (X).
PN WO9309804-A1.
PD 27-MAY-1993.
PA (SCRI) SCRIPPS RES INST.
Query Match 7.0%; Score 278; DB 2; Length 448;
Best Local Similarity 24.0%; Pred. No. 3.2e-07;
RESULT 1421
ID AAR22511 standard; protein; 488 AA.
DE Human Factor Xa1.
PN WO9204378-A.
PD 19-MAR-1992.
PA (CORT-) COR THERAPEUTICS INC.
Query Match 7.0%; Score 278; DB 2; Length 488;
Best Local Similarity 24.0%; Pred. No. 3.4e-07;
RESULT 1422
ID ADQ17444 standard; protein; 488 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 261.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 7.0%; Score 278; DB 8; Length 488;
Best Local Similarity 24.0%; Pred. No. 3.4e-07;
RESULT 1423
ID AAR09232 standard; protein; 523 AA.
DE t-PA deletion variant d297-300.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 278; DB 2; Length 523;
Best Local Similarity 23.2%; Pred. No. 3.7e-07;
RESULT 1424
ID AAR09244 standard; protein; 525 AA.
DE t-PA deletion variant d297, d300.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 278; DB 2; Length 525;
Best Local Similarity 23.2%; Pred. No. 3.7e-07;
RESULT 1425
ID AAR05806 standard; protein; 527 AA.
DE Thrombolytic protein with secondary structure of human tissue plasminogen activator.
PN JP02145184-A.
PD 04-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 527;
Best Local Similarity 22.9%; Pred. No. 3.7e-07;
RESULT 1426
ID AAR22621 standard; protein; 527 AA.
DE Mutated recombinant tPA.
PN JP04094684-A.
PD 26-MAR-1992.
PA (KANF) KANEKA CORP.
Query Match 7.0%; Score 278; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 3.7e-07;
RESULT 1427
ID AAR70896 standard; protein; 527 AA.
DE Human t-PA variant (N103,A339,A342).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 278; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.7e-07;
RESULT 1428
ID AAR70858 standard; protein; 527 AA.
DE Human t-PA variant (N67,A296,A297,A298,A299).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 278; DB 2; Length 527;
Best Local Similarity 23.3%; Pred. No. 3.7e-07;
RESULT 1429
ID AAR70897 standard; protein; 527 AA.
DE Human t-PA variant (N103,A347,A348,A349,A351).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 278; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.7e-07;
RESULT 1430
ID AAR70856 standard; protein; 527 AA.
DE Human t-PA variant (N67,A267).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 278; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 3.7e-07;
RESULT 1431
ID AAR70873 standard; protein; 527 AA.
DE Human t-PA variant (N67,A477).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.

Query Match 7.0%; Score 278; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.7e-07;
RESULT 1432
ID AAP71450 standard; protein; 528 AA.
DE Modified human tissue plasminogen activator.
PN EP238304-A.
PD 23-SEP-1987.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 278; DB 1; Length 528;
Best Local Similarity 22.9%; Pred. No. 3.7e-07;
RESULT 1433
ID AAR07033 standard; protein; 528 AA.
DE Thrombolytic protein with secondary structure of human tissue plasminogen
DE activator.
PN JP02145184-A.
PD 04-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 528;
Best Local Similarity 22.9%; Pred. No. 3.7e-07;
RESULT 1434
ID AAP70881 standard; protein; 530 AA.
DE Thrombolytic protein 1-12-1-18 having t-PA activity, deleted or replaced
DE R275 is and containing a modified N-linked glycosylation site.
PN W08704722-A.
PD 13-AUG-1987.
PA (GEMY) GENETICS INST INC.
PA (LARS) LARSEN G R.
Query Match 7.0%; Score 278; DB 1; Length 530;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1435
ID AAR07034 standard; protein; 531 AA.
DE Thrombolytic protein with secondary structure of human tissue plasminogen
DE activator.
PN JP02145184-A.
PD 04-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 531;
Best Local Similarity 22.9%; Pred. No. 3.7e-07;
RESULT 1436
ID AAR13153 standard; protein; 558 AA.
DE T-PA with -ve charged finger and/or kringle domain (8) .
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 558;
Best Local Similarity 23.0%; Pred. No. 3.9e-07;
RESULT 1437
ID AAR13151 standard; protein; 559 AA.
DE T-PA with -ve charged finger and/or kringle domain (4) .
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 559;
Best Local Similarity 23.0%; Pred. No. 3.9e-07;
RESULT 1438
ID AAR13155 standard; protein; 559 AA.
DE T-PA variant having Lys416 substitution (4) .
PN JP03061484-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 559;
Best Local Similarity 23.0%; Pred. No. 3.9e-07;
RESULT 1439
ID AAR13154 standard; protein; 559 AA.
DE T-PA variant having Lys416 substitution (2) .
PN JP03061484-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 559;
Best Local Similarity 23.0%; Pred. No. 3.9e-07;
RESULT 1440
ID AAP81359 standard; protein; 562 AA.
DE Pre-pro tissue plasminogen activator.

PN EP293934-A.
PD 07-DEC-1988.
PA (ZYMO) ZYMOGENETICS INC.
PA (NOVO) NOVO IND AS.
PA (EISA) EISA CO LTD.
Query Match 7.0%; Score 278; DB 1; Length 562;
Best Local Similarity 23.2%; Pred. No. 3.9e-07;
RESULT 1441
ID AAR07079 standard; protein; 562 AA.
DE Thrombolytic protein with secondary structure of human tissue plasminogen
DE activator.
PN JP02145184-A.
PD 04-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 562;
Best Local Similarity 22.9%; Pred. No. 3.9e-07;
RESULT 1442
ID AAR04702 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA C87S; K419S
DE with altered residues 87 and 419.
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.0%; Score 278; DB 2; Length 562;
Best Local Similarity 22.7%; Pred. No. 3.9e-07;
RESULT 1443
ID AAR3809 standard; protein; 562 AA.
DE t-PA (Glu 299) mutant.
PN W09206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.0%; Score 278; DB 2; Length 562;
Best Local Similarity 23.5%; Pred. No. 3.9e-07;
RESULT 1444
ID ADI27177 standard; protein; 1113 AA.
DE Mouse LRP binding family protein #17.
PN W02003106657-A2.
PD 24-DEC-2003.
PA (STON-) STOWERS INST MEDICAL RES.
Query Match 7.0%; Score 278; DB 8; Length 1113;
Best Local Similarity 20.7%; Pred. No. 7.4e-07;
RESULT 1445
ID ADR29372 standard; protein; 1113 AA.
DE Murine Lrp4 dopaminergic neuronal marker SEQ ID NO:3.
PN W02004065599-A1.
PD 05-AUG-2004.
PA (EISA) EISAI CO LTD.
Query Match 7.0%; Score 278; DB 8; Length 1113;
Best Local Similarity 20.7%; Pred. No. 7.4e-07;
RESULT 1446
ID AAO30596 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/K337A/V158D) .
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1447
ID AAO30549 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/K337A) .
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.6%; Pred. No. 3.1e-07;
RESULT 1448
ID AAO30561 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/K337A) .
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;

Best Local Similarity 22.6%; Pred. No. 3.1e-07;
RESULT 1449
ID AAO30570 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1450
ID AAO30588 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/K337A).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1451
ID AAO30623 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/E296V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1452
ID AAO30611 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158D).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1453
ID AAO30567 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158D).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1454
ID AAO30529 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/K316Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.6%; Pred. No. 3.1e-07;
RESULT 1455
ID AAO30548 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1456
ID AAO30564 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1457
ID AAO30609 standard; protein; 406 AA.
DE Human factor VII variant (K316H/L305V/V158T/E296V/M298Q/K337A).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;

RESULT 1458
ID AAO30579 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/E296V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1459
ID AAO30581 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/E296V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1460
ID AAO30593 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/K337A/V158T).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1461
ID AAO30624 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158D/E296V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1462
ID AAO30632 standard; protein; 406 AA.
DE Human factor VII variant (L305V/K337A).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1463
ID AAO30552 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1464
ID AAO30580 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/E296V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1465
ID AAO30614 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1466
ID AAO30608 standard; protein; 406 AA.
DE Human factor VII variant (K316H/L305V/V158D/E296V/M298Q/K337A).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1467

ID AAO30625 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T/E296V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1468
ID AAO30560 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1469
ID ADJ55906 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1470
ID ADJ56001 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ M298Q/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1471
ID ADJ56022 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ K337A/ M298Q/ V158D.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1472
ID ADJ56024 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ K337A/ M298Q/ V158T.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1473
ID ADJ55878 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1474
ID ADJ55983 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1475
ID ADJ56019 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ K337A/ S314E/ V158T.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1476
ID ADJ56037 standard; protein; 406 AA.

DE Human factor VII polypeptide mutant F374Y/ S314E/ E296V/ M298Q/ L305V.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1477
ID ADJ55909 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 3.1e-07;
RESULT 1478
ID ADJ55953 standard; protein; 406 AA.
DE Human factor VII protein mutant V158T/ E296V/ M298Q/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1479
ID ADJ55955 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1480
ID ADJ55893 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 3.1e-07;
RESULT 1481
ID ADJ55932 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1482
ID ADJ55897 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1483
ID ADJ55956 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1484
ID ADJ56036 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ E296V/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1485
ID ADJ55875 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ L305V/ K337A.

PN WO2004000366-A1.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1486
ID ADJ55912 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ L305V/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1487
ID ADJ55940 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1488
ID ADJ56029 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ V158T.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1489
ID ADJ56059 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158D/ E296V/ M298Q/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.1%; Pred. No. 3.1e-07;
RESULT 1490
ID ADJ55891 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant S314E/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 3.1e-07;
RESULT 1491
ID ADJ55923 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant E296V/ M298Q/ L305V/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1492
ID ADJ55925 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ E296V/ M298Q/ L305V/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1493
ID ADJ55939 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1494
ID ADJ55968 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ E296V/ M298Q/ L305V/ K316Q.
PN WO2004000366-A1.

PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1495
ID ADJ55969 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ E296V/ M298Q/ L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1496
ID ADJ56010 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/ V158D/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1497
ID ADJ56026 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ V158D.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1498
ID ADJ55861 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1499
ID ADJ55950 standard; protein; 406 AA.
DE Human factor VII protein mutant V158D/ E296V/ M298Q/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1500
ID ADJ56020 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ K337A/ S314E/ V158D.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 3.1e-07;

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 8, 2005, 15:31:03 ; Search time 77 Seconds
(without alignments)
4788.273 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 3945

Sequence: 1 MELGCWTQLGLFLQLLLIS.....LSTAFKVLPPKDWIERNMK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3945	100.0	720	2 Q6UXH9	Q6uxh9 homo sapien
2	3936	99.8	720	2 Q6N062	Q6n062 homo sapien
3	3921.5	99.4	737	2 Q96JW2	Q96jw2 homo sapien
4	3612	91.6	720	2 Q8BU25	Q8bu25 m mus muscu
5	3612	91.6	720	2 Q8K2B8	Q8k2b8 mus musculus
6	2823	71.6	722	2 Q6DIV5	Q6div5 xenopus tro
7	2059	52.2	417	2 Q7IRE9	Q7ire9 homo sapien
8	949	24.1	181	2 Q9Y432	Q9y432 homo sapien
9	678	17.2	1019	2 Q8T9S1	Q8t9s1 tachypleus
10	672	17.0	1019	1 LFC TACTR	P28175 tachypleus
11	665	16.9	1019	1 LFC_CARRO	Q26422 carcinoscor
12	665	16.9	1083	2 Q26423	Q26423 carcinoscor
13	608.5	15.4	680	2 Q868H7	Q868h7 branchiosteo
14	604	15.3	680	2 Q868H5	Q868h5 branchiosteo
15	597	15.1	688	2 Q868H6	Q868h6 branchiosteo
16	576.5	14.6	688	2 Q868H4	Q868h4 branchiosteo
17	507.5	12.9	698	2 Q6GPF9	Q6gpf9 xenopus lae
18	490.5	12.4	730	2 Q6QIQ8	Q6qiq8 gallus gall
19	489.5	12.4	698	2 Q9PU71	Q9pu71 xenopus lae
20	483	12.2	701	2 Q9JJS9	Q9jjs9 rattus norv
21	482.5	12.2	703	2 Q8CHN8	Q8chn8 rattus norv
22	482	12.2	717	2 Q8AXR1	Q8axr1 xenopus lae
23	478	12.1	699	1 CRAR_HUMAN	P48740 h complemen
24	475	12.0	704	1 CRAR_MOUSE	P98064 mus musculus
25	468	11.9	728	2 Q9GRS4	Q9grs4 homo sapien
26	467	11.8	697	2 Q8CG43	Q8cg43 rattus norv
27	466	11.8	717	2 Q8AXR0	Q8axr0 xenopus lae
28	459	11.6	733	2 Q8CD27	Q8cd27 mus musculus
29	457	11.6	719	2 Q9PVY2	Q9pyv2 triakis scy
30	452	11.5	733	2 Q920S0	Q920s0 mus musculus
31	448	11.4	745	2 Q9PVY3	Q9pyv3 cyprinus ca

32	447	11.3	686	2 Q6QIQ9	Q6qiq9 gallus gall
33	436.5	11.1	681	2 Q7ZT70	Q7zt70 lampetra ja
34	428	10.8	707	1 C1R_MOUSE	Q8cgl6 mus musculus
35	424	10.7	678	2 Q9JJS8	Q9jjs8 rattus norv
36	421.5	10.7	688	2 Q9PVY4	Q9pyv4 xenopus lae
37	420	10.6	643	2 Q9QX84	Q9qx84 rattus norv
38	417	10.6	685	2 Q9LWP0	Q9lwp0 mus musculus
39	416.5	10.6	706	2 Q8CFG9	Q8cfg9 mus musculus
40	412	10.4	685	2 Q9Z338	Q9z338 mus musculus
41	403.5	10.2	705	1 C1R_HUMAN	P00736 homo sapien
42	401.5	10.2	496	2 Q8CHP7	Q8chp7 cavia porce
43	401.5	10.2	746	2 Q8IAD8	Q8iad8 halocynthia
44	400.5	10.2	686	1 MAS2_HUMAN	O00187 homo sapien
45	398.5	10.1	746	2 O01654	O01654 halocynthia
46	395	10.0	721	2 Q7ZT69	Q7zt69 lampetra ja
47	395	10.0	721	2 Q7ZT69	Q7zt69 lampetra ja
48	384	9.7	688	2 Q8CFG8	Q8cfg8 mus musculus
49	382.5	9.7	752	2 O01655	O01655 halocynthia
50	382	9.7	722	2 Q8AW90	Q8aw90 lampetra ja
51	381	9.7	722	2 Q9PSZ5	Q9psz5 lampetra ja
52	380.5	9.6	687	2 Q69DK8	Q69dk8 sus scrofa
53	378.5	9.6	695	1 CASP_MESAU	P15156 mesocricetu
54	376	9.5	623	2 Q9JJF3	Q9jjf3 rattus norv
55	372.5	9.4	752	2 Q8IAD7	Q8iad7 halocynthia
56	371.5	9.4	541	2 Q9QX90	Q9qx90 rattus norv
57	370	9.4	688	2 Q8CG14	Q8cg14 mus musculus
58	369	9.4	694	2 Q8BJC4	Q8bjc4 mus musculus
59	368	9.3	685	2 Q9DGC1	Q9dgc1 cyprinus ca
60	366	9.3	685	2 Q9DGC0	Q9dgc0 cyprinus ca
61	364	9.2	688	2 Q8CH28	Q8ch28 mus musculus
62	364	9.2	694	2 Q8VBY4	Q8vby4 mus musculus
63	357	9.0	676	2 Q6DUJ6	Q6duj6 cyprinus ca
64	354	9.0	1524	2 Q91674	Q91674 xenopus lae
65	342	8.7	694	2 Q8R099	Q8r099 mus musculus
66	340.5	8.6	694	2 Q70542	Q70542 rattus norv
67	340.5	8.6	694	2 Q6P6T1	Q6p6t1 rattus norv
68	339.5	8.6	707	2 Q70W31	Q70w31 oncorhynch
69	335	8.5	645	2 Q6PY92	Q6py92 anopheles g
70	335	8.5	666	2 Q69BL0	Q69bl0 manduca sex
71	334	8.5	503	2 Q8AYE4	Q8aye4 brachydanio
72	334	8.5	688	1 C1S_HUMAN	P09871 homo sapien
73	331.5	8.4	1019	1 ENTK_HUMAN	P98073 homo sapien
74	329.5	8.4	1034	1 ENTK_PIG	P98074 sus scrofa
75	329.5	8.4	3565	1 CSM1_HUMAN	Q96z27 homo sapien
76	329	8.3	3564	1 CSM1_MOUSE	Q92313 mus musculus
77	328	8.3	855	1 ST14_HUMAN	Q9Y5V6 homo sapien
78	318	8.1	3487	1 CSM2_HUMAN	Q7Z408 homo sapien
79	317.5	8.0	1035	1 ENTK_BOVIN	P98072 bos taurus
80	316.5	8.0	460	1 PRTC_MOUSE	P33587 mus musculus
81	315	8.0	444	1 FA7_RABIT	P98139 oryctolagus
82	314.5	8.0	475	1 FA10_CHICK	P25155 gallus gall
83	314	8.0	855	1 ST14_MOUSE	P56677 mus musculus
84	313	7.9	855	2 Q9JJ17	Q9jj17 rattus norv
85	311	7.9	446	1 FA7_RAT	Q8k3u6 rattus norv
86	310.5	7.9	434	2 Q7T3B6	Q7t3b6 brachydanio
87	310.5	7.9	461	1 PRTC_HUMAN	P04070 homo sapien
88	309.5	7.8	799	2 Q6PF94	Q6pf94 mus musculus
89	309.5	7.8	811	1 TMS6_MOUSE	Q9dbi0 mus musculus
90	305	7.7	456	1 PRTC_CANFA	Q28278 canis famil
91	304	7.7	1069	1 ENTK_MOUSE	P97435 mus musculus
92	302.5	7.7	446	1 FA7_MOUSE	P70375 mus musculus
93	301.5	7.6	433	2 Q8JHD0	Q8jhd0 brachydanio
94	300.5	7.6	463	2 Q6IT10	Q6it10 pseudonaja
95	299.5	7.6	467	2 Q6IT09	Q6it09 pseudonaja
96	299	7.6	1111	2 Q80YN4	Q80yn4 rattus norv
97	298.5	7.6	433	2 Q90YK1	Q90yk1 brachydanio
98	298.5	7.6	553	2 Q6P719	Q6p719 xenopus lae
99	297.5	7.5	543	2 Q8BU99	Q8bu99 homo sapien
100	297.5	7.5	777	2 Q8CAN9	Q8can9 mus musculus
101	297	7.5	459	1 PRTC_PIG	Q9glp2 sus scrofa
102	296	7.5	458	1 PRTC_RABIT	Q28661 oryctolagus
103	295.5	7.5	336	2 Q8CIR9	Q8cir9 mus musculus
104	295.5	7.5	441	2 Q804X2	Q804x2 fugu rubrip

1419	172.5	4.4	4.4	1	PCOL HUMAN	Q15113	homo sapien
1420	172.5	4.4	4.4	863	Q6AXF9	Q6AXF9	mus musculus
1421	172.5	4.4	4.4	923	Q91X64	Q91X64	mus musculus
1422	172.5	4.4	4.4	1202	1 JAG2 RAT	P97607	rattus norv
1423	172	4.4	4.4	157	1 PRTC CADHI	Q28315	capra hirc
1424	172	4.4	4.4	235	2 Q66P68	Q66P68	fugu rubrip
1425	172	4.4	4.4	242	2 FIBC LUNRU	P83238	lumbicus r
1426	172	4.4	4.4	242	2 Q96687	Q96687	lumbicus r
1427	172	4.4	4.4	249	2 Q7KRD0	Q7KRD0	drosofila
1428	172	4.4	4.4	249	2 Q9W6K0	Q9W6K0	notothenia
1429	172	4.4	4.4	254	1 TRYP SARBU	P51588	sarcophaga
1430	172	4.4	4.4	254	2 Q765Z0	Q765Z0	stomoxys ca
1431	172	4.4	4.4	260	1 ESTA CANFA	P09582	canis famil
1432	172	4.4	4.4	260	2 Q9V7G4	Q9V7G4	drosofila
1433	172	4.4	4.4	261	1 KLK8 MOUSE	P07628	mus musculus
1434	172	4.4	4.4	261	2 Q6H320	Q6H320	bos taurus
1435	172	4.4	4.4	262	1 TRYT DROME	P42278	drosofila
1436	172	4.4	4.4	262	2 Q8S2Q7	Q8S2Q7	drosofila
1437	172	4.4	4.4	262	2 Q9V5Y0	Q9V5Y0	drosofila
1438	172	4.4	4.4	390	2 Q81927	Q81927	hyphantria
1439	172	4.4	4.4	415	1 ACRO PIG	P08001	sus scrofa
1440	172	4.4	4.4	415	2 Q29015	Q29015	sus sp. pre
1441	172	4.4	4.4	441	2 Q81917	Q81917	manduca sex
1442	172	4.4	4.4	441	2 Q81925	Q81925	hyphantria
1443	172	4.4	4.4	655	2 Q7KKR0	Q7KKR0	drosofila
1444	172	4.4	4.4	721	2 Q95Y90	Q95Y90	ciona savig
1445	172	4.4	4.4	721	2 Q91902	Q91902	xenopus lae
1446	172	4.4	4.4	1208	2 Q80YA8	Q80YA8	mus musculus
1447	172	4.4	4.4	1247	1 JAG2 MOUSE	Q9QV5	mus musculus
1448	171.5	4.3	4.3	241	2 Q9G0Q2	Q9G0Q2	biophalari
1449	171.5	4.3	4.3	261	2 Q8IR82	Q8IR82	drosofila
1450	171.5	4.3	4.3	261	2 Q6H322	Q6H322	equus cabal
1451	171.5	4.3	4.3	262	1 KLK1 HUMAN	P06870	homo sapien
1452	171.5	4.3	4.3	262	2 Q7PX38	Q7PX38	anopheles g
1453	171.5	4.3	4.3	277	2 Q9VFN8	Q9VFN8	drosofila
1454	171.5	4.3	4.3	278	2 Q8MQ02	Q8MQ02	drosofila
1455	171.5	4.3	4.3	282	2 Q9NGY4	Q9NGY4	heliothis v
1456	171.5	4.3	4.3	321	2 Q6IE60	Q6IE60	rattus norv
1457	171.5	4.3	4.3	373	2 Q7PVJ0	Q7PVJ0	anopheles g
1458	171.5	4.3	4.3	1785	2 Q9Y211	Q9Y211	homo sapien
1459	171.5	4.3	4.3	1785	2 Q9Y4V9	Q9Y4V9	homo sapien
1460	171.5	4.3	4.3	2403	2 Q9UGM2	Q9UGM2	homo sapien
1461	171.5	4.3	4.3	2413	2 Q96DU4	Q96DU4	homo sapien
1462	171.5	4.3	4.3	2413	2 Q9UKJ4	Q9UKJ4	homo sapien
1463	171.5	4.3	4.3	2426	2 Q9UGM3	Q9UGM3	homo sapien
1464	171	4.3	4.3	175	2 Q6PLJ9	Q6PLJ9	scylla ora
1465	171	4.3	4.3	245	2 Q17439	Q17439	boltenia vi
1466	171	4.3	4.3	248	2 Q8T4P2	Q8T4P2	lepeophthei
1467	171	4.3	4.3	258	2 Q6ISM6	Q6ISM6	homo sapien
1468	171	4.3	4.3	260	1 GRAA MOUSE	P11032	mus musculus
1469	171	4.3	4.3	262	2 Q7Z1D6	Q7Z1D6	lepeophthei
1470	171	4.3	4.3	266	1 EL1 RAT	P00773	rattus norv
1471	171	4.3	4.3	273	1 TRY5 ANOGA	P35040	anopheles g
1472	171	4.3	4.3	277	1 KLK2 HUMAN	Q9UKR3	homo sapien
1473	171	4.3	4.3	319	2 Q9VAQ4	Q9VAQ4	drosofila
1474	171	4.3	4.3	358	2 Q45029	Q45029	drosofila
1475	171	4.3	4.3	426	2 Q8CFX9	Q8CFX9	mus musculus
1476	171	4.3	4.3	454	2 Q8TB42	Q8TB42	homo sapien
1477	171	4.3	4.3	609	2 Q9GLF0	Q9GLF0	canis famil
1478	171	4.3	4.3	611	1 LEM2 CANFA	P33730	canis famil
1479	171	4.3	4.3	737	2 Q81YT0	Q81YT0	homo sapien
1480	171	4.3	4.3	737	2 Q8NFT8	Q8NFT8	homo sapien
1481	171	4.3	4.3	832	2 Q9JLB4	Q9JLB4	mus musculus
1482	171	4.3	4.3	2139	1 CRB DROME	P10040	drosofila
1483	171	4.3	4.3	2146	2 Q9VC97	Q9VC97	drosofila
1484	171	4.3	4.3	2412	2 Q9UJ57	Q9UJ57	homo sapien
1485	170.5	4.3	4.3	259	2 Q45048	Q45048	anopheles g
1486	170.5	4.3	4.3	273	2 Q57659	Q57659	gallus gall
1487	170.5	4.3	4.3	282	2 Q7PV7	Q7PV7	anopheles g
1488	170.5	4.3	4.3	328	2 Q6BEA2	Q6BEA2	rattus norv
1489	170.5	4.3	4.3	350	2 Q9V5E3	Q9V5E3	drosofila
1490	170.5	4.3	4.3	377	2 Q9VB68	Q9VB68	drosofila
1491	170.5	4.3	4.3	390	2 Q9Y157	Q9Y157	drosofila
1492	170.5	4.3	4.3	408	2 Q8MR95	Q8MR95	drosofila
1493	170.5	4.3	4.3	473	2 Q7PV63	Q7PV63	anopheles g
1494	170.5	4.3	4.3	669	2 Q922H0	Q922H0	mus musculus
1495	170.5	4.3	4.3	705	2 Q6MZN4	Q6MZN4	homo sapien
1496	170.5	4.3	4.3	772	2 Q6DI48	Q6DI48	brachydanio
1497	170.5	4.3	4.3	802	2 Q57462	Q57462	brachydanio
1498	170	4.3	4.3	239	2 Q8T4P3	Q8T4P3	lepeophthei
1499	170	4.3	4.3	239	2 Q63275	Q63275	rattus norv
1500	170	4.3	4.3	245	1 MCT1_SHEEP	P80931	ovis aries

ALIGNMENTS

RESULT 1

Q6UXH9	PRELIMINARY;	PRT;	720 AA.
ID	Q6UXH9	PRELIMINARY;	PRT;
AC	Q6UXH9;		
DT	05-JUL-2004 (TREMBlrel. 27, Created)		
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)		
DE	05-JUL-2004 (TREMBlrel. 27, Last annotation update)		
DE	ELGCG99.		
GN	ORFNames=UNO699;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
NCBI_TaxID=9606;			
[1]			
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22887236; PubMed=12975309; DOI=10.1101/gr.1393003;		
RA	Clark H.F., Gurney A.D., Abaya E., Baker K., Baldwin D., Brush J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,		
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seshgiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,		
RA	Vandenberg R., Watanabe C., Wileand D., Woods K., Xie M.H., Yansura D.,		
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,		
RA	Godowski P.;		
RT	"The secreted protein discovery initiative (SPDI), a large-scale		
RT	effort to identify novel human secreted and transmembrane proteins: a		
RT	bioinformatics assessment.";		
CC	Genome Res. 13:2285-2270(2003).		
CC	-I- SIMILARITY: Belongs to peptidase family S1.		
CC	-I- SIMILARITY: Contains 1 EGF-like domain.		
DR	EMBL: AY358346; AAQ88712.1; -		
DR	HSSP: P00734; 1BB0.		
DR	GO: GO:0005509; F:calcium ion binding; IEA.		
DR	GO: GO:0004263; F:chymotrypsin activity; IEA.		
DR	GO: GO:0008233; F:peptidase activity; IEA.		
DR	GO: GO:0004295; F:trypsin activity; IEA.		
DR	GO: GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro: IPR000859; CUB.		
DR	InterPro: IPR000742; EGF_2.		
DR	InterPro: IPR001881; EGF_Ca.		
DR	InterPro: IPR006209; EGF_like.		
DR	InterPro: IPR006210; IEGF.		
DR	InterPro: IPR001254; Peptidase S1.		
DR	InterPro: IPR001314; Peptidase_S1A.		
DR	InterPro: IPR009003; Pept_Ser_Cys.		
DR	Pfam: PF00431; CUB; 1.		
DR	Pfam: PF00008; EGF; 1.		
DR	Pfam: PF00084; Sushi; 1.		
DR	PRINTS: PR00722; CHYMOTRYPSIN.		
DR	SMART: SM00032; CCF; 2.		
DR	SMART: SM00042; CUB; 1.		
DR	SMART: SM00181; EGF; 2.		
DR	SMART: SM00179; EGF_Ca; 1.		
DR	SMART: SM00020; Tryp_SPC; 1.		
DR	PROSITE: PS01180; CUB; 1.		
DR	PROSITE: PS00022; EGF_1; 1.		
DR	PROSITE: PS01186; EGF_2; 1.		

DR PROSITE; PS50026; EGF 3; 1.
DR PROSITE; PS50923; SUSHI; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 720 AA; 80196 MW; DC989BC7241289D3 CRC64;

Query Match 100.0%; Score 3945; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.6e-287;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60
DB 1 MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60
QY 61 VVGTYTPCCNNEECDSCLIHPGCTIFENCKSCRNCSWGGLTDDFVVGKGYCAECRAGW 120
DB 61 VVGTYTPCCNNEECDSCLIHPGCTIFENCKSCRNCSWGGLTDDFVVGKGYCAECRAGW 120
QY 121 YGDCMRCGVLRAPKGQILLESYPLNAHCETIHAKEPVIQLRFVMLSLEFDYMCQYD 180
DB 121 YGDCMRCGVLRAPKGQILLESYPLNAHCETIHAKEPVIQLRFVMLSLEFDYMCQYD 180
QY 181 YVEVRDGDNRDQGIIRKVCNERNPAPIQSGSSLHVLFHSDGSKNFGFHAIEEITACS 240
DB 181 YVEVRDGDNRDQGIIRKVCNERNPAPIQSGSSLHVLFHSDGSKNFGFHAIEEITACS 240
QY 241 SSPCFHDGTCVLDKAGSKYKACLAGYTGRCENLLEERNCSDPGPGVNGYQKITGGPGLI 300
DB 241 SSPCFHDGTCVLDKAGSKYKACLAGYTGRCENLLEERNCSDPGPGVNGYQKITGGPGLI 300
QY 301 NGRHAKITGVVSFFCNNSYVLSGNEKRTCOQNGEWSGKQPICIKACREPKISDLVRRRL 360
DB 301 NGRHAKITGVVSFFCNNSYVLSGNEKRTCOQNGEWSGKQPICIKACREPKISDLVRRRL 360
QY 361 PMQVQSRETLHLQLYSAAFSKQLQSAPTCKKPPALPGDLPWGQYQHLHTQLQYECISPFYR 420
DB 361 PMQVQSRETLHLQLYSAAFSKQLQSAPTCKKPPALPGDLPWGQYQHLHTQLQYECISPFYR 420
QY 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWQAAIYRRTSGVHDGSL 480
DB 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWQAAIYRRTSGVHDGSL 480
QY 481 HKGAFLVCSGALVNERVTVAAHCVTDLGKVTMIKTADLKVLGKPYRDDDRDEKTIQS 540
DB 481 HKGAFLVCSGALVNERVTVAAHCVTDLGKVTMIKTADLKVLGKPYRDDDRDEKTIQS 540
QY 541 LQISAILLHPNYDPIILLDADIALKLLDKARISTRVQPICLAASRDLSFSQESHITVAG 600
DB 541 LQISAILLHPNYDPIILLDADIALKLLDKARISTRVQPICLAASRDLSFSQESHITVAG 600
QY 601 WNVLDVRSFGFNDRTRSGVSVVDSLLCEQEHEDHGIPVSVTDNMFCASWEPTAPSDI 660
DB 601 WNVLDVRSFGFNDRTRSGVSVVDSLLCEQEHEDHGIPVSVTDNMFCASWEPTAPSDI 660
QY 661 CTAETGGIAAVSPGRASPRRHLMLGVSWSYDKTCSHRLSTAFKVLFPKDWIERNMK 720
DB 661 CTAETGGIAAVSPGRASPRRHLMLGVSWSYDKTCSHRLSTAFKVLFPKDWIERNMK 720

RESULT 2
Q6N062 ID Q6N062 PRELIMINARY; PRT; 720 AA.
AC Q6N062;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686N24154.
GN Name=DKFZp686N24154;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Colon endothel.
RG The German CDNA Consortium;
RA Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; BX640676; CAE45808.1; -.
DR HSSP; P00734; 1BBO.
DR GO; GO:000509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase SLA.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sush1; 1.
DR PRINTS; PF0722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_Ca; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS50923; SUSHI; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW EGF-like domain; Hydrolase; Hypothetical protein; Protease;
KW Serine protease.
SQ SEQUENCE 720 AA; 80196 MW; E98A9F9948EE777D CRC64;

Query Match 99.8%; Score 3936; DB 2; Length 720;
Best Local Similarity 99.7%; Pred. No. 7.5e-287;
Matches 718; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60
DB 1 MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60
QY 61 VVGTYTPCCNNEECDSCLIHPGCTIFENCKSCRNCSWGGLTDDFVVGKGYCAECRAGW 120
DB 61 VVGTYTPCCNNEECDSCLIHPGCTIFENCKSCRNCSWGGLTDDFVVGKGYCAECRAGW 120
QY 121 YGDCMRCGVLRAPKGQILLESYPLNAHCETIHAKEPVIQLRFVMLSLEFDYMCQYD 180
DB 121 YGDCMRCGVLRAPKGQILLESYPLNAHCETIHAKEPVIQLRFVMLSLEFDYMCQYD 180
QY 181 YVEVRDGDNRDQGIIRKVCNERNPAPIQSGSSLHVLFHSDGSKNFGFHAIEEITACS 240
DB 181 YVEVRDGDNRDQGIIRKVCNERNPAPIQSGSSLHVLFHSDGSKNFGFHAIEEITACS 240
QY 241 SSPCFHDGTCVLDKAGSKYKACLAGYTGRCENLLEERNCSDPGPGVNGYQKITGGPGLI 300
DB 241 SSPCFHDGTCVLDKAGSKYKACLAGYTGRCENLLEERNCSDPGPGVNGYQKITGGPGLI 300
QY 301 NGRHAKITGVVSFFCNNSYVLSGNEKRTCOQNGEWSGKQPICIKACREPKISDLVRRRL 360
DB 301 NGRHAKITGVVSFFCNNSYVLSGNEKRTCOQNGEWSGKQPICIKACREPKISDLVRRRL 360
QY 361 PMQVQSRETLHLQLYSAAFSKQLQSAPTCKKPPALPGDLPWGQYQHLHTQLQYECISPFYR 420
DB 361 PMQVQSRETLHLQLYSAAFSKQLQSAPTCKKPPALPGDLPWGQYQHLHTQLQYECISPFYR 420


```

361 PMVQSRTPHLQLYSAFSAFQKQLOSAFTKPKALPFGDLPMGYOHLHTQLQYECISPPYR 420
421 RLSSRRTRCLRTGKWSGRAPSCIPICCKIENITAPKTQGLRWPMQAAIYRTSGVHDGSL 480
421 RLSSRRTRCLRTGKWSGRAPSCIPICCKIENITAPKTQGLRWPMQAAIYRTSGVHDGSL 480
481 HKGAWFLVCSGALVNERVTVAAHCVTDLGKVTMIKTADLKVLGKPYRDDRDDEKTIQS 540
481 HKGAWFLVCSGALVNERVTVAAHCVTDLGKVTMIKTADLKVLGKPYRDDRDDEKTIQS 540
541 LQISAIILHNPYDPIILLADIAILKLDKARISTRVQIPICLAASRDLSLTSFQESHITVAG 600
541 LRISAIILHNPYDPIILLADIAILKLDKARISTRVQIPICLAASRDLSLTSFQESHITVAG 600
601 WNVLADVRSPGFKNDRTRSGVSVVDSLLCEEQHEHGHGIPSVVTDNNMFCASWEPPTAPSDI 660
601 WNVLADVRSPGFKNDRTRSGVSVVDSLLCEEQHEHGHGIPSVVTDNNMFCASWEPPTAPSDI 660
661 CTAETGGIAAVSPGRASPPRHLMLGLVSWSDYDKTCSHRLSTAFKVLFPKDWIERNMK 720
661 CTAETGGIAAVSPGRASPPRHLMLGLVSWSDYDKTCSHRLSTAFKVLFPKDWIERNMK 720

RESULT 3
Q96JW2 PRELIMINARY; PRT; 737 AA.
ID Q96JW2 AC Q96JW2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ14935.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sakine M., Obayashi M., Nishi Y., Isono Y., Nakamura Y., Negahari K.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Negahari K.,
RA Murakami K., Saito T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Iehibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirao K., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohnori Y.,
RA Kawabata A., Hakihi T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togaashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC EMBL; AK027841; BAB55404.1; -
DR

```

```

HSSP; P00735; LGPZ.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000859; CUB.
InterPro; IPR000742; EGF_2.
InterPro; IPR006209; EGF_like.
InterPro; IPR006210; IEGF.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR009003; Peptidase S1A.
InterPro; IPR000436; Sushi_Scr_CCP.
Pfam; PF00431; CUB; 1.
Pfam; PF00008; EGF; 1.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00032; CCP; 2.
SMART; SM00042; CUB; 1.
SMART; SM00181; EGF; 2.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50026; EGF_3; 1.
PROSITE; PS50923; SUSHI; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
EGF-like domain; Hydrolase; Protease; Serine protease.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 737 AA; 81952 MW; 4F51689C5EB32B44 CRC64;

Query Match 99.4%; Score 3921.5; DB 2; Length 737;
Best Local Similarity 97.6%; Pred. No. 9.5e-286;
Matches 719; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

QY 1 MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCCECEYDQIECVCKRE 60
DB 1 MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCCECEYDQIECVCKRE 60
QY 61 VVGVTTPCCRNENECDCLIHGCTIFENCKSCRNCSWGGLDDFVVGKGFYCAECRAGW 120
DB 61 VVGVTTPCCRNENECDCLIHGCTIFENCKSCRNCSWGGLDDFVVGKGFYCAECRAGW 120
QY 121 YGSDCMRCQGVLRAPKGQILLSEYPLNAHCEWTHAKPGFVIQLRFVMSLEFDYMCQYD 180
DB 121 YGSDCMRCQGVLRAPKGQILLSEYPLNAHCEWTHAKPGFVIQLRFVMSLEFDYMCQYD 180
QY 181 YVEVRDGNRDQIILKRVCGNERPAPIQSIGSLHLVPHSDGSKNPDGFHAIYEETACS 240
DB 181 YVEVRDGNRDQIILKRVCGNERPAPIQSIGSLHLVPHSDGSKNPDGFHAIYEETACS 240
QY 241 SSPCFHDGTCLVDKAGSYKACLAGYTGORCENL-----LEERNCSDP 283
DB 241 SSPCFHDGTCLVDKAGSYKACLAGYTGORCENL-----LEERNCSDP 283
QY 284 GGPVNGYQKITGGPGLNGRHAHAKIGTVSFFCNNSYVLSGNEKRTCCQNGWESGKQIPCI 343
DB 301 GGPVNGYQKITGGPGLNGRHAHAKIGTVSFFCNNSYVLSGNEKRTCCQNGWESGKQIPCI 360
QY 344 KACREPKISDLVRRVRLPMQVQSRRETPHLQLYSAFSAFQKQLOSAFTKPKALPFGDLPMGY 403
DB 361 KACREPKISDLVRRVRLPMQVQSRRETPHLQLYSAFSAFQKQLOSAFTKPKALPFGDLPMGY 420
QY 404 QHLHTQLQYECISPPFYRRRLGSSRRRTCLRTGKWSGRAPSCIPICCKIENITAPKTQGLRW 463
DB 421 QHLHTQLQYECISPPFYRRRLGSSRRRTCLRTGKWSGRAPSCIPICCKIENITAPKTQGLRW 480
QY 464 WQAAIYVRTSGVHDGSLHKGAWFLVCSGALVNERVTVAAHCVTDLGKVTMIKTADLKVV 523
DB 481 WQAAIYVRTSGVHDGSLHKGAWFLVCSGALVNERVTVAAHCVTDLGKVTMIKTADLKVV 540
QY 524 LGKPYRDDRDDEKTIQSLOISAILHPNVPDPIILLADIAILKLDKARISTRVQIPICLAA 583

```

```
Db 541 LGRFYRDDDEXTKIQSLQISAILHPNVPYDILLADIALKLLDKARISTRVQPICLAA 600
Qy 584 SRLDSTSFQESHITVAGNVLADVRSPGKNDTLRSGVSVVDSILCEQHEDHGIPVSU 643
Db 601 SRLDSTSFQESHITVAGNVLADVRSPGKNDTLRSGVSVVDSILCEQHEDHGIPVSU 660
Qy 644 TDMNFCASBEPTAPSDICTAETGIIAASVSPGRASPEPRWHLMLGLVSWSDYDKTCSHRLST 703
Db 661 TDMNFCASBEPTAPSDICTAETGIIAASVSPGRASPEPRWHLMLGLVSWSDYDKTCSHRLST 720
Qy 704 AFTKVLFPKDWIERNMK 720
Db 721 AFTKVLFPKDWIERNMK 737

RESULT 4
Q8BU25 PRELIMINARY; PRT; 720 AA.
AC Q8BU25;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
DE length enriched library, clone:E430002G05 product:hypothetical EGF-
DE like domain, CUB domain, Sushi domain / SCR repeat / CCP module and
DE Serine proteases, trypsin family domain containing protein, full
DE insert sequence.
GN Name=E430002G05Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RN [5]
RN SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RN [5]
```

```
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
RN [6]
RN SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akanishi A., Muramatsu M., Hayashizaki Y.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; AK088017; BAC40098.1; -.
DR HSSP; P00736; IGPZ.
DR MGD; MGI:2445082; E430002G05Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept Ser Cys.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00923; SUSHI; 2.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
KW EGF-like domain; Hydrolase; Hypothetical protein; Protease;
KW Serine protease.
SQ SEQUENCE 720 AA; 80300 MW; C098E076D903A5A0 CRC64;

Query Match 91.6%; Score 3612; DB 2; Length 720;
Best Local Similarity 90.1%; Pred. No. 1.6e-262;
Matches 649; Conservative 33; Mismatches 38; Indels 0; Gaps 0;

Qy 1 MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAENWIMCRECEYDQIECVCPKRE 60
Db 1 MELDRWAQLGLVFLQLLLISSLPREYTVINEACPGAENWIMCRECEYDQIECLCPKKE 60
Qy 61 VVGTYTPCCFNEENECDSCLIHFGCTIFENCKSCRNCSWGSGTLLDDFYVKGFYCAECRAG 120
Db 61 VVGTYTPCCFNEENECDSCLIHFGCTIFENCKSCRNCSWGSGTLLDDFYVKGFYCAECRAG 120
Qy 121 YGGDCMRCGGQVLRAKQGLLESYPNAHCEWTHAKPGFVIQLRFWMLSEFDYMCQYD 180
Db 121 YGGDCMRCGGQVLRAKQGLLESYPNAHCEWTHAKPGFVIQLRFWMLSEFDYMCQYD 180
Qy 181 YVVRGDNRDGOI IKRVCCNERPAPIQSTIGSSILHVLFDHSDGSKNDFGFHAYEEITACS 240
Db 181 YVVRGDNRDSDPIIKRVCCNERPAPIRSTIGSSILHVLFDHSDGSKNDFGFHAYEEITACS 240
Qy 241 SSPCFHDGTCVLDKAGSKYKCACLAGYTGQRCENLLBERNCSDPGPGPVNGYQKITGGPLI 300
```

```
Db 241 SSCFDHGTCLLDTTSGFKACACAGTGCRCENLLEERNCSLDGGPVNGYKKITEGPGLL 300
Qy 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPCIKACREPKISDLVRRVRL 360
Db 301 NEHHVIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPCIKACREPKISDLVRRVRL 360
Qy 361 PMQVQSRRTPLHQLYSAPFSKQKQSAFTKPKPALPGDLPNGYHQLHTQLOVEICISPFYR 420
Db 361 SMQVQSRRTPLHQLYSTAFSKQLQDASTKPKPALPGDLPNGYHQLHTQLOVEICISPFYR 420
Qy 421 RLSSRRRTCLRTGWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480
Db 421 RLSSRRRTCLRTGWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480
Qy 481 HKGAWFLVCSGALVNERVTVAACHVCTDLGKVTMIKTADLKVVLGKGYRDDDEKTIQS 540
Db 481 HKGAWFLVCSGALVNERVTVAACHVCTDLGKVTMIKTADLKVVLGKGYRDDDEKTIQS 540
Qy 541 LQISAILHPNYDPIILLDADIALKLDKARISTRVQPICLAAASRLDLSFQESHITVAG 600
Db 541 LRVSAILHPNYDPIILLDADIALKLDKARISTRVQPICLAAASRLDLSFQESHITVAG 600
Qy 601 WNVLDVRSFGKNDTLRSQVSVVDSLCEOEHDGIPVSVTDNMFCASWPTAPSDI 660
Db 601 WNVLDVRSFGKNDTLRSQVSVVDSLCEOEHDGIPVSVTDNMFCASWPTAPSDI 660
Qy 661 CTAETGGIAAVSPGPRHLMGLVSWSDYDKTCSHRLSTAFKTVLPFKDWIERNMK 720
Db 661 CTAETGGIAAVSPGPRHLMGLVSWSDYDKTCSHRLSTAFKTVLPFKDWIERNMK 720
RESULT 5
Q8K2B8 PRELIMINARY; PRT; 720 AA.
AC Q8K2B8;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Regeneration associated muscle protease.
GN Name=E430002G05Rik;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RP Strausberg R.;
```

```
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; BC031841; AAH31841.1; -.
DR EMBL; BC057685; AAH57685.1; -.
DR HSSP; P00736; 1GPZ.
DR MGD; MGI:2445082; E430002G05Rik.
DR CO; Q0:0005615; C-extracellular space; TAS.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00923; SUSHI; 2.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 720 AA; 80377 MW; 7172B7F1E690FD0E CRC64;
Query Match 91.6%; Score 3612; DB 2; Length 720;
Best Local Similarity 90.1%; Pred. No. 1.6e-262;
Matches 649; Conservative 33; Mismatches 38; Indels 0; Gaps 0;
Qy 1 MELGCVTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60
Db 1 MELDRWAQLGLVFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECLCPGKKE 60
Qy 61 VVGVTYTPCCRNENECDSCLIHGCTIPENCCKSCRNCSGGTLLDDPVKGFYCAECRAGW 120
Db 61 VVGVTYTPCCRNENECDSCLIHGCTIPENCCKSCRNCSGGTLLDDPVKGFYCEECRAGW 120
Qy 121 YGDCMRCQGVLRAPKQGLLESYPLNAHCEWTIHAKPGFVQLRFLVMSLEFDYMCQYD 180
Db 121 YGDCMRCQGVLRASKQGLLESYPLNAHCEWTIHARPGFIQLRFGMLSLDFDYMCQYD 180
Qy 181 YVEVRDGDNRDQIINKVCGNERPAPIQSIGSSLHLVLFHSDGSKNFDGFHAIYEETACS 240
Db 181 YVEVRDGDNSDPIIKRPGCNERPAPIRSTGSSLHLVLFHSDGSKNFDGFHAFVEETACS 240
Qy 241 SSPCFHDGTCLVDKAGSYKACACLAGYTGRCENLLEERNCSDPGGPVNGYKITEGPGLI 300
Db 241 SSPCFHDGTCLDITTTGSPFKACLAGYTGRCENLLEERNCSDLGGPVNGYKKITEGPGLL 300
Qy 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPCIKACREPKISDLVRRVRL 360
Db 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPCIKACREPKISDLVRRVRL 360
Qy 361 PMQVQSRRTPLHQLYSAPFSKQKQSAFTKPKPALPGDLPNGYHQLHTQLOVEICISPFYR 420
Db 361 SMQVQSRRTPLHQLYSTAFSKQLQDASTKPKPALPGDLPNGYHQLHTQLOVEICISPFYR 420
Qy 421 RLSSRRRTCLRTGWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480
Db 421 RLSSRRRTCLRTGWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480
Qy 481 HKGAWFLVCSGALVNERVTVAACHVCTDLGKVTMIKTADLKVVLGKGYRDDDEKTIQS 540
Db 481 HKGAWFLVCSGALVNERVTVAACHVCTDLGKVTMIKTADLKVVLGKGYRDDDEKTIQS 540
```

```
QY 541 LOISAILHPNYDPILLDADIATLKLLDKARISTRVQPICLASRDLSSTSFQESHITVAG 600
DB 541 LRVSAILHPNYDPILLDTDIATLKLLDKARISTRVQPICLATVTRDLSSTSFQESHITVAG 600
QY 601 WNVLADVRSPGKNDLTRSGVSWVDSLLCEQEHEDHGIPVSVTDNMFCASWEPTAPSDI 660
DB 601 WNVLADVRSPGKNDLTRSGVSWVDSLLCEQEHEDHGIPVSVTDNMFCASWDPTSPSDI 660
QY 661 CTAETGGIAAVSPGPRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLFPKDWIERNMK 720
DB 661 CTAETGGIAALSFPGRASPEPRWHLVGLVSWSYDKTCSNGLSTAFTKVLFPKDWIERNMK 720

RESULT 6
Q6DIV5 PRELIMINARY; PRT; 722 AA.
AC Q6DIV5;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE MGC89196 protein.
GN Name=MGC89196;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Capeton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
[2]
RC SEQUENCE FROM N.A.
RP TISSUE=Whole body;
RA Klein S., Gerhard D.S.; to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; BC075430; AAH75430.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004295; F:tryptase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sushi; 2.
DR Pfam; PF00089; Trypsin; 1.
```

```
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; TYP_SPC; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00923; SUSHI; 2.
DR PROSITE; PS02040; TRYPsin DOM; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 722 AA; 80366 MW; F173563206DLA582 CRC64;

Query Match 71.6%; Score 2823; DB 2; Length 722;
Best Local Similarity 66.9%; Pred. No. 2.9e-203;
Matches 483; Conservative 110; Mismatches 127; Indels 2; Gaps 1;

QY 1 MELGCWTQLGLTFLQLLLISLP--REYTVINEACPGAENWIMCRCCCEYDQIECVCPGK 58
DB 1 MALLVWSSLVVASLHLGLTAAPSRKSYTVINENCFGAENWIMCRCCCEYDQIECVCPGK 60
QY 59 REVVGVTIPCCRNEECDSLIHPGCTTIPENCKSCRNCSWGCTLDDFFYKGYCAECRA 118
DB 61 NQKVGVTIPCCRNEECDSLIHPGCTTIPENCKSCRNCSWGCTLDDFFYKGYCAECRM 120
QY 119 GWYGGDMRCGVLRAPKQILLESYPLNAHCETTHAKPGFVIQLRFVWLSLEFDYMCQ 178
DB 121 GWYGGDMRCGEVIQAARGEIMLESYPPNARCEWSIQVAPGYTVELRFGMLSLSEFDYMCQ 180
QY 179 YDVEVRDGDNRDQIIRKVCNGNERPAPIOSIGSSHLVLFHSDGSKNFDGFHAIYBEITA 238
DB 181 YDLEVRDGDNDVAKILKFCGNQRPISLSTGNSLHLFQSDGSKNFDGFYTFEEVTG 240
QY 239 CSSSPCFHDTGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDDPGSPVNGYQKITGGPG 298
DB 241 CSSTPCFHDGTCTIADKTGYRACLAGYTGRCHEVIEEKSKDPCGAPMNGYRKLPDGAG 300
QY 299 LINGRAKIGTVVSFFCNNSYVLNGEKTCCQNGSWGSKQPIKACKEPKISDLVRRR 358
DB 301 LSLANHIKVGFKIHYFCNNSYVLNGEQRACQAGQWQSGKQPVCIKACKEPKVADLVROK 360
QY 359 VLPQVQSRETPLHOLYSAAFSKQLQSAFTKPKPALPFGDLPNGYQHLHTQLQYECISPF 418
DB 361 VLPQVQSRETPLHOLYSAAFSKQEKTDILPTKPPALPFGELPGYQHLHTQLQYDCVSPF 420
QY 419 YRRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRTSGVHDG 478
DB 421 YRRTGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRTSGVHDG 480
QY 479 SLHKGAWFLVCSGALVNERTVVVAACHVTDLGKVTMKTADLKVLGKFYRDDDDREKTI 538
DB 481 SLRKGSMVLVCSGALLNERTVVAACHVTDLGKSSIIKVSMDKVLGKFRDDDDREKTSQ 540
QY 539 QSLQISAILHPNYDPILLDADIATLKLLDKARISTRVQPICLASRDLSSTSFQESHITV 598
DB 541 QHLHISAVINPNYDPILLDSDIAVILKLDKARVSDYVQVCLTLATEMITSPQYITVI 600
QY 599 AGNVLADVRSPGKNDLTRSGVSWVDSLLCEQEHEDHGIPVSVTDNMFCASWEPTAPS 658
DB 601 SGWKILSDPRAPGSKNETTRAGAIEPVDSILQCEQVEENGISVSVTESMFCQKQEPSP 660
QY 659 DICTAETGGIAAVSPGPRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLFPKDWIERN 718
DB 661 SICPSETGGITTVLLPSPSPSPSGSWHLILGLVSWGYDKSCRDLTYGTIKVTTFKWLK 720
QY 719 MK 720
DB 721 MK 722

RESULT 7
Q71RE9
```

```

ID Q71R99 PRELIMINARY; PRT; 417 AA.
AC Q71R99;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FP938
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF370388; AAQ15224.1; -.
DR HSSP; P00734; 1BB0.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Peptidase_S1A.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00923; SUSHI; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 417 AA; 46703 MW; 2546A52A3697C1C4 CRC64;

Query Match 52.2%; Score 2059; DB 2; Length 417;
Best Local Similarity 95.6%; Pred. No. 3 5e-146;
Matches 389; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

QY 314 FCNNSVYLGNEKRTCCQNGESGKQPIKACREPKISDLVRRVPLPMQVQSRRTPLHQ 373
DB 11 FVTPMFLVAMRKELASRMERWSGKQPIKACREPKISDLVRRVPLPMQVQSRRTPLHQ 70
QY 374 LYSAAESKQKQLOAPTKKPPALPGDLPNGYQHLLHTQLEYECISPFYRRLLGSSRRRTCLRTG 433
DB 71 LYSAAESKQKQLOAPTKKPPALPGDLPNGYQHLLHTQLEYECISPFYRRLLGSSRRRTCLRTG 130
QY 434 KNSGRAPSCIPICGKIENITAPKTQGLRWEPQAAIYRRTSQVHDSGLHKGAWFLVCSGAL 493
DB 131 KNSGRAPSCIPICGKIENITAPKTQGLRWEPQAAIYRRTSQVHDSGLHKGAWFLVCSGAL 190
QY 494 VNERTVVAACHVTDLGKVTMIKTADLKVVLGKPYRDDDDREKTIQSLQISAILLHPNYD 553
DB 191 VNERTVVAACHVTDLGKVTMIKTADLKVVLGKPYRDDDDREKTIQSLQISAILLHPNYD 250
QY 554 PILLDADIAILLKLDKARISTRVQPICLAASRDLSFQESHITVAGWNVLDVRSFGPK 613
DB 251 PILLDADIAILLKLDKARISTRVQPICLAASRDLSFQESHITVAGWNVLDVRSFGPK 310
QY 614 NDLTRSGVSVVDSLLCEQHEHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSF 673
DB 311 NDLTRSGVSVVDSLLCEQHEHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSF 370
QY 674 PGRASPEPRWHLMLVSWSDYKTCSHRLSTAFTKVLPPFKDWIERNMK 720
DB 371 PGRASPEPRWHLMLVSWSDYKTCSHRLSTAFTKVLPPFKDWIERNMK 417

RESULT 8
QY432
AC QY432;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

```

```

DE Hypothetical protein DKF2p586H2123 (Fragment).
GN Name=DKF2p586H2123;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ansoerge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050214; CAB43317.1; -.
DR PIR; T08805; T08805.
DR HSSP; P00736; 1MD7.
DR MEROPS; S01.998; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR009003; Peptidase_S1A.
DR SMART; SM00089; Trypsin; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
KW Hydrolase; Hypothetical protein; Protease; Serine protease.
FT NON_TER 1
SQ SEQUENCE 181 AA; 19962 MW; ABC793BE8682D439 CRC64;

Query Match 24.1%; Score 949; DB 2; Length 181;
Best Local Similarity 99.4%; Pred. No. 2.9e-63;
Matches 180; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 540 SLQISAILLHPNYDPIILLDADIAILLKLDKARISTRVQPICLAASRDLSFQESHITVA 599
DB 1 SLRISAILLHPNYDPIILLDADIAILLKLDKARISTRVQPICLAASRDLSFQESHITVA 60
QY 600 GNVLDVRSFGPKNDLTRSGVSVVDSLLCEQHEHGIPVSVTDNMFCASWEPTAPSD 659
DB 61 GNVLDVRSFGPKNDLTRSGVSVVDSLLCEQHEHGIPVSVTDNMFCASWEPTAPSD 120
QY 660 ICTAETGGIAAVSFGRASPEPRWHLMLVSWSDYKTCSHRLSTAFTKVLPPFKDWIERNM 719
DB 121 ICTAETGGIAAVSFGRASPEPRWHLMLVSWSDYKTCSHRLSTAFTKVLPPFKDWIERNM 180
QY 720 K 720
DB 181 K 181

RESULT 9
QY432
ID Q8T9S1 PRELIMINARY; PRT; 1019 AA.
AC Q8T9S1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Factor C precursor.
OS Tachyplesus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachyplesus.
NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21955715; PubMed=11958140;
RA Wang D., Liu J., Chen L., Wang L., Yang G., Wu X., Zhang W.;
RT "Cloning and expression of Tachyplesus tridentatus factor C.";
RL Acta Biochim. Biophys. Sin. 34:77-82(2002).
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF467804; AAL75577.1; -.
DR HSSP; P00746; 1FDP.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.

```

```

DR GO: G0:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR006209; EGF_Like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR004043; LCCL.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR Pfam: PF003815; LCCL; 1.
DR Pfam: PF00059; Lectin_C; 1.
DR Pfam: PF00084; Sushi_3.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00032; CCP; 5.
DR SMART: SM00034; CLECT; 1.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00603; LCCL; 1.
DR SMART: SM00020; Tryp_SFC; 1.
DR PROSITE: PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS00026; EGF_3; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00820; LCCL; 1.
DR PROSITE: PS00923; SUSHI; 5.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL 1
FT CHAIN 26 1019
SQ SEQUENCE 1019 AA; 112248 MW; B8E51730AE595993 CRC64;

Query Match 17.2%; Score 678; DB 2; Length 1019;
Best Local Similarity 25.68; Pred. No. 5.5e-42;
Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;

QY 34 PGAEWNIM-----CRECEYDQIE---CVCFGKREVGVGTYTPCCRNENECDSCLIHPGCT 86
DB 184 PNGQWSFPKCIKRECAKVSSPEHGKVTAPSGNMIEGATL-----RFSCHS-----PHYL 233
QY 87 IFENCKSCR-NGSWGGLT-----
DB 234 IGOETLTCCGNGQWSGQIPQCKLVFCPDLDPVNHAEHVQKIGVEQKYGFPQGTETVYTT 293
QY 104 --DDFYKGFVCAECR--AGWYGG--DCMR-----CGQVLR--APKG 137
DB 294 CSGNYFLMGNTLKNLDGWSGSGQSCVKVADREVDVDCSKAVDFLDDVGEVRIHCPAG 353
QY 138 QILLES-----YPLNAHCEWTIHA-----KPGFVI-----Q 163
DB 354 CSLTAGTVGWTATVYHELSSVCRAIHAGKLPNSGAVHVHNGPYSDFLGSLDNGIKSEE 413
QY 164 LRFVMLSLEFDYM-----COYDVFEVRD-----GNRDGQIIRKVCN--ERPAP 206
DB 414 LKSLARSFRFDYVSSSTAGRSGCPDGMFEVENCVVYTSQRAWERAQGVCTNNAARLAV 473
QY 207 IQS--IGSSLHLVLFHSDG--SKNFDGFH-----ALYEBITACSSSPCF 245
DB 474 LDKDVIPTSSITEALRGKGLTTTIGLRLDAERPFVWELMDRNVNLDNLTFWASGEPG 533
QY 246 HDGTCV-LDKAGS-----YKCACLAGYTGQRCENLLEERN---CSDPGGPNVGKYGKTTGGP 297
DB 534 NEITNCVYLDIRDQIQPVWTKTKSCFPSSFACMMDLSDRNAKAKDDPGSLENGHATLHGQS 593
QY 298 GLINGRAHAKGTVVVSFFCNNSYVLGNEKTKCOQNGEWSGKQPTCIK--ACREPKISDLV 355
DB 594 --IDGFYA--GSSIRYCEVHLVLSGTETVTTCTTNGTWSAPKPKCIKVTCONPPVPSYG 649
QY 356 RRRVLPQVOSRETPLHQLYSAAPSKQLQ---SAPTKKPAIPGD-----LP 400

```

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; D90271; BAA14315.1; -;
 EMBL; D90272; BAA14316.1; -;
 PIR; A38738; A38738.
 HSP; P00746; 1FDP.
 MEROPS; S01_219; -;
 InterPro; IPR000742; EGF_2.
 InterPro; IPR006209; EGF_like.
 InterPro; IPR006210; IEGF.
 InterPro; IPR004043; LCCL.
 InterPro; IPR001304; Lectin C.
 InterPro; IPR001254; Peptidase_S1.
 InterPro; IPR001314; Peptidase_S1A.
 InterPro; IPR009003; Pept_Ser_Cys.
 InterPro; IPR000436; Sushi_SCR_CCP.
 Pfam; PF03815; LCCL; 1.
 Pfam; PF00059; Lectin_C; 1.
 Pfam; PF00084; Sushi; 5.
 Pfam; PF00089; Trypsin; 1.
 PRINTS; PR00722; CHYMOTRYPSIN.
 SMART; SM00032; CCP; 5.
 SMART; SM00034; CLECT; 1.
 SMART; SM00181; EGF; 1.
 SMART; SM00603; LCCL; 1.
 SMART; SM00020; Tryp_Spc; 1.
 PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
 PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
 PROSITE; PS00022; EGF_1; 1.
 PROSITE; PS01186; EGF_2; FALSE_NEG.
 PROSITE; PS00026; EGF_3; 1.
 PROSITE; PS00820; LCCL; 1.
 PROSITE; PS00923; SUSHI; 5.
 PROSITE; PS0240; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 PROSITE; PS00135; TRYPSIN_SER; 1.
 Alternative splicing; Cell adhesion; Direct protein sequencing;
 EGF-like domain; Glycoprotein; Hemolymph clotting; Hydrolase; Lectin;
 Repeat; Serine protease; Signal; Sushi.
 SIGNAL 1 25 Limulus clotting factor C.
 CHAIN 26 1019 Limulus clotting factor C heavy chain.
 CHAIN 26 690 Limulus clotting factor C light chain.
 CHAIN 691 1019 Limulus clotting factor C chain A.
 CHAIN 763 1019 Limulus clotting factor C chain B.
 CHAIN 102 137 EGF-like.
 DOMAIN 140 197 Sushi 1.
 DOMAIN 140 197 Sushi 1.
 DOMAIN 198 256 Sushi 2.
 DOMAIN 258 323 Sushi 3.
 DOMAIN 325 421 LCCL.
 DOMAIN 436 568 C-type lectin.
 DOMAIN 574 636 Sushi 4.
 DOMAIN 689 750 Sushi 5.
 DOMAIN 763 1019 Serine protease.
 ACT_SITE 809 809 Charge relay system (By similarity).
 ACT_SITE 865 865 Charge relay system (By similarity).
 ACT_SITE 966 966 Charge relay system (By similarity).
 BINDING 960 960 Substrate (By similarity).
 DOMAIN 643 689 pro-rich.
 DISULFID 106 118 By similarity.
 DISULFID 112 125 By similarity.
 DISULFID 127 136 By similarity.
 DISULFID 436 447 By similarity.
 DISULFID 464 564 By similarity.
 DISULFID 538 556 By similarity.
 DISULFID 794 810 By similarity.
 DISULFID 932 932 By similarity.

FT DISULFID 962 996 By similarity.
 FT CARBOHYD 523 534 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 534 534 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 624 624 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 740 740 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 767 767 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 912 912 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 492 498 LTTTWIG -> TDNVTAT (in isoform Short).
 FT VARSPLIC 499 1019 Missing (in isoform Short).
 FT VARSPLIC 499 1019 /FTId=VSP_005413.
 FT VARSPLIC 499 1019 /FTId=VSP_005414.
 SQ SEQUENCE 1019 AA; 112346 MW; 58C2864C6715289B CRC64;
 Query Match 17.0%; Score 672; DB 1; Length 1019;
 Best Local Similarity 25.6%; Pred. No. 1.6e-41;
 Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;
 QY 34 PGAENIM-----CRECEYDQIE---CVCPRKEVVGVTIPCCNEENECDCSLHFGCT 86
 DB 184 PNGOWSSFPKCIKRECAKVSSEPHGVNAPSNGMIEGATL-----RFSCDS-----PYYL 233
 QY 87 IFENCKSCR-NGSWGGLT-----
 DB 234 IGQETLTCCQNGQWSGOIPCKKLVPCLDLPVNHAEHQVIGVEQKYGFPGQTEVYT 293
 QY 104 --DDFYKGYCAECR--AGWYGG--DCMR-----CGQVLR--APKG 137
 DB 294 CSGNYFLMGFNTLKNPDGSGWSQSCVKVADREVDCDSKAVDFLDVGEVRIHPAG 353
 QY 138 QILLES-----YPLNAHCETIHA---KGFVI-----Q 163
 DB 354 CSLTAGTVMGTATYHELSSVCAAAIHAGKLPNSGGAVHVYVNGPYSDFLGSLNGIKSEE 413
 QY 164 LRFVMLSLEFDY-----COYDVEVRD-----GDRDQGITKRCGN--ERPAP 206
 DB 414 LKSLARSPFDYVSSSTAGSGCGPDGWFVEENCVYTSKORAWERAGQVCTNWAARLAV 473
 QY 207 IQS--IGSSLHLVFLHSDG-SKNFDGPH-----AIYEITACSSSPCF 245
 DB 474 LDKDLIPSSLTETLRGKGLTTTWIGLHRLDAEKPFWELMDRNVVLDNLNLTFWASCEPG 533
 QY 246 HDGTCV-LDKAGS-----YKACACLAGYTGRCENLLERN---CSDPGGVNGYQKITGGP 297
 DB 534 NETCYVLDIRDQLQPVWTKSCFPSSFACMDLSDRNKAKCDPGLPENGHATLHGQS 593
 QY 298 GLINGRHAKIGTVVFFCNNSYVLSGNEKRTCCQNGESGKQPICIK--ACREPKISDLV 355
 DB 594 --JDGFYA--GSSIRYSCVELHYLSGTETVCTTNGTWSAPKPRCIVITCQNPVPSYG 649
 QY 356 RRVLPMPQVQSRETPLHQLYSAAFSKQKLQ---SAPTKKPPALPFGD-----LP 400
 DB 650 SVEIKP---PSRTNSISRVSPPFLRLPLPLARAAPKPPKPRSSQPSVTLASKVKLP 706
 QY 401 MGVOHLHTQLQYECISPPFRRLGSSRRRTCLRTKNSGRAPSCIPICGKIENITAP----- 455
 DB 707 EGHYRVGSRAIYTCESRYELLYSGQRCDSNGWSGRPASCIPIVCGRSDSPSPFTWNG 766
 QY 456 -KTQGLRWPQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVAACHVDLGLKVTM 514
 DB 767 NSTEIQWNPQAGISRWLA-----DHNNWFLQCGSLNLRKWIYTAACHVITYSATAEI 819
 QY 515 IKTADLVVLGKPYRDDDEKTIQSLQISAITLHPNYDPILLADIALKLDKARIST 574
 DB 820 IDPSQPKIYLGKYVRDSDDDYVQVREALEIHVNPNYDPGNLNFDAIQLATPVLT 879
 QY 575 RVQPICLASRLSTSFQESHI-----TVAGNNVLADVRSPGKNDTLRSVVSVVDSL 628
 DB 880 RVQPICLPT--DITT---REHLKEGTLAVVTGNG-----LNENNTYSEMIQAAVLPVVAAS 930
 QY 629 LCBEQHEHGIPVSVTDNNMFCASWEPTAPSDICTAETGGIAVSPFGRASPEPRHLMGL 688
 DB 931 TCEEGYKEADLPVTVTENMFCAGYK-KGRYDACSQSGG--PLVFADDSKTERRWVLEGI 987

QY 689 VWSYDKTCSH-RLSTAFKVLFPKDWIER 717
 DB 988 VSWGSPSGCKANQYGGFTKVNFLSWIRQ 1017

RESULT 11
 LFC_CARRO STANDARD; PRT: 1019 AA.
 AC Q26422;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Limulus clotting factor C precursor (EC 3.4.21.84) (FC).
 OS Carinoscorpius rotundicauda (Southeast Asian horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Carinoscorpius.
 OX NCBI_TaxID=6848;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=95268506; PubMed=7538401;
 RA Ding J.L., Navas M.A. III, Ho B.;
 RT "Molecular cloning and sequencing analysis of factor C cDNA from the
 RL Singapore horseshoe crab, Carinoscorpius rotundicauda.";
 RL Mol. Mar. Biol. Biotechnol. 4:90-103(1995).
 CC -!- FUNCTION: This enzyme is closely associated with an endotoxin-
 CC sensitive hemolymph coagulation system which may play important
 CC roles in both hemostasis and host defense mechanisms. Its active
 CC form catalyzes the activation of factor B.
 CC -!- CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-Ser-104 and
 CC 124-Ile-Ile-125 bonds in Limulus clotting factor B to form
 CC activated factor B. Cleavage of Pro-Arg-Xaa bonds in synthetic
 CC substrates.
 CC -!- ENZYME REGULATION: Activated by Gram-negative bacterial
 CC lipopolysaccharides and chymotrypsin (By similarity).
 CC -!- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
 CC a disulfide bond (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted in hemolymph.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 1 LCCL domain.
 CC -!- SIMILARITY: Contains 5 Sushi (CCP/SCR) domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: S77063; AAB34361.1; -.
 CC HSP: P00746; 1PDP.
 CC DR MEROPS: S01.219; -.
 CC InterPro: IPR000742; EGF 2.
 CC InterPro: IPR006209; EGF-like.
 CC InterPro: IPR006210; IEGF.
 CC InterPro: IPR004043; LCCL.
 CC InterPro: IPR001304; Lectin C.
 CC InterPro: IPR001254; Peptidase S1.
 CC InterPro: IPR001314; Peptidase_S1.
 CC InterPro: IPR009003; Pept_Ser_Cys.
 CC InterPro: IPR004036; Sushi_SCR_CCP.
 CC Pfam: PF03815; LCCL; 1.
 CC Pfam: PF00059; Lectin C; 1.
 CC Pfam: PF00084; Sushi; 5.
 CC Pfam: PF00089; Trypsin; 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC SMART: SM00032; CCP; 5.
 CC SMART: SM00034; CLECT; 1.
 CC SMART: SM00181; EGF; 1.
 CC SMART: SM00603; LCCL; 1.

DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
 DR PROSITE; PS00441; C_TYPE_LLECTIN_2; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS00820; LCCL; 1.
 DR PROSITE; PS00923; SUSHI; 5.
 DR PROSITE; PS02400; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Cell adhesion; EGF-like domain; Glycoprotein; Hemolymph clotting;
 KW Hydrolase; Lectin; Repeat; Serine protease; Signal; Sushi.
 FT SIGNAL 1 25
 FT CHAIN 26 1019
 FT CHAIN 26 690
 FT CHAIN 691 1019
 FT CHAIN 691 762
 FT CHAIN 763 1019
 FT DOMAIN 102 137
 FT DOMAIN 140 197
 FT DOMAIN 198 256
 FT DOMAIN 258 323
 FT DOMAIN 325 421
 FT DOMAIN 436 568
 FT DOMAIN 574 636
 FT DOMAIN 689 750
 FT DOMAIN 763 1019
 FT ACT_SITE 809 809
 FT ACT_SITE 865 865
 FT ACT_SITE 966 966
 FT BINDING 960 960
 FT DOMAIN 643 689
 FT DISULFID 106 118
 FT DISULFID 112 125
 FT DISULFID 127 136
 FT DISULFID 436 447
 FT DISULFID 464 564
 FT DISULFID 538 556
 FT DISULFID 794 810
 FT DISULFID 932 951
 FT DISULFID 962 996
 FT CARBOHYD 523 523
 FT CARBOHYD 534 534
 FT CARBOHYD 624 624
 FT CARBOHYD 740 740
 FT CARBOHYD 767 767
 FT CARBOHYD 912 912
 SQ SEQUENCE 1019 AA; 112429 MW; 918A1ED8B817B6C3 CRC64;

Query Match 16.9%; Score 665; DB 1; Length 1019;
 Best Local Similarity 25.4%; Pred. No. 5.2e-41;
 Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAEWIMRCCEYDQIECVCPGKRE-----VVGYTTPCCRNENECDSCLIH 82
 DB 184 PNGQWSNFPKICR-----ECAMVSSPHGKVNALSGDMIEGATL-----RFSCDS----- 229
 QY 83 PGCTIFENCKSCR-NGSWGOTL----- 103
 DB 230 PYYLIGQETLTCCQNGQWNGQIPQCKNLVFCPLDPVNHAEHKVIGVEQYQGFPGTE 289
 QY 104 -----DDFYVKGFYCAECR--AGWYGG--DCMR-----CQQLR-- 133
 DB 290 VVTCTGNGYFLMGFDTLKCNPDGSGWSGSQSCVKVADREVDCKSAVDLDDVGEPRIH 349
 QY 134 APKQIILLES-----YPLNAHCETIHA-----KPGFVI----- 162
 DB 350 CPAGCSLTAGTVNGTAIYHELSSVCRAAIHAGKLPSNGGAVHVNNNGPYSDFLGSLNGI 409
 QY 163 ---OLRFVMLSLEFDYM-----CQDYVEVRD-----GDRRGQIILKRCGN--E 202
 DB 410 KSEBELKSARSFRFDYVRSSTAGKSGCPDGWFEVDENCVCVYTSKQRAWERAQGVCTNMAA 469

Db 827 IWNGNSTEQWQAGISRWLA-----DHNWFLQCGSLNKKWIVTAACVITYSA 879
QY 511 KVTMIKTADLKVVGLKGYRDRDDREKTIQSLQISAILLHPNYDPILLDADIALKLLDKA 570
Db 880 TABIIDPNQPMYLGKYYRDSDDDDYVQVREALEIHVNENYDPGNLNFIDIALIQLKTPV 939
QY 571 RISTRVQPICLAASRDLSFQESHII-----TVAGNVLADVRSPGFKNDTLRSQVVSU 624
Db 940 TLTRIVQPICLPT--DITT---REHLKEGTLAVVTGWG-----LNENNTVSETIQQAVLPV 990
QY 625 VDSLLCEEQHEHIGIPVSTNNMFCASWEPTAPSDICTAFTGGIAAVSPFGRASPPRHH 684
Db 991 VAASTCEGYKEADLPITVENMFCAGYK-KGRYDACSGDSGG--PLVFADDSRTERRWV 1047
QY 685 LMGLVSWSYDKTCSH-RLSTAFKVLFPFKDWIER 717
Db 1048 LEGIVSWGSPSGCGKANQYGFTKVNVLFSWIRQ 1081

RESULT 13

Q868H7 PRELIMINARY; PRT; 680 AA.
ID Q868H7
AC Q868H7;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Mannose-binding lectin associated serine protease-1.
GN Name=MASP-1;
OS Branchiostoma belcheri (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7741;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Notochord;
RX MEDLINE=22593355; PubMed=12707349;
RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Matsusita A., Takabashi M.,
Matsushita M., Fujita T.,
RT "Origin of mannose-binding lectin-associated serine protease (MASP)-1
and MASP-3 involved in the lectin complement pathway traced back to
the invertebrate, amphioxus";
RT J. Immunol. 170:4701-4707(2003).
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR ENBL; AB089267; BAC75886.1; -.
DR HSP; P00736; IAPQ.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006956; P:complement activation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR011361; Pept_S1 Comp Act.
DR InterPro; IPR009003; Pept_Set_Cys.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sushi; 2.
DR Pfam; PF00089; Trypsin; 1.
DR PIRSF; PIRSF001155; Clr_Cis_MASP; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; Tryp_Spc; 1.

DR PROSITE; PS00010; ASX HYDROXYL; UNKNOWN_1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS0923; SUSHI; 2.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Lectin; Protease; Serine protease.
SQ SEQUENCE 680 AA; 75871 MW; 496985A94A728318 CRC64;

Query Match 15.4%; Score 608.5; DB 2; Length 680;
Best Local Similarity 26.3%; Pred. No. 5.5e-37;
Matches 195; Conservative 92; Mismatches 239; Indels 215; Gaps 35;

QY 46 CEYDQIECV-----CFGKEV-----VGYT 65
Db 84 CEYDYKVMGDKLVGLFCGTEDTDEKVPGRVIESTGSLSEPKSPSNVDRHKGFV 143
QY 66 IPCRNEENECDSLIHPGCTIFENCKSCRNCSWGGLDDFYVKGFCACRAG-WYGGD 124
Db 144 VHYRVVDRDEC-AVDNGGCHHF-----CHN-----YISGYCS-CRAGYWMKD 185
QY 125 ---C-MRCG-QVLRAPKQIILLES---YPLNAHCEWTTHAKPGFVIQIRFVMSLEFD- 174
Db 186 RETCKFGCGQVLTQLSGTISSEYPRLYPKVLDLDCDWKIQVEPGYVVTLOF---DDDFDV 242
QY 175 ---YMCQYDYVEVRDGNRDQIIRKVCNERPAPIQISGSSLSLHVLHSDGSKNFDGF 229
Db 243 EQHPEVSCPYDHLKVQAGDEKYP-----YCGKTVPTTITSTDHKMHVFFHSDSGENKGF 298
QY 230 HAIYEBITACSSSPCPHDGTCVLCDKAGSYKACLAGYTGQRCENLLEERNCSDPGGPVNG 289
Db 299 RATYFT-----TARPCAL-----SAP----- 315
QY 290 YQKITGGPGLNGRHAKIGTVVSVFFCNNSYVLSGNEKRTCCQNGEWSGKQPICAKREP 349
Db 316 ---AYGTMESNFTYSQKVSFACGEGYLDGPDHRCVQADGWSGVQPTC----- 362
QY 350 KISDIARRRVLPQVOSRSTPLHOLYSAAFSKQLOSAPTKKFPALPGDLPMGYQHLHTQ 409
Db 363 ---ELVNCGLP-NISNGEIEVDGNFS-----YADIAI----- 391
QY 410 LOYECISPFYRRLGSSRRRTCLRTKWSGRAPSCIPICGKIENITAPKTOGLR-----WP 463
Db 392 --YRC-DQFVEMAGEGTRFCEADGKKTGNEPSCKTCGKPEFVTRGKLVGRPAMRGAWP 448
QY 464 WQAAIYRTSGVHDGSLHKGAMFLVCSGALVNERTVVVAACHVTDLGKVTMIKTADLKVV 523
Db 449 WMAMLHRTPRG-----FCGGTLLGQWVLTAAHCLVSPVTSDFILKDSFSVI 496
QY 524 LGKF-YRDDRDEKTIQSLQISAILLHPNYDPILLDADIALKLLDKARISTRVQPICLA 582
Db 497 LGHKARDKDTTEQTV---QVAQIVVHPAPFTFLADIALLKLESAPRLNPYITICLL 553
QY 583 ASRDLSTSF---QESHITVAGWNVLADVRSPGFKNDTLRSQVVSVDLLCEQHEDHGI 639
Db 554 SEEEATATLVPGREAAVT--GWG-----HSDQGFANLELREVFLPLDVTSTCNKTYD---- 603
QY 640 PVSVDNMFCAWSEPTAPSDICTAFTGGIAAVSPFGRASPEPRWHLMGLVSWSYDKTCSH 699
Db 604 -FTVTSMDICAGFQ-EGGKDACRDSGG--PLAFFERTA--EKWQGVQVVTWGWG--CGR 655

QY 700 RLS-TAFTKVLFPFKDWIERNM 719
Db 656 KNKYGYVTNVIQYLPWIDEVM 676

RESULT 14

Q868H5 PRELIMINARY; PRT; 680 AA.
ID Q868H5
AC Q868H5;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)

[illegible]

DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR011361; Pept_S1 Comp Act.
DR InterPro; IPR009003; Pept_Set_Cys.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sushi; 2.
DR Pfam; PF00089; Trypsin; 1.
DR PIRSF; PIRSF001155; Chr_Cls_MASP; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00923; SUSHI; 2.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Lectin; Protease; Serine protease.
SQ. SEQUENCE 688 AA; 76890 MW; 14B3AD8215BD4D15 CRC64;

Query Match 15.1%; Score 597; DB 2; Length 688;
Best Local Similarity 26.6%; Pred. No. 4.1e-36;
Matches 197; Conservative 88; Mismatches 244; Indels 212; Gaps 36;

QY 46 CEYDQIECV-----CPGKEV-----VGYT 65
DB 84 CEYDYKVMGDKLVGLFCGTEDTDEQVFGDRVIESTGSQLSLEPKSDFSNADRHKGFA 143

QY 66 IPCRNEENECDSCLHPGCTIIFENCKSCRNKSGWGTLDLDFYKGYCAECRAG-WYGGD 124
DB 144 VHYRVVDREDC--AVDNGGCHF-----CHN-----YISGYYS-CRAGYIMKD 185

QY 125 ---C-MRCG-QVLRAPKQILLES---YPLNAHCWTHAKPGFVQLRPFVMSLEFD- 174
DB 186 RETCKFGCGRQVLTKLSGTISSEYPRLYPKVLDCKWKIQVEFGYVVLQF---DDDFDV 242

QY 175 -----YMCQYDYVEVRDGNRDGQIIKRVCGNERPAPIQSIGSLHVLPHSDGSKNPDGF 229
DB 243 EQHPEVSCPYDHLKVKAGDEKYG----YCGKTVPTITSTDHNMHVFFHSDSGENKGF 298

QY 230 HAIYEITACSSPFCFHDGTCVLDKAGSYKACACLAGYTGQRCENLLEERCNSDPGPGVNG 289
DB 299 RATYFT-----TARPCAL-----SAP----- 315

QY 290 YQKITGGPGLNGRHAKIGTVGFFCNNSVYLSGNEKRTCOONGESGKOPICIKACREP 349
DB 316 -----AYGTWEGSNFTYSQKVSFACGEGYLDGPHRVQADGWSGVQPTC----- 362

QY 350 KISDLVRRVLPQVQSRETPLHQLYSAAFSKQKLSAPTCKPALPFGDLPMGYQHLHTQ 409
DB 363 ---ELVNCGPLP-NISNGEIVDGNFS-----YADIAI----- 391

QY 410 LQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKI-----ENIT--APKTQGLRW 462
DB 392 --YRC-DQFYEMAGEGRFCEAGGKWTGNEFPCKPICGESSFPSRDRIVGGGPKKG-AW 447

QY 463 PQQAAIVRRTSVGHDSLHGAWFL---VCSGALVNERTVVAHCVTDLKGVTMIKTAD 519
DB 448 PQQAMV-----IHQAPRIRKPFCCGALVDKKWILTAAHCV---GENDILPTGY 493

QY 520 LKVVLGKFYRDDREKTIQSLQISAJILHPNVDPIILLDADIAILKLLDKARISTRVQPI 579
DB 494 FNVSLGLHKKEPDNDVVPF--EVERIRHPDWDKDNFDSIALLELKEEVDLTDYIRPV 551

QY 580 CLAAS--RDLSTSFQBSHI-TVAGMNVLADVRSPGFKNDTLRSGVSVVVDLLICEQHED 636
DB 552 CLQSRGRQSAQDVQEGRAGVVTGWGRTSNLP--GSEANTLQEBVEVPVVDQEECVSAYEG 609
QY 637 HGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPRKWHLMGLVSWSYDKT 696
DB 610 ---DYPVTGNMLCAGLR-IGGKSDCDGSGPILLFQDPDTT-----RFYVAGLVSWGEPSE 661

QY 697 CSH-RLSTAFATKVLFPKDWIE 716
DB 662 CGRARKYGYVYARVENFVQMIK 682

Search completed: May 8, 2005, 16:08:27
Job time : 109 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 8, 2005, 13:11:48 ; Search time 25 Seconds
(without alignments)
2149.893 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 3945

Sequence: 1 MELGWTQGLTFLQLLIS.....LSTAFKVLFPKDWIERNMK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2946.5	74.7	570	4	US-10-067-422-9
2	665	16.9	1019	1	US-08-296-014A-4
3	665	16.9	1019	2	US-08-596-405-4
4	665	16.9	1019	4	US-08-877-620-4
5	665	16.9	1019	4	US-08-287-368-4
6	665	16.9	1019	4	US-09-626-795-4
7	665	16.9	1083	1	US-08-296-014A-2
8	665	16.9	1083	2	US-08-596-405-2
9	665	16.9	1083	4	US-08-877-620-2
10	665	16.9	1083	4	US-09-287-368-2
11	665	16.9	1083	4	US-09-626-795-2
12	482	12.2	699	4	US-09-949-016-6138
13	475	12.0	717	4	US-09-949-016-11182
14	399.5	10.1	691	4	US-09-949-016-7775
15	337	8.3	855	2	US-09-027-337-2
16	337	8.3	855	4	US-09-644-600-2
17	337	8.3	855	4	US-09-654-600A-2
18	321	8.1	460	6	5270178-16
19	321	8.1	460	6	5270178-16
20	317.5	8.0	798	1	US-08-200-900A-2
21	317.5	8.0	798	4	US-08-794-042-2
22	317.5	8.0	798	5	PCT-US94-00616-2
23	311.5	7.9	461	6	5460953-3
24	311.5	7.9	461	6	5460953-3
25	310.5	7.9	409	3	US-09-065-872-2
26	310.5	7.9	409	4	US-09-667-570A-2
27	310.5	7.9	410	3	US-09-065-872-1

28	310.5	7.9	410	4	US-09-667-570A-1	Sequence 1, Appli
29	310.5	7.9	419	1	US-08-295-411-1	Sequence 1, Appli
30	310.5	7.9	419	2	US-08-955-471-1	Sequence 1, Appli
31	310.5	7.9	419	4	US-09-667-570A-3	Sequence 3, Appli
32	310.5	7.9	419	4	US-10-182-263-1	Sequence 1, Appli
33	310.5	7.9	419	5	PCT-US92-10242-1	Sequence 1, Appli
34	310.5	7.9	460	2	US-08-756-506-2	Sequence 2, Appli
35	310.5	7.9	460	2	US-08-756-506-4	Sequence 2, Appli
36	310.5	7.9	461	4	US-10-182-263-2	Sequence 2, Appli
37	310.5	7.9	461	4	US-09-054-272-32	Sequence 32, Appli
38	310.5	7.9	461	4	US-09-949-016-5921	Sequence 5921, Ap
39	310.5	7.9	461	6	525537-2	Patent No. 525537
40	310.5	7.9	461	6	525537-2	Patent No. 525537
41	310.5	7.9	485	4	US-09-949-016-10882	Sequence 10882, A
42	310	7.9	419	4	US-10-182-263-6	Sequence 6, Appli
43	309	7.8	419	4	US-10-182-263-3	Sequence 3, Appli
44	309	7.8	419	4	US-10-182-263-5	Sequence 5, Appli
45	309	7.8	461	6	5270178-2	Patent No. 5270178
46	309	7.8	461	6	5270178-2	Patent No. 5270178
47	308	7.8	419	4	US-10-182-263-4	Sequence 4, Appli
48	307	7.8	460	6	5270178-15	Patent No. 5270178
49	307	7.8	460	6	5270178-15	Patent No. 5270178
50	305	7.7	460	6	5270178-13	Patent No. 5270178
51	305	7.7	460	6	5270178-14	Patent No. 5270178
52	305	7.7	460	6	5270178-13	Patent No. 5270178
53	305	7.7	460	6	5270178-14	Patent No. 5270178
54	302.5	7.7	461	6	5270178-17	Patent No. 5270178
55	302.5	7.7	461	6	5270178-18	Patent No. 5270178
56	302.5	7.7	461	6	5270178-17	Patent No. 5270178
57	302.5	7.7	461	6	5270178-18	Patent No. 5270178
58	288.5	7.3	902	4	US-09-644-600-10	Sequence 10, Appli
59	288.5	7.3	902	4	US-09-654-600A-10	Sequence 10, Appli
60	287.5	7.3	356	4	US-09-054-272-18	Sequence 18, Appli
61	283.5	7.2	587	4	US-09-949-016-11501	Sequence 11501, A
62	282	7.1	527	6	5520913-1	Patent No. 5520913
63	282	7.1	527	6	5520913-1	Patent No. 5520913
64	281	7.1	487	1	US-08-469-486-53	Sequence 53, Appli
65	281	7.1	487	2	US-08-469-658-53	Sequence 53, Appli
66	281	7.1	488	4	US-09-367-777-44	Sequence 44, Appli
67	281	7.1	488	4	US-09-367-791A-27	Sequence 27, Appli
68	281	7.1	492	1	US-08-469-486-2	Sequence 2, Appli
69	281	7.1	492	2	US-08-469-658-2	Sequence 2, Appli
70	280.5	7.1	267	4	US-09-949-016-9575	Sequence 9575, Ap
71	280	7.1	527	1	US-07-609-510B-16	Sequence 16, Appli
72	280	7.1	527	2	US-08-811-949-39	Sequence 39, Appli
73	280	7.1	527	4	US-09-600-985-1	Sequence 1, Appli
74	280	7.1	527	4	US-09-612-314A-51	Sequence 51, Appli
75	280	7.1	527	5	PCT-US91-01025A-2	Sequence 2, Appli
76	280	7.1	527	6	5185259-8	Patent No. 5185259
77	280	7.1	527	6	5185259-8	Patent No. 5185259
78	280	7.1	562	2	US-08-811-949-43	Sequence 43, Appli
79	280	7.1	562	2	US-08-560-098A-50	Sequence 50, Appli
80	280	7.1	562	2	US-08-883-795A-38	Sequence 38, Appli
81	280	7.1	562	4	US-09-703-695A-4	Sequence 4, Appli
82	280	7.1	562	4	US-10-443-701-4	Sequence 4, Appli
83	280	7.1	562	6	5185259-3	Patent No. 5185259
84	280	7.1	562	6	5200340-2	Patent No. 5200340
85	280	7.1	562	6	5344773-2	Patent No. 5344773
86	280	7.1	562	6	5185259-3	Patent No. 5185259
87	280	7.1	562	6	5200340-2	Patent No. 5200340
88	280	7.1	562	6	5344773-2	Patent No. 5344773
89	279	7.1	527	4	US-09-600-985-2	Sequence 2, Appli
90	278.5	7.1	466	1	US-07-882-202A-4	Sequence 4, Appli
91	278.5	7.1	466	1	US-08-021-615A-4	Sequence 4, Appli
92	278.5	7.1	466	1	US-08-321-777-4	Sequence 4, Appli
93	278.5	7.1	466	3	US-09-009-217-14	Sequence 14, Appli
94	278.5	7.1	466	3	US-09-009-656-14	Sequence 14, Appli
95	278.5	7.1	466	5	PCT-US93-04493-4	Sequence 4, Appli
96	278.5	7.1	483	4	US-09-949-016-9523	Sequence 9523, Ap
97	278	7.0	448	5	PCT-US92-10068-1	Sequence 1, Appli
98	278	7.0	496	4	US-09-949-016-9524	Sequence 9524, Ap
99	276.5	7.0	655	1	US-08-148-910-12	Sequence 12, Appli
100	276.5	7.0	655	1	US-08-448-937A-12	Sequence 12, Appli

101	276	7.0	448	1	US-08-295-411-3	Sequence 3, Appli	174	248.5	6.3	262	1	US-07-720-189-1	Sequence 1, Appli
102	276	7.0	448	2	US-08-955-471-3	Sequence 3, Appli	175	248	6.3	230	2	US-08-944-483-62	Sequence 62, Appl
103	276	7.0	448	5	PCT-US92-10242-3	Sequence 3, Appli	176	248	6.3	231	3	US-09-027-337-6	Sequence 6, Appli
104	276	7.0	527	4	US-09-600-985-3	Sequence 3, Appli	177	248	6.3	231	4	US-09-644-600-6	Sequence 6, Appli
105	275.5	7.0	406	1	US-08-295-411-5	Sequence 5, Appli	178	248	6.3	231	4	US-09-654-600A-6	Sequence 2, Appli
106	275.5	7.0	406	2	US-08-955-471-5	Sequence 5, Appli	179	247	6.3	764	2	US-08-177-109A-2	Sequence 2, Appli
107	275.5	7.0	406	4	US-09-782-587B-1	Sequence 1, Appli	180	247	6.3	764	2	US-08-687-706-2	Sequence 2, Appli
108	275.5	7.0	406	4	US-09-782-587B-1	Sequence 1, Appli	181	247	6.3	798	4	US-09-949-016-11021	Sequence 11021, A
109	275.5	7.0	406	5	PCT-US92-10242-5	Sequence 5, Appli	182	247	6.3	986	4	US-09-949-016-6690	Sequence 6690, Ap
110	275.5	7.0	444	1	US-08-475-845-2	Sequence 2, Appli	183	246.5	6.2	259	3	US-08-944-483-52	Sequence 52, Appl
111	275.5	7.0	444	2	US-08-327-690-2	Sequence 2, Appli	184	246.5	6.2	295	3	US-08-338-368-2	Sequence 2, Appli
112	275.5	7.0	444	2	US-08-660-289-2	Sequence 2, Appli	185	246.5	6.2	376	3	US-08-558-269-10	Sequence 10, Appl
113	275.5	7.0	444	2	US-08-537-807-2	Sequence 2, Appli	186	246.5	6.2	376	3	US-09-410-882-10	Sequence 10, Appl
114	275.5	7.0	444	2	US-08-871-003-2	Sequence 2, Appli	187	246.5	6.2	579	1	US-08-295-411-4	Sequence 4, Appli
115	275.5	7.0	444	3	US-08-464-233-2	Sequence 2, Appli	188	246.5	6.2	579	2	US-08-955-471-4	Sequence 4, Appli
116	275.5	7.0	444	3	US-09-189-607-2	Sequence 2, Appli	189	246.5	6.2	579	3	US-09-117-708-14	Sequence 14, Appl
117	275.5	7.0	444	3	US-09-378-907-2	Sequence 2, Appli	190	246.5	6.2	579	5	PCT-US92-10242-4	Sequence 4, Appli
118	275.5	7.0	444	5	PCT-US94-05779-2	Sequence 2, Appli	191	246.5	6.2	615	1	US-07-998-972A-3	Sequence 3, Appli
119	275.5	7.0	461	4	US-09-949-016-8839	Sequence 8839, Ap	192	246.5	6.2	615	1	US-08-463-953-3	Sequence 3, Appli
120	275	7.0	562	6	5244676-5	Patent No. 5244676	193	246.5	6.2	615	1	US-08-462-261-3	Sequence 3, Appli
121	275	7.0	562	6	5244676-5	Patent No. 5244676	194	246.5	6.2	615	5	PCT-US92-11357-3	Sequence 3, Appli
122	275	7.0	1113	4	US-09-959-392-4	Sequence 4, Appli	195	246.5	6.2	622	3	US-08-952-967-8	Sequence 8, Appli
123	273	6.9	560	4	US-09-949-016-6458	Sequence 6458, Ap	196	246.5	6.2	622	3	US-09-054-272-42	Sequence 42, Appl
124	273	6.9	560	4	US-09-912-559-3	Sequence 3, Appli	197	246	6.2	622	4	US-08-991-761A-7	Sequence 7, Appli
125	273	6.9	560	4	US-09-912-559-4	Sequence 4, Appli	198	245	6.2	812	4	US-08-278-091-10	Sequence 10, Appl
126	272	6.9	488	1	US-08-487-037-1	Sequence 1, Appli	199	245	6.2	228	1	US-08-483-859-10	Sequence 10, Appl
127	271.5	6.9	244	4	US-08-361-393-1	Sequence 1, Appli	200	245	6.2	228	1	US-08-472-173-10	Sequence 10, Appl
128	271.5	6.9	325	4	US-09-949-016-7713	Sequence 7713, Ap	201	245	6.2	228	2	US-08-487-167-10	Sequence 10, Appl
129	270.5	6.9	415	1	US-08-295-411-2	Sequence 2, Appli	202	245	6.2	228	2	US-08-482-816-10	Sequence 10, Appl
130	270.5	6.9	415	2	US-08-955-471-2	Sequence 2, Appli	203	245	6.2	228	2	US-08-296-149-10	Sequence 10, Appl
131	270.5	6.9	415	5	PCT-US92-10242-2	Sequence 2, Appli	204	245	6.2	228	2	US-08-801-499-10	Sequence 10, Appl
132	268.5	6.8	406	1	US-08-293-778-24	Sequence 24, Appl	205	245	6.2	228	2	US-08-615-271-10	Sequence 10, Appl
133	264.5	6.7	415	2	US-08-073-531B-1	Sequence 1, Appli	206	245	6.2	228	3	US-09-074-660-10	Sequence 10, Appl
134	264.5	6.7	415	2	US-08-766-288-1	Sequence 1, Appli	207	245	6.2	228	3	US-09-106-468-10	Sequence 10, Appl
135	263	6.7	431	4	US-09-101-272G-1	Sequence 1, Appli	208	245	6.2	228	3	US-09-106-466A-10	Sequence 10, Appl
136	263	6.7	431	6	5188829-1	Patent No. 5188829	209	245	6.2	228	3	US-09-106-467-10	Sequence 10, Appl
137	263	6.7	431	6	5188829-1	Patent No. 5188829	210	245	6.2	228	3	US-09-106-467-10	Sequence 10, Appl
138	262.5	6.7	461	3	US-08-742-877-2	Sequence 2, Appli	211	244.5	6.2	269	4	US-09-715-994-2	Sequence 2, Appli
139	262.5	6.7	461	3	US-09-053-871A-21	Sequence 21, Appl	212	242.5	6.1	416	2	US-09-000-846-2	Sequence 2, Appli
140	262.5	6.7	461	3	US-10-133-907-5	Sequence 5, Appli	213	242	6.1	730	3	US-08-872-757-2	Sequence 2, Appli
141	262.5	6.7	461	6	5521070-2	Patent No. 5521070	214	242	6.1	730	4	US-08-850-048A-2	Sequence 2, Appli
142	262.5	6.7	461	6	5521070-2	Patent No. 5521070	215	241.5	6.1	347	2	US-08-811-949-1	Sequence 1, Appli
143	262.5	6.7	480	4	US-09-949-016-11123	Sequence 11123, A	216	241.5	6.1	788	1	US-08-572-225-1	Sequence 1, Appli
144	262.5	6.7	1042	4	US-09-959-392-2	Sequence 2, Appli	217	241	6.1	354	2	US-08-811-949-61	Sequence 61, Appl
145	261.5	6.6	415	4	US-09-118-748-2	Sequence 2, Appli	218	241	6.1	986	3	US-08-872-757-4	Sequence 4, Appli
146	260.5	6.6	437	1	US-08-487-037-2	Sequence 2, Appli	219	241	6.1	986	3	US-08-872-757-4	Sequence 4, Appli
147	260	6.6	477	2	US-08-560-098A-51	Sequence 51, Appl	220	240.5	6.1	356	1	US-08-427-640-8	Sequence 8, Appli
148	258.5	6.6	411	1	US-08-087-163-1	Sequence 1, Appli	221	240.5	6.1	3571	4	US-09-911-842A-2	Sequence 2, Appli
149	258.5	6.6	411	1	US-08-286-748B-18	Sequence 18, Appl	222	240	6.1	242	4	US-09-959-392-34	Sequence 34, Appl
150	258.5	6.6	411	1	US-08-153-799-18	Sequence 18, Appl	223	240	6.1	432	2	US-08-560-098A-47	Sequence 47, Appl
151	258.5	6.6	411	3	US-09-181-816-1	Sequence 1, Appli	224	239.5	6.1	1015	4	US-09-285-385C-2	Sequence 2, Appli
152	258.5	6.6	411	3	US-09-181-816-1	Sequence 1, Appli	225	239.5	6.1	3594	4	US-09-911-842A-4	Sequence 4, Appli
153	257.5	6.5	430	6	5219569-2	Patent No. 5219569	226	239	6.1	230	4	US-09-601-318-3	Sequence 3, Appli
154	257.5	6.5	430	6	5219569-2	Patent No. 5219569	227	239	6.1	356	2	US-08-681-151-1	Sequence 1, Appli
155	256.5	6.5	411	4	US-09-403-736-2	Sequence 2, Appli	228	239	6.1	389	2	US-08-811-949-67	Sequence 67, Appl
156	256.5	6.5	430	1	US-07-942-157A-3	Sequence 3, Appli	229	238.5	6.0	437	2	US-08-811-949-49	Sequence 49, Appl
157	255.5	6.5	244	4	US-09-618-259-11	Sequence 11, Appl	230	238.5	6.0	437	2	US-08-811-949-51	Sequence 51, Appl
158	254.5	6.5	437	1	US-08-487-037-3	Sequence 3, Appli	231	238.5	6.0	437	2	US-08-811-949-55	Sequence 55, Appl
159	254	6.4	261	6	5270178-21	Patent No. 5270178	232	238.5	6.0	437	2	US-08-811-949-57	Sequence 57, Appl
160	254	6.4	261	6	5270178-21	Patent No. 5270178	233	238	6.0	237	3	US-08-163-919A-3	Sequence 3, Appli
161	251	6.4	261	6	5270178-5	Patent No. 5270178	234	238	6.0	237	4	US-08-462-515-3	Sequence 3, Appli
162	251	6.4	261	6	5270178-5	Patent No. 5270178	235	238	6.0	237	5	PCT-US94-14073-3	Sequence 3, Appli
163	250.5	6.3	229	2	US-08-557-146-13	Sequence 13, Appl	236	236.5	6.0	274	2	US-08-978-404B-5	Sequence 5, Appli
164	250.5	6.3	229	2	US-09-154-344-13	Sequence 13, Appl	237	236.5	6.0	355	1	US-08-137-116-1	Sequence 1, Appli
165	250.5	6.3	401	4	US-08-560-098A-48	Sequence 48, Appl	238	236.5	6.0	355	1	US-08-217-618-1	Sequence 2, Appli
166	249.5	6.3	413	2	US-09-880-503-6	Sequence 6, Appli	239	236.5	6.0	355	1	US-08-427-640-2	Sequence 2, Appli
167	249.5	6.3	986	4	US-09-285-385C-19	Sequence 19, Appl	240	236.5	6.0	355	1	US-08-427-640-6	Sequence 6, Appli
168	249	6.3	251	3	US-08-944-483-47	Sequence 47, Appl	241	236.5	6.0	355	1	US-08-217-617A-1	Sequence 1, Appli
169	248.5	6.3	250	3	US-08-944-483-51	Sequence 51, Appl	242	236.5	6.0	355	1	US-08-217-616-1	Sequence 1, Appli
170	248.5	6.3	261	6	5270178-19	Patent No. 5270178	243	236.5	6.0	355	2	US-08-811-949-45	Sequence 45, Appl
171	248.5	6.3	261	6	5270178-20	Patent No. 5270178	244	236.5	6.0	355	2	US-08-811-949-47	Sequence 47, Appl
172	248.5	6.3	261	6	5270178-19	Patent No. 5270178	245	236.5	6.0	355	3	US-08-794-528-1	Sequence 1, Appli
173	248.5	6.3	261	6	5270178-20	Patent No. 5270178	246	236.5	6.0	355	6	5223256-1	Patent No. 5223256

247	236.5	6.0	355	6	5223256-1	Patent No. 5223256	320	228	5.8	812	4	US-09-192-012-3	Sequence 3, Appli
248	236.5	6.0	356	1	US-08-427-640-4	Sequence 4, Appli	321	228	5.8	812	4	US-09-335-325-1	Sequence 1, Appli
249	236.5	6.0	378	3	US-09-553-498-10	Sequence 10, Appl	322	228	5.8	812	4	US-08-991-761A-12	Sequence 12, Appl
250	236.5	6.0	378	4	US-09-618-869-10	Sequence 10, Appl	323	228	5.8	812	5	PCr-US95-05107-1	Sequence 1, Appli
251	236.5	6.0	472	2	US-08-811-949-63	Sequence 63, Appl	324	227	5.8	241	4	US-09-657-986B-2	Sequence 2, Appli
252	236.5	6.0	871	3	US-09-245-041-19	Sequence 19, Appl	325	227	5.8	285	4	US-09-023-942A-26	Sequence 26, Appl
253	236.5	6.0	871	4	US-09-358-055B-19	Sequence 19, Appl	326	227	5.8	308	3	US-08-705-875A-10	Sequence 10, Appl
254	236.5	6.0	871	4	US-09-893-238-19	Sequence 19, Appl	327	227	5.8	308	4	US-09-242-999-10	Sequence 10, Appl
255	236.5	6.0	1013	2	US-08-866-650-3	Sequence 3, Appli	328	226.5	5.7	454	3	US-09-518-046-2	Sequence 2, Appli
256	236.5	6.0	1013	2	US-09-021-287-3	Sequence 3, Appli	329	226.5	5.7	2787	3	US-09-245-041-15	Sequence 15, Appl
257	236.5	6.0	1013	3	US-09-240-473-3	Sequence 3, Appli	330	226.5	5.7	2787	4	US-09-358-055B-15	Sequence 15, Appl
258	236.5	6.0	1350	3	US-09-245-041-17	Sequence 17, Appl	331	226.5	5.7	2787	4	US-09-893-238-15	Sequence 15, Appl
259	236.5	6.0	1350	4	US-09-358-055B-17	Sequence 17, Appl	332	226	5.7	406	4	US-09-851-588-6	Sequence 6, Appli
260	236.5	6.0	1350	4	US-09-893-238-17	Sequence 17, Appl	333	226	5.7	423	4	US-09-656-002-2	Sequence 2, Appli
261	236	6.0	355	2	US-08-811-949-53	Sequence 53, Appl	334	226	5.7	435	3	US-09-656-002-2	Sequence 2, Appli
262	236	6.0	355	2	US-08-811-949-59	Sequence 59, Appl	335	226	5.7	435	3	US-09-008-271A-6	Sequence 6, Appli
263	235	6.0	270	2	US-08-811-949-59	Sequence 59, Appl	336	226	5.7	435	4	US-09-607-745-2	Sequence 2, Appli
264	233.5	5.9	252	3	US-08-944-483-72	Sequence 72, Appl	337	226	5.7	437	4	US-09-851-588-8	Sequence 8, Appli
265	233.5	5.9	253	2	US-09-027-337-8	Sequence 8, Appli	338	226	5.7	481	4	US-09-949-016-9238	Sequence 9238, Ap
266	233.5	5.9	253	4	US-09-644-600-8	Sequence 8, Appli	339	226	5.7	481	4	US-09-949-016-9239	Sequence 9239, Ap
267	233.5	5.9	253	4	US-09-654-600A-8	Sequence 8, Appli	340	226	5.7	637	4	US-09-949-016-11538	Sequence 11538, A
268	233.5	5.9	383	2	US-08-558-269-6	Sequence 6, Appli	341	225.5	5.7	637	4	US-09-949-016-11539	Sequence 11539, A
269	233.5	5.9	383	3	US-09-410-882-6	Sequence 6, Appli	342	224.5	5.7	348	4	US-09-949-016-6979	Sequence 6979, Ap
270	233.5	5.9	546	6	5200340-6	Patent No. 5200340	343	224.5	5.7	232	3	US-08-944-483-65	Sequence 65, Appl
271	233.5	5.9	546	6	5200340-6	Patent No. 5200340	344	224	5.7	275	2	US-09-016-366A-17	Sequence 17, Appl
272	232.5	5.9	259	4	US-10-165-442-2	Sequence 2, Appli	345	224	5.7	275	2	US-08-978-404B-12	Sequence 12, Appl
273	232.5	5.9	295	4	US-10-165-442-1	Sequence 1, Appli	346	224	5.7	276	4	US-09-880-503-5	Sequence 5, Appli
274	232.5	5.9	1013	2	US-08-866-650-5	Sequence 5, Appli	347	224	5.7	306	2	US-08-560-098A-45	Sequence 45, Appl
275	232.5	5.9	1013	2	US-09-021-287-5	Sequence 5, Appli	348	224	5.7	323	4	US-09-880-503-7	Sequence 7, Appli
276	232.5	5.9	1013	3	US-08-991-408-2	Sequence 2, Appli	349	224	5.7	331	2	US-08-560-098A-46	Sequence 46, Appl
277	232.5	5.9	1013	3	US-09-240-473-5	Sequence 5, Appli	350	223.5	5.7	245	3	US-08-944-483-69	Sequence 69, Appl
278	232.5	5.9	1013	3	US-09-432-473-2	Sequence 2, Appli	351	223.5	5.7	346	4	US-09-949-016-9000	Sequence 9000, Ap
279	232.5	5.9	1013	4	US-09-285-385C-20	Sequence 20, Appl	352	223	5.7	521	3	US-08-944-483-64	Sequence 64, Appl
280	232	5.9	638	2	US-08-681-151-3	Sequence 3, Appli	353	223	5.7	521	4	US-09-949-016-11081	Sequence 11081, A
281	231.5	5.9	389	2	US-08-811-949-65	Sequence 65, Appl	354	223	5.7	521	4	US-09-949-016-11082	Sequence 11082, A
282	231.5	5.9	417	4	US-09-820-002-4	Sequence 4, Appli	355	223	5.7	521	4	US-09-949-016-11083	Sequence 11083, A
283	231	5.9	365	1	US-08-093-741-83	Sequence 83, Appl	356	222.5	5.6	452	4	US-09-949-016-7182	Sequence 7182, Ap
284	231	5.9	365	1	US-08-720-012-83	Sequence 83, Appl	357	222.5	5.6	790	4	US-08-991-761A-13	Sequence 13, Appl
285	231	5.9	393	2	US-08-560-098A-44	Sequence 44, Appl	358	222	5.6	274	2	US-09-016-366A-21	Sequence 21, Appl
286	231	5.9	393	3	US-08-967-024C-24	Sequence 24, Appl	359	222	5.6	274	2	US-08-978-404B-16	Sequence 16, Appl
287	231	5.9	393	3	US-08-967-024C-25	Sequence 25, Appl	360	222	5.6	407	3	US-09-734-675-4	Sequence 4, Appli
288	231	5.9	1012	4	US-09-285-385C-4	Sequence 4, Appli	361	221	5.6	253	3	US-08-944-483-73	Sequence 73, Appl
289	230.5	5.8	259	4	US-10-165-442-4	Sequence 4, Appli	362	221	5.6	273	2	US-08-978-404B-6	Sequence 6, Appli
290	230.5	5.8	295	4	US-10-165-442-3	Sequence 3, Appli	363	221	5.6	300	3	US-08-705-875A-6	Sequence 6, Appli
291	230.5	5.8	302	3	US-09-220-731-26	Sequence 26, Appl	364	221	5.6	300	4	US-09-242-999-6	Sequence 6, Appli
292	230.5	5.8	302	4	US-09-242-999-22	Sequence 22, Appl	365	221	5.6	1193	4	US-09-949-016-10498	Sequence 10498, A
293	230	5.8	232	3	US-09-959-392-31	Sequence 31, Appl	366	220.5	5.6	376	4	US-09-820-002-2	Sequence 2, Appli
294	230	5.8	248	3	US-08-944-483-63	Sequence 63, Appl	367	220	5.6	273	2	US-09-016-366A-19	Sequence 19, Appl
295	230	5.8	387	3	US-09-032-215-8	Sequence 8, Appli	368	220	5.6	273	2	US-08-978-404B-14	Sequence 14, Appl
296	230	5.8	387	3	US-09-032-215-13	Sequence 13, Appl	369	219.5	5.6	254	3	US-08-944-483-50	Sequence 50, Appl
297	229	5.8	242	3	US-09-004-731-36	Sequence 36, Appl	370	219.5	5.6	255	2	US-09-027-337-7	Sequence 7, Appli
298	229	5.8	242	4	US-08-749-699-36	Sequence 36, Appl	371	219.5	5.6	255	4	US-09-644-600-7	Sequence 7, Appli
299	229	5.8	242	4	US-09-004-729-36	Sequence 36, Appl	372	219.5	5.6	255	4	US-09-654-600A-7	Sequence 7, Appli
300	229	5.8	400	3	US-09-004-731-30	Sequence 30, Appl	373	218.5	5.5	244	4	US-09-601-318-4	Sequence 4, Appli
301	229	5.8	400	3	US-09-004-731-33	Sequence 33, Appl	374	218.5	5.5	244	4	US-09-601-318-5	Sequence 5, Appli
302	229	5.8	400	3	US-08-749-699-30	Sequence 30, Appl	375	218.5	5.5	244	4	US-09-601-318-6	Sequence 6, Appli
303	229	5.8	400	3	US-08-749-699-33	Sequence 33, Appl	376	218.5	5.5	244	4	US-09-601-318-7	Sequence 7, Appli
304	229	5.8	400	4	US-09-004-729-30	Sequence 30, Appl	377	218.5	5.5	245	3	US-09-079-970A-6	Sequence 6, Appli
305	229	5.8	400	4	US-08-248-629A-1	Sequence 1, Appli	378	218.5	5.5	245	4	US-09-601-318-1	Sequence 1, Appli
306	228.5	5.8	235	3	US-08-807-151-3	Sequence 3, Appli	379	218.5	5.5	249	3	US-09-079-970A-5	Sequence 5, Appli
307	228.5	5.8	235	3	US-09-478-957-3	Sequence 3, Appli	380	217.5	5.5	1198	3	US-09-245-041-131	Sequence 131, App
308	228	5.8	591	3	US-08-991-408-4	Sequence 4, Appli	381	217.5	5.5	1198	3	US-09-794-236-3	Sequence 3, Appli
309	228	5.8	809	4	US-09-432-473-4	Sequence 4, Appli	382	217.5	5.5	1198	3	US-09-358-055B-132	Sequence 132, App
310	228	5.8	812	1	US-08-248-629A-1	Sequence 1, Appli	383	217.5	5.5	1429	3	US-09-245-041-130	Sequence 130, App
311	228	5.8	812	1	US-08-451-932-1	Sequence 1, Appli	384	217.5	5.5	1429	3	US-09-358-055B-131	Sequence 131, App
312	228	5.8	812	1	US-08-451-932-1	Sequence 1, Appli	385	217	5.5	239	3	US-08-944-483-61	Sequence 61, Appl
313	228	5.8	812	1	US-08-452-260-1	Sequence 1, Appli	386	217	5.5	268	4	US-09-613-822B-2	Sequence 2, Appli
314	228	5.8	812	1	US-08-326-785-1	Sequence 1, Appli	387	217	5.5	273	2	US-08-978-404B-3	Sequence 3, Appli
315	228	5.8	812	2	US-08-612-788-1	Sequence 1, Appli	388	217	5.5	791	3	US-08-643-219-1	Sequence 1, Appli
316	228	5.8	812	2	US-08-605-988B-1	Sequence 1, Appli	389	217	5.5	791	3	US-08-851-350-1	Sequence 1, Appli
317	228	5.8	812	2	US-08-429-743-1	Sequence 1, Appli	390	217	5.5	2703	1	US-08-185-432-19	Sequence 19, Appl
318	228	5.8	812	2	US-08-866-735-1	Sequence 1, Appli	391	217	5.5	2703	4	US-08-899-232-4	Sequence 4, Appli
319	228	5.8	812	3	US-09-066-028-1	Sequence 1, Appli	392	217	5.5	2703	4	US-09-121-457-4	Sequence 4, Appli

393	216	5.5	267	2	US-09-016-366A-23	Sequence 23, Appl	466	211	5.3	1218	4	US-09-917-254-85	Sequence 85, Appl
394	216	5.5	267	2	US-08-978-404B-18	Sequence 18, Appl	467	211	5.3	1218	4	US-09-195-524-6	Sequence 6, Appl
395	216	5.5	267	4	US-09-917-254-101	Sequence 101, App	468	211	5.3	1218	4	US-09-579-536C-1	Sequence 1, Appl
396	216	5.5	268	1	US-08-568-031-2	Sequence 2, Appl	469	211	5.3	1218	4	US-09-949-016-10297	Sequence 5902, App
397	216	5.5	268	2	US-08-966-319-2	Sequence 2, Appl	470	211	5.3	1254	4	US-09-949-016-10297	Sequence 62, Appl
398	216	5.5	268	3	US-09-153-304-2	Sequence 2, Appl	471	210.5	5.3	418	4	US-09-370-838-62	Sequence 62, Appl
399	216	5.5	299	3	US-08-944-483-66	Sequence 66, Appl	472	210.5	5.3	418	4	US-08-854-133-62	Sequence 5, Appl
400	216	5.5	319	4	US-09-386-642-12	Sequence 12, Appl	473	210.5	5.3	1219	4	US-08-882-046-5	Sequence 5, Appl
401	216	5.5	328	4	US-09-386-642-11	Sequence 11, Appl	474	210.5	5.3	1219	4	US-09-566-047-5	Sequence 5, Appl
402	216	5.5	790	1	US-08-469-486-54	Sequence 54, Appl	475	210	5.3	154	3	US-09-261-416-5	Sequence 24, Appl
403	216	5.5	790	2	US-08-469-658-54	Sequence 54, Appl	476	210	5.3	248	3	US-08-944-483-24	Sequence 2, Appl
404	216	5.5	810	6	5200340-8	Patent No. 5200340	477	210.5	5.3	446	4	US-10-177-661-4	Sequence 2, Appl
405	216	5.5	810	6	5200340-8	Patent No. 5200340	478	209.5	5.3	477	4	US-10-177-661-2	Sequence 2, Appl
406	215.5	5.5	317	4	US-09-386-629-7	Sequence 7, Appl	479	209.5	5.3	562	4	US-09-879-792-12	Sequence 12, Appl
407	215.5	5.5	317	4	US-09-907-794A-263	Sequence 263, App	480	208.5	5.3	492	4	US-09-685-166A-895	Sequence 895, App
408	215.5	5.5	317	4	US-09-905-125A-263	Sequence 263, App	481	208.5	5.3	492	4	US-09-879-792-14	Sequence 14, Appl
409	215.5	5.5	317	4	US-09-902-775A-263	Sequence 263, App	482	208.5	5.3	492	4	US-09-679-426-895	Sequence 895, App
410	215.5	5.5	317	4	US-09-906-700-263	Sequence 263, App	483	208.5	5.3	492	4	US-09-759-143-895	Sequence 2, Appl
411	215.5	5.5	317	4	US-09-903-603A-263	Sequence 263, App	484	208	5.3	268	1	US-08-270-584A-2	Sequence 2, Appl
412	215.5	5.5	317	4	US-09-904-920A-263	Sequence 263, App	485	208	5.3	268	2	US-08-765-192-2	Sequence 2, Appl
413	215.5	5.5	317	4	US-09-909-064-263	Sequence 263, App	486	208	5.3	268	3	US-09-199-793-2	Sequence 2, Appl
414	215.5	5.5	317	4	US-09-905-381A-263	Sequence 263, App	487	208	5.3	271	1	US-08-467-155A-10	Sequence 10, Appl
415	215.5	5.5	317	4	US-09-906-618-263	Sequence 263, App	488	208	5.3	271	2	US-08-628-198-10	Sequence 10, Appl
416	215	5.4	713	4	US-09-949-016-9983	Sequence 9983, App	489	208	5.3	271	3	US-09-201-038-10	Sequence 10, Appl
417	215	5.4	791	2	US-09-131-995-1	Sequence 1, Appl	490	208	5.3	271	5	PCT-US96-07343-10	Sequence 10, Appl
418	215	5.4	791	2	US-08-832-087B-1	Sequence 1, Appl	491	207.5	5.3	241	3	US-08-944-483-59	Sequence 59, Appl
419	215	5.4	791	3	US-09-132-154-1	Sequence 1, Appl	492	206.5	5.2	255	1	US-08-650-129-5	Sequence 5, Appl
420	215	5.4	791	4	US-08-991-761A-6	Sequence 6, Appl	493	206.5	5.2	255	3	US-08-984-417-5	Sequence 5, Appl
421	215	5.4	791	4	US-08-924-287A-1	Sequence 1, Appl	494	206.5	5.2	284	3	US-09-387-375-7	Sequence 7, Appl
422	215	5.4	810	1	US-07-854-603-2	Sequence 2, Appl	495	206.5	5.2	284	4	US-10-041-400A-7	Sequence 7, Appl
423	215	5.4	810	1	US-08-147-000B-29	Sequence 29, Appl	496	206.5	5.2	284	4	US-10-042-091A-7	Sequence 9, Appl
424	215	5.4	810	3	US-09-086-514-1	Sequence 1, Appl	497	206.5	5.2	316	4	US-09-387-375-9	Sequence 9, Appl
425	215	5.4	810	4	US-09-192-012-5	Sequence 1, Appl	498	206.5	5.2	316	4	US-10-041-400A-9	Sequence 9, Appl
426	215	5.4	810	4	US-09-403-736-1	Sequence 1, Appl	499	206.5	5.2	316	4	US-10-042-091A-9	Sequence 9, Appl
427	215	5.4	810	4	US-09-701-265-1	Sequence 1, Appl	500	205.5	5.2	235	3	US-08-944-483-48	Sequence 48, Appl
428	214	5.4	254	2	US-08-560-098A-49	Sequence 49, Appl	501	205.5	5.2	269	2	US-08-978-404B-10	Sequence 10, Appl
429	214	5.4	292	4	US-09-607-745-9	Sequence 9, Appl	502	205.5	5.2	288	4	US-09-386-642-13	Sequence 8, Appl
430	213.5	5.4	255	3	US-08-944-483-67	Sequence 67, Appl	503	205.5	5.2	327	4	US-09-386-629-8	Sequence 2, Appl
431	213.5	5.4	256	2	US-09-027-337-3	Sequence 3, Appl	504	205.5	5.2	492	3	US-09-342-749-2	Sequence 2, Appl
432	213.5	5.4	256	4	US-09-644-600-3	Sequence 3, Appl	505	205.5	5.2	492	4	US-09-691-840-2	Sequence 2, Appl
433	213.5	5.4	256	4	US-09-654-600A-3	Sequence 3, Appl	506	205.5	5.2	492	4	US-09-759-143-932	Sequence 932, App
434	212.5	5.4	256	4	US-09-205-258-427	Sequence 427, App	507	205.5	5.2	510	4	US-09-949-016-11074	Sequence 11074, A
435	212.5	5.4	282	3	US-09-025-059-1	Sequence 1, Appl	508	205	5.2	393	4	US-09-759-143-934	Sequence 934, App
436	212.5	5.4	289	4	US-09-386-642-14	Sequence 14, Appl	509	204.5	5.2	439	4	US-09-949-016-9260	Sequence 9260, App
437	212	5.4	260	3	US-09-025-059-3	Sequence 3, Appl	510	204	5.2	260	3	US-09-070-526-2	Sequence 2, Appl
438	212	5.4	260	4	US-09-618-259-8	Sequence 8, Appl	511	204	5.2	260	4	US-09-618-259-7	Sequence 7, Appl
439	212	5.4	814	1	US-08-750-711-1	Sequence 1, Appl	512	203.5	5.2	224	3	US-08-944-483-34	Sequence 34, Appl
440	211.5	5.4	418	1	US-08-508-448C-19	Sequence 19, Appl	513	203.5	5.2	249	4	US-09-949-016-8770	Sequence 8770, App
441	211.5	5.4	418	1	US-08-508-448C-25	Sequence 25, Appl	514	203.5	5.2	3623	4	US-09-341-461-2	Sequence 2, Appl
442	211.5	5.4	418	4	US-09-370-838-82	Sequence 82, Appl	515	203	5.1	283	3	US-08-807-151-1	Sequence 1, Appl
443	211.5	5.4	418	4	US-09-370-838-83	Sequence 82, Appl	516	203	5.1	283	4	US-09-478-957-1	Sequence 1, Appl
444	211.5	5.4	418	4	US-09-854-133-82	Sequence 82, Appl	517	202	5.1	2321	4	US-09-230-652-2	Sequence 2, Appl
445	211.5	5.4	418	4	US-09-854-133-83	Sequence 83, Appl	518	200.5	5.1	226	1	US-08-650-129-4	Sequence 4, Appl
446	211	5.3	276	2	US-09-016-366A-15	Sequence 15, Appl	519	200.5	5.1	226	3	US-08-984-417-4	Sequence 4, Appl
447	211	5.3	276	2	US-08-978-404B-21	Sequence 21, Appl	520	200.5	5.1	232	1	US-08-278-091-8	Sequence 8, Appl
448	211	5.3	300	3	US-08-705-875A-4	Sequence 4, Appl	521	200.5	5.1	232	1	US-08-483-859-8	Sequence 8, Appl
449	211	5.3	300	3	US-09-220-731-21	Sequence 21, Appl	522	200.5	5.1	232	1	US-08-472-173-8	Sequence 8, Appl
450	211	5.3	300	4	US-09-242-999-4	Sequence 4, Appl	523	200.5	5.1	232	2	US-08-487-167-8	Sequence 8, Appl
451	211	5.3	433	4	US-09-949-016-8220	Sequence 8220, App	524	200.5	5.1	232	2	US-08-482-816-8	Sequence 8, Appl
452	211	5.3	1010	3	US-08-882-046-7	Sequence 7, Appl	525	200.5	5.1	232	2	US-08-296-149-8	Sequence 8, Appl
453	211	5.3	1010	3	US-09-566-047-7	Sequence 7, Appl	526	200.5	5.1	232	2	US-08-801-499-8	Sequence 8, Appl
454	211	5.3	1036	3	US-09-068-740A-6	Sequence 6, Appl	527	200.5	5.1	232	2	US-08-615-271-8	Sequence 8, Appl
455	211	5.3	1067	3	US-09-579-536C-18	Sequence 18, Appl	528	200.5	5.1	232	3	US-09-074-660-8	Sequence 8, Appl
456	211	5.3	1187	3	US-09-068-740A-7	Sequence 7, Appl	529	200.5	5.1	232	3	US-09-106-468-8	Sequence 8, Appl
457	211	5.3	1208	4	US-09-199-865-1	Sequence 1, Appl	530	200.5	5.1	232	3	US-09-106-468A-8	Sequence 8, Appl
458	211	5.3	1208	4	US-10-213-329-1	Sequence 1, Appl	531	200.5	5.1	232	3	US-09-106-467-8	Sequence 2, Appl
459	211	5.3	1218	2	US-08-400-159-6	Sequence 6, Appl	532	200.5	5.1	232	2	US-08-956-267A-2	Sequence 2, Appl
460	211	5.3	1218	3	US-08-611-729A-6	Sequence 6, Appl	533	200.5	5.1	247	2	US-09-636-382A-2	Sequence 104, App
461	211	5.3	1218	3	US-08-882-046-2	Sequence 2, Appl	534	200.5	5.1	415	4	US-09-907-794A-104	Sequence 104, App
462	211	5.3	1218	3	US-09-214-278-7	Sequence 7, Appl	535	200.5	5.1	415	4	US-09-905-125A-104	Sequence 104, App
463	211	5.3	1218	3	US-09-068-740A-11	Sequence 11, Appl	536	200.5	5.1	415	4	US-09-902-775A-104	Sequence 104, App
464	211	5.3	1218	4	US-09-855-722-7	Sequence 7, Appl	537	200.5	5.1	415	4	US-09-906-700-104	Sequence 104, App
465	211	5.3	1218	4	US-09-566-047-2	Sequence 2, Appl	538	200.5	5.1	415	4		

539	200.5	5.1	415	4	US-09-903-603A-104	Sequence 104, App	612	193	4.9	228	3	US-08-944-483-44	Sequence 44, Appl
540	200.5	5.1	415	4	US-09-904-920A-104	Sequence 104, App	613	193	4.9	253	6	5223425-8	Patent No. 5223425
541	200.5	5.1	415	4	US-09-909-064-104	Sequence 104, App	614	193	4.9	253	6	5223425-8	Patent No. 5223425
542	200.5	5.1	415	4	US-09-905-381A-104	Sequence 104, App	615	193	4.9	268	3	US-09-032-215-42	Sequence 42, Appl
543	200.5	5.1	415	4	US-09-906-618-104	Sequence 104, App	616	192.5	4.9	225	2	US-08-557-146-12	Sequence 12, Appl
544	200.5	5.1	769	4	US-09-949-016-11019	Sequence 11019, A	617	192.5	4.9	225	2	US-09-154-344-12	Sequence 12, Appl
545	200.5	5.1	810	4	US-08-991-761A-11	Sequence 11, Appl	618	192.5	4.9	281	1	US-08-467-155A-7	Sequence 7, Appl
546	200	5.1	385	4	US-09-163-951-16	Sequence 16, Appl	619	192.5	4.9	281	2	US-08-628-198-7	Sequence 7, Appl
547	200	5.1	385	4	US-09-345-881-16	Sequence 16, Appl	620	192.5	4.9	281	2	US-08-628-198-7	Sequence 7, Appl
548	199.5	5.1	1193	2	US-08-400-159-10	Sequence 10, Appl	621	192.5	4.9	281	5	PCT-US96-07343-7	Sequence 7, Appl
549	199.5	5.1	1193	3	US-08-611-729A-10	Sequence 10, Appl	622	192	4.9	149	3	US-09-518-046-20	Sequence 20, Appl
550	199.5	5.1	1193	4	US-09-195-524-10	Sequence 10, Appl	623	191.5	4.9	221	4	US-09-959-392-33	Sequence 33, Appl
551	199.5	5.1	2556	1	US-08-185-432-17	Sequence 17, Appl	624	191.5	4.9	224	2	US-08-766-982-13	Sequence 13, Appl
552	199.5	5.1	2556	1	US-08-083-590A-20	Sequence 20, Appl	625	191.5	4.9	224	3	US-08-944-483-36	Sequence 36, Appl
553	199.5	5.1	2556	3	US-08-532-384-20	Sequence 20, Appl	626	191.5	4.9	224	3	US-09-296-219-13	Sequence 13, Appl
554	199.5	5.1	2556	1	US-08-899-232-2	Sequence 2, Appl	627	191.5	4.9	225	2	US-09-027-337-5	Sequence 5, Appl
555	199.5	5.1	2556	4	US-09-121-457-2	Sequence 2, Appl	628	191.5	4.9	225	4	US-09-644-600-5	Sequence 5, Appl
556	199	5.0	249	4	US-09-949-016-8151	Sequence 8151, Ap	629	191.5	4.9	225	4	US-09-654-600A-5	Sequence 5, Appl
557	199	5.0	260	3	US-09-008-271A-7	Sequence 7, Appl	630	191.5	4.9	233	4	US-09-636-382A-24	Sequence 24, Appl
558	199	5.0	278	1	US-08-392-828C-4	Sequence 4, Appl	631	191.5	4.9	830	1	US-08-110-158-4	Sequence 4, Appl
559	199	5.0	278	3	US-09-330-945-4	Sequence 4, Appl	632	191	4.8	250	6	5223425-4	Patent No. 5223425
560	198.5	5.0	223	1	US-08-278-091-9	Sequence 9, Appl	633	191	4.8	250	6	5223425-4	Patent No. 5223425
561	198.5	5.0	223	1	US-08-483-859-9	Sequence 9, Appl	634	191	4.8	254	3	US-09-439-313-525	Sequence 525, App
562	198.5	5.0	223	1	US-08-472-173-9	Sequence 9, Appl	635	191	4.8	254	4	US-09-636-215-525	Sequence 525, App
563	198.5	5.0	223	2	US-08-487-167-9	Sequence 9, Appl	636	191	4.8	254	4	US-09-685-166A-525	Sequence 525, App
564	198.5	5.0	223	2	US-08-482-816-9	Sequence 9, Appl	637	191	4.8	254	4	US-09-679-426-525	Sequence 525, App
565	198.5	5.0	223	2	US-08-296-149-9	Sequence 9, Appl	638	191	4.8	254	4	US-09-759-143-525	Sequence 525, App
566	198.5	5.0	223	2	US-08-801-499-9	Sequence 9, Appl	639	191	4.8	254	4	US-09-651-236-525	Sequence 525, App
567	198.5	5.0	223	2	US-08-615-271-9	Sequence 9, Appl	640	191	4.8	455	3	US-09-261-416-2	Sequence 2, Appl
568	198.5	5.0	223	3	US-09-074-660-9	Sequence 9, Appl	641	190	4.8	284	4	US-09-386-642-54	Sequence 54, Appl
569	198.5	5.0	223	3	US-09-074-659-9	Sequence 9, Appl	642	189	4.8	220	3	US-09-439-313-327	Sequence 327, App
570	198.5	5.0	223	3	US-09-106-468-9	Sequence 9, Appl	643	189	4.8	220	3	US-09-352-616A-327	Sequence 327, App
571	198.5	5.0	223	3	US-09-106-466A-9	Sequence 9, Appl	644	189	4.8	220	4	US-09-232-149A-327	Sequence 327, App
572	198.5	5.0	223	3	US-09-106-467-9	Sequence 9, Appl	645	189	4.8	220	4	US-09-636-215-327	Sequence 327, App
573	198.5	5.0	223	3	US-09-601-318-2	Sequence 2, Appl	646	189	4.8	220	4	US-09-685-166A-327	Sequence 327, App
574	198.5	5.0	223	3	US-09-120-582-2	Sequence 2, Appl	647	189	4.8	220	4	US-09-688-489-327	Sequence 327, App
575	198.5	5.0	232	2	US-08-378-404B-45	Sequence 45, Appl	648	189	4.8	220	4	US-09-679-426-327	Sequence 327, App
576	198.5	5.0	849	4	US-09-949-016-10271	Sequence 10271, A	649	189	4.8	220	4	US-09-759-143-327	Sequence 327, App
577	198	5.0	242	3	US-08-944-483-57	Sequence 57, Appl	650	189	4.8	220	4	US-09-651-236-327	Sequence 327, App
578	197.5	5.0	221	3	US-08-944-483-54	Sequence 54, Appl	651	189	4.8	224	3	US-08-944-483-33	Sequence 33, Appl
579	197.5	5.0	222	1	US-08-456-840-46	Sequence 46, Appl	652	189	4.8	224	2	US-09-027-337-4	Sequence 4, Appl
580	197.5	5.0	222	1	US-08-266-407A-46	Sequence 46, Appl	653	189	4.8	225	4	US-09-644-600-4	Sequence 4, Appl
581	197.5	5.0	222	2	US-08-892-544-46	Sequence 46, Appl	654	189	4.8	225	4	US-09-654-600A-4	Sequence 4, Appl
582	197	5.0	338	4	US-08-991-761A-10	Sequence 10, Appl	655	189	4.8	238	6	5223425-5	Patent No. 5223425
583	196.5	5.0	241	3	US-08-944-483-60	Sequence 60, Appl	656	189	4.8	238	6	5223425-5	Patent No. 5223425
584	196.5	5.0	248	3	US-08-944-483-71	Sequence 71, Appl	657	189	4.8	238	6	5223425-5	Patent No. 5223425
585	196.5	5.0	300	1	US-08-148-910-1	Sequence 1, Appl	658	189	4.8	253	2	US-08-557-146-2	Sequence 2, Appl
586	196.5	5.0	300	1	US-08-448-937A-1	Sequence 1, Appl	659	189	4.8	253	2	US-08-824-874-3	Sequence 2, Appl
587	196.5	5.0	2523	1	US-08-185-432-18	Sequence 18, Appl	660	189	4.8	253	2	US-09-154-344-2	Sequence 2, Appl
588	196.5	5.0	2523	4	US-08-899-232-3	Sequence 3, Appl	661	189	4.8	253	3	US-08-930-188-2	Sequence 2, Appl
589	196.5	5.0	2523	4	US-09-121-457-3	Sequence 3, Appl	662	189	4.8	253	3	US-09-210-084-3	Sequence 3, Appl
590	195.5	5.0	232	3	US-08-944-483-45	Sequence 45, Appl	663	189	4.8	253	5	PCT-US96-04294-2	Sequence 2, Appl
591	195.5	5.0	241	1	US-08-330-978-4	Sequence 4, Appl	664	189	4.8	265	4	US-09-949-016-7716	Sequence 7716, Ap
592	195.5	5.0	241	1	US-08-474-042-4	Sequence 4, Appl	665	189	4.8	312	4	US-09-023-942A-4	Sequence 4, Appl
593	195.5	5.0	241	1	US-08-484-558-4	Sequence 4, Appl	666	189	4.8	449	4	US-09-636-215-617	Sequence 617, App
594	195.5	5.0	241	1	US-08-774-592-4	Sequence 4, Appl	667	189	4.8	449	4	US-09-685-166A-617	Sequence 617, App
595	195.5	5.0	254	1	US-08-330-978-3	Sequence 3, Appl	668	189	4.8	449	4	US-09-679-426-617	Sequence 617, App
596	195.5	5.0	254	1	US-08-474-042-3	Sequence 3, Appl	669	189	4.8	449	4	US-09-759-143-617	Sequence 617, App
597	195.5	5.0	254	1	US-08-484-558-3	Sequence 3, Appl	670	189	4.8	449	4	US-09-651-236-617	Sequence 617, App
598	195.5	5.0	254	1	US-08-774-592-3	Sequence 3, Appl	671	188.5	4.8	290	4	US-09-386-653A-7	Sequence 7, Appl
599	195.5	5.0	306	1	US-08-330-978-1	Sequence 1, Appl	672	188	4.8	248	1	US-08-744-026-1	Sequence 1, Appl
600	195.5	5.0	306	1	US-08-474-042-1	Sequence 1, Appl	673	188	4.8	248	2	US-09-102-732-1	Sequence 1, Appl
601	195.5	5.0	306	1	US-08-484-558-1	Sequence 1, Appl	674	188	4.8	248	3	US-09-261-767-1	Sequence 1, Appl
602	195.5	5.0	306	1	US-08-774-592-1	Sequence 1, Appl	675	188	4.8	254	3	US-09-439-313-523	Sequence 523, App
603	195.5	5.0	2471	1	US-08-185-432-16	Sequence 16, Appl	676	188	4.8	254	4	US-09-636-215-523	Sequence 523, App
604	195.5	5.0	2471	1	US-08-083-590A-19	Sequence 19, Appl	677	188	4.8	254	4	US-09-685-166A-523	Sequence 523, App
605	195.5	5.0	2471	3	US-08-532-384-19	Sequence 19, Appl	678	188	4.8	254	4	US-09-679-426-523	Sequence 523, App
606	195.5	5.0	2471	1	US-08-899-232-1	Sequence 1, Appl	679	188	4.8	254	4	US-09-759-143-523	Sequence 523, App
607	195.5	5.0	2471	4	US-09-121-457-1	Sequence 1, Appl	680	188	4.8	254	4	US-09-651-236-523	Sequence 523, App
608	194.5	4.9	246	2	US-08-978-404B-44	Sequence 44, Appl	681	188	4.8	263	2	US-08-790-137-4	Sequence 4, Appl
609	194.5	4.9	415	3	US-09-032-523-2	Sequence 2, Appl	682	188	4.8	263	2	US-08-824-874-5	Sequence 5, Appl
610	194.5	4.9	415	4	US-09-802-633-2	Sequence 2, Appl	683	188	4.8	263	3	US-08-807-151-5	Sequence 5, Appl
611	194	4.9	113	4	US-09-438-046-20	Sequence 20, Appl	684	188	4.8	263	3	US-09-210-084-5	Sequence 5, Appl

685	188	4.8	263	3	US-09-478-957-5	Sequence 5, Appli	758	181.5	4.6	258	1	US-07-990-301A-2	Sequence 2, Appli
686	188	4.8	263	4	US-09-764-762-5	Sequence 5, Appli	759	181.5	4.6	299	1	US-08-467-155A-8	Sequence 8, Appli
687	188	4.8	333	4	US-08-991-761A-8	Sequence 8, Appli	760	181.5	4.6	299	2	US-08-628-198-8	Sequence 8, Appli
688	187.5	4.8	224	3	US-08-944-483-35	Sequence 35, Appl	761	181.5	4.6	299	3	US-09-201-038-8	Sequence 8, Appli
689	187.5	4.8	242	3	US-08-944-483-29	Sequence 29, Appl	762	181.5	4.6	299	5	PCT-US96-07343-8	Sequence 86, Appl
690	187.5	4.8	255	3	US-08-906-769-83	Sequence 83, Appl	763	181	4.6	396	4	US-09-800-729-86	Sequence 6948, Ap
691	187.5	4.8	255	3	US-08-906-616-83	Sequence 83, Appl	764	180	4.6	254	4	US-09-949-016-6948	Patent No. 5223425
692	187.5	4.8	255	3	US-08-817-795-83	Sequence 83, Appl	765	180	4.6	260	6	5223425-10	Patent No. 5223425
693	187.5	4.8	255	3	US-08-639-075A-83	Sequence 83, Appl	766	180	4.6	260	6	5223425-10	Sequence 176, App
694	187.5	4.8	255	3	US-09-012-431-83	Sequence 83, Appl	767	179.5	4.6	205	3	US-09-020-956-176	Sequence 176, App
695	187.5	4.8	255	3	US-09-012-692-83	Sequence 83, Appl	768	179.5	4.6	205	3	US-09-030-607-176	Sequence 176, App
696	187.5	4.8	255	3	US-08-906-613-83	Sequence 83, Appl	769	179.5	4.6	205	3	US-09-439-313-176	Sequence 176, App
697	187.5	4.8	255	5	PCT-US95-1442A-83	Sequence 83, Appl	770	179.5	4.6	205	3	US-09-352-616A-176	Sequence 176, App
698	186	4.7	110	4	US-09-341-461-28	Sequence 28, Appl	771	179.5	4.6	205	4	US-09-232-149A-176	Sequence 176, App
699	186	4.7	230	1	US-08-456-840-47	Sequence 47, Appl	772	179.5	4.6	205	4	US-09-159-812-176	Sequence 176, App
700	186	4.7	230	1	US-08-266-407A-47	Sequence 47, Appl	773	179.5	4.6	205	4	US-09-636-215-176	Sequence 176, App
701	186	4.7	230	2	US-08-892-544-47	Sequence 47, Appl	774	179.5	4.6	205	4	US-09-685-166A-176	Sequence 176, App
702	186	4.7	230	2	US-08-766-983-12	Sequence 12, Appl	775	179.5	4.6	205	4	US-09-115-453-176	Sequence 176, App
703	186	4.7	230	3	US-08-944-483-53	Sequence 53, Appl	776	179.5	4.6	205	4	US-09-688-489-176	Sequence 176, App
704	186	4.7	230	3	US-09-296-219-12	Sequence 12, Appl	777	179.5	4.6	205	4	US-09-679-426-176	Sequence 176, App
705	186	4.7	232	2	US-08-897-340-31	Sequence 31, Appl	778	179.5	4.6	205	4	US-09-759-143-176	Sequence 176, App
706	186	4.7	232	3	US-09-252-329-31	Sequence 31, Appl	779	179.5	4.6	205	4	US-09-651-236-176	Sequence 176, App
707	186	4.7	326	3	US-09-411-977-3	Sequence 3, Appli	780	179.5	4.6	259	6	5223425-2	Patent No. 5223425
708	186	4.7	326	4	US-10-057-951-3	Sequence 3, Appli	781	179.5	4.6	259	6	5223425-2	Patent No. 5223425
709	185.5	4.7	256	3	US-09-032-215-27	Sequence 27, Appl	782	179.5	4.6	728	3	US-08-981-392-2	Sequence 2, Appli
710	185.5	4.7	261	3	US-08-163-913A-2	Sequence 2, Appli	783	179.5	4.6	728	4	US-09-908-322-2	Sequence 2, Appli
711	185.5	4.7	261	4	US-08-462-515-2	Sequence 2, Appli	784	179.5	4.6	830	5	PCT-US91-05059-2	Sequence 2, Appli
712	185.5	4.7	261	5	PCT-US94-14073-2	Sequence 2, Appli	785	179	4.5	230	1	US-08-379-621-2	Sequence 2, Appli
713	185.5	4.7	306	4	US-09-386-643-53	Sequence 53, Appl	786	179	4.5	230	1	US-08-147-000B-2	Sequence 2, Appli
714	185.5	4.7	711	1	US-08-184-012C-8	Sequence 8, Appli	787	179	4.5	230	2	US-08-889-078-2	Sequence 2, Appli
715	185.5	4.7	711	1	US-08-334-177-2	Sequence 2, Appli	788	179	4.5	253	3	US-09-578-303-4	Sequence 22, Appl
716	185.5	4.7	711	2	US-08-666-082B-1	Sequence 1, Appli	789	179	4.5	384	3	US-09-032-215-22	Sequence 4, Appli
717	185.5	4.7	711	5	PCT-US95-13830-2	Sequence 2, Appli	790	178.5	4.5	250	3	US-08-944-483-68	Sequence 68, Appl
718	185.5	4.7	713	3	US-08-872-855-5	Sequence 5, Appli	791	178.5	4.5	315	4	US-09-386-653A-9	Sequence 9, Appli
719	185	4.7	247	3	US-08-944-483-49	Sequence 49, Appl	792	178.5	4.5	401	2	US-08-839-008-5	Sequence 5, Appli
720	185	4.7	258	1	US-08-744-026-3	Sequence 3, Appli	793	178.5	4.5	468	2	US-08-839-008-7	Sequence 7, Appli
721	185	4.7	258	2	US-09-102-732-3	Sequence 3, Appli	794	178.5	4.5	468	3	US-09-032-523-8	Sequence 8, Appli
722	185	4.7	258	3	US-09-261-767-3	Sequence 3, Appli	795	178.5	4.5	468	4	US-09-802-633-8	Sequence 8, Appli
723	185	4.7	314	4	US-09-023-942A-6	Sequence 6, Appli	796	178.5	4.5	922	4	US-09-116-473-4	Sequence 4, Appli
724	184	4.7	144	4	US-09-618-259-1	Sequence 1, Appli	797	178.5	4.5	923	3	US-08-936-135-6	Sequence 6, Appli
725	184	4.7	314	3	US-09-008-271A-3	Sequence 3, Appli	798	178.5	4.5	923	4	US-09-439-711C-6	Sequence 3, Appli
726	184	4.7	314	4	US-09-907-794A-257	Sequence 257, App	799	177.5	4.5	248	2	US-08-851-974-3	Sequence 3, Appli
727	184	4.7	314	4	US-09-905-125A-257	Sequence 257, App	800	177.5	4.5	248	3	US-09-213-390-3	Sequence 1, Appli
728	184	4.7	314	4	US-09-902-775A-257	Sequence 257, App	801	177.5	4.5	1964	2	US-09-467-997-1	Sequence 7, Appli
729	184	4.7	314	4	US-09-906-700-257	Sequence 257, App	802	177	4.5	1102	3	US-09-374-135-7	Sequence 29, Appl
730	184	4.7	314	4	US-09-903-603A-257	Sequence 257, App	803	177	4.5	1103	4	US-09-341-461-29	Sequence 45768, A
731	184	4.7	314	4	US-09-904-920A-257	Sequence 257, App	804	177	4.5	1103	4	US-09-270-767-45768	Sequence 11, Appl
732	184	4.7	314	4	US-09-909-064-257	Sequence 257, App	805	177	4.5	223	1	US-08-278-091-11	Sequence 11, Appl
733	184	4.7	314	4	US-09-905-381A-257	Sequence 257, App	806	177	4.5	240	1	US-08-483-859-11	Sequence 11, Appl
734	184	4.7	314	4	US-09-906-618-257	Sequence 257, App	807	177	4.5	240	1	US-08-472-173-11	Sequence 11, Appl
735	183.5	4.7	711	2	US-08-766-982-2	Sequence 2, Appli	808	177	4.5	240	2	US-08-487-167-11	Sequence 11, Appl
736	183.5	4.7	711	3	US-09-296-219-2	Sequence 2, Appli	809	177	4.5	240	2	US-08-482-816-11	Sequence 11, Appl
737	183.5	4.7	711	4	US-09-600-991-20	Sequence 20, Appl	810	177	4.5	240	2	US-08-296-149-11	Sequence 11, Appl
738	183.5	4.7	711	4	US-09-601-040A-12	Sequence 12, Appl	811	177	4.5	240	2	US-08-801-499-11	Sequence 11, Appl
739	183.5	4.7	711	4	US-09-949-016-6981	Sequence 6981, Ap	812	177	4.5	240	2	US-08-615-271-11	Sequence 11, Appl
740	183.5	4.7	722	3	US-08-981-392-12	Sequence 12, Appl	813	177	4.5	240	3	US-09-074-659-11	Sequence 11, Appl
741	183.5	4.7	722	4	US-09-908-322-12	Sequence 12, Appl	814	177	4.5	240	3	US-09-106-468-11	Sequence 11, Appl
742	183	4.6	418	4	US-10-177-661-6	Sequence 6, Appli	815	177	4.5	240	3	US-09-106-466A-11	Sequence 11, Appl
743	182.5	4.6	258	4	US-09-023-942A-8	Sequence 8, Appli	816	177	4.5	240	3	US-09-106-467-11	Sequence 11, Appl
744	182.5	4.6	484	2	US-08-252-493C-9	Sequence 9, Appli	817	177	4.5	729	3	US-08-872-855-8	Sequence 8, Appli
745	182.5	4.6	484	3	US-09-276-197-9	Sequence 9, Appli	818	177	4.5	830	6	5378464-2	Patent No. 5378464
746	182.5	4.6	720	3	US-08-872-855-4	Sequence 4, Appli	819	177	4.5	830	6	5378464-2	Patent No. 5378464
747	182	4.6	405	3	US-09-734-675-2	Sequence 2, Appli	820	177	4.5	930	1	US-07-990-301A-4	Sequence 4, Appli
748	182	4.6	721	3	US-08-872-855-7	Sequence 7, Appli	821	176.5	4.5	232	1	US-08-936-135-22	Sequence 22, Appl
749	182	4.6	1055	3	US-09-214-278-2	Sequence 2, Appli	822	176.5	4.5	901	3	US-09-439-711C-22	Sequence 22, Appl
750	182	4.6	1055	4	US-09-855-722-2	Sequence 2, Appli	823	176.5	4.5	901	3	US-08-936-135-24	Sequence 24, Appl
751	182	4.6	1055	2	US-08-400-159-8	Sequence 8, Appli	824	176.5	4.5	906	3	US-08-936-135-24	Sequence 24, Appl
752	182	4.6	1212	3	US-09-214-278-3	Sequence 3, Appli	825	176.5	4.5	906	3	US-09-439-711C-24	Sequence 8, Appli
753	182	4.6	1212	4	US-09-855-722-3	Sequence 3, Appli	826	176.5	4.5	909	3	US-08-936-135-8	Sequence 10, Appl
754	182	4.6	1238	3	US-09-214-278-5	Sequence 5, Appli	827	176.5	4.5	909	4	US-08-936-135-10	Sequence 8, Appli
755	182	4.6	1238	4	US-09-855-722-5	Sequence 5, Appli	828	176.5	4.5	909	4	US-09-439-711C-8	Sequence 10, Appl
756	182	4.6	1257	3	US-08-611-729A-8	Sequence 8, Appli	829	176.5	4.5	909	4	US-09-439-711C-10	Sequence 10, Appl
757	182	4.6	1257	4	US-09-195-524-8	Sequence 8, Appli	830	176.5	4.5	914	3	US-08-936-135-12	Sequence 12, Appl

831	176.5	4.5	914	4	US-09-439-711C-12	Sequence 12, Appl	904	170	4.3	213	3	US-08-906-769-149	Sequence 149, App
832	176.5	4.5	925	3	US-09-116-473-2	Sequence 2, Appl	905	170	4.3	213	3	US-08-906-616-149	Sequence 149, App
833	176.5	4.5	926	3	US-08-936-135-14	Sequence 14, Appl	906	170	4.3	213	3	US-08-639-075A-149	Sequence 149, App
834	176.5	4.5	926	3	US-09-439-711C-14	Sequence 14, Appl	907	170	4.3	213	3	US-09-012-431-149	Sequence 149, App
835	176.5	4.5	931	3	US-08-936-135-16	Sequence 16, Appl	908	170	4.3	213	3	US-09-012-692-149	Sequence 149, App
836	176.5	4.5	931	3	US-09-439-711C-16	Sequence 16, Appl	909	170	4.3	213	3	US-08-906-613-149	Sequence 149, App
837	176	4.5	933	3	US-09-004-731-27	Sequence 27, Appl	910	170	4.3	217	4	US-09-601-040A-8	Sequence 8, Appl
838	176	4.5	933	3	US-08-749-699-27	Sequence 27, Appl	911	170	4.3	717	4	US-09-601-040A-8	Sequence 8, Appl
839	176	4.5	933	3	US-09-004-729-27	Sequence 27, Appl	912	170	4.3	729	4	US-09-601-040A-4	Sequence 4, Appl
840	176	4.5	933	3	US-08-944-483-58	Sequence 58, Appl	913	170	4.3	1148	3	US-08-882-046-4	Sequence 4, Appl
841	176	4.5	933	3	US-09-004-731-24	Sequence 24, Appl	914	169	4.3	95	3	US-09-566-047-4	Sequence 8, Appl
842	176	4.5	933	3	US-08-749-699-24	Sequence 24, Appl	915	169	4.3	95	3	US-09-374-135-8	Sequence 8, Appl
843	176	4.5	933	3	US-09-004-729-24	Sequence 24, Appl	916	169	4.3	95	3	US-09-341-461-25	Sequence 25, Appl
844	175.5	4.4	921	4	US-09-439-711C-4	Sequence 4, Appl	917	169	4.3	237	1	US-08-096-946-11	Sequence 11, Appl
845	175	4.4	112	4	US-09-438-046-21	Sequence 21, Appl	918	169	4.3	237	5	PCT-US94-07329-11	Sequence 11, Appl
846	175	4.4	909	3	US-08-936-135-18	Sequence 18, Appl	919	169	4.3	237	5	PCT-US95-06157-1	Sequence 1, Appl
847	175	4.4	909	3	US-09-439-711C-18	Sequence 18, Appl	920	168.5	4.3	375	4	US-09-755-100A-11	Sequence 11, Appl
848	175	4.4	926	3	US-08-936-135-20	Sequence 20, Appl	921	168.5	4.3	375	4	US-09-755-100A-11	Sequence 11, Appl
849	175	4.4	926	3	US-09-439-711C-20	Sequence 20, Appl	922	168.5	4.3	375	4	US-09-755-100A-11	Sequence 11, Appl
850	175	4.4	931	4	US-09-583-638-4	Sequence 4, Appl	923	168.5	4.3	375	4	US-09-755-100A-11	Sequence 11, Appl
851	174	4.4	265	2	US-08-177-109A-57	Sequence 57, Appl	924	168	4.3	375	4	US-09-755-100A-11	Sequence 11, Appl
852	174	4.4	265	2	US-08-687-706-57	Sequence 57, Appl	925	168	4.3	375	4	US-09-755-100A-11	Sequence 11, Appl
853	174	4.4	286	1	US-08-467-155A-9	Sequence 9, Appl	926	168	4.3	375	4	US-09-755-100A-11	Sequence 11, Appl
854	174	4.4	286	1	US-08-628-198-9	Sequence 9, Appl	927	168	4.3	375	4	US-09-755-100A-11	Sequence 11, Appl
855	174	4.4	286	3	US-09-201-038-9	Sequence 9, Appl	928	168	4.3	375	4	US-09-755-100A-11	Sequence 11, Appl
856	174	4.4	286	5	PCT-US96-07343-9	Sequence 9, Appl	929	167.5	4.2	261	1	US-08-744-026-5	Sequence 5, Appl
857	173.5	4.4	294	4	US-09-800-729-146	Sequence 146, Appl	930	167.5	4.2	261	1	US-08-744-026-5	Sequence 5, Appl
858	173.5	4.4	294	4	US-10-067-423-12	Sequence 12, Appl	931	167.5	4.2	261	1	US-09-102-732-5	Sequence 5, Appl
859	173.5	4.4	414	4	US-09-270-767-46426	Sequence 46426, A	932	167.5	4.2	261	3	US-09-083-521-6	Sequence 6, Appl
860	173.5	4.4	717	3	US-08-872-855-9	Sequence 9, Appl	933	167.5	4.2	261	3	US-09-261-767-5	Sequence 5, Appl
861	173	4.4	211	3	US-09-220-731-25	Sequence 25, Appl	934	167.5	4.2	261	4	US-09-413-049-1	Sequence 1, Appl
862	173	4.4	211	3	US-09-242-999-20	Sequence 20, Appl	935	167.5	4.2	261	4	US-09-907-402-1	Sequence 1, Appl
863	172.5	4.4	449	2	US-08-839-008-2	Sequence 2, Appl	936	167.5	4.2	261	4	US-09-618-259-10	Sequence 10, Appl
864	172.5	4.4	449	2	US-08-839-008-9	Sequence 9, Appl	937	167.5	4.2	262	1	US-08-744-026-4	Sequence 4, Appl
865	172.5	4.4	449	4	US-09-919-497-89	Sequence 89, Appl	938	167.5	4.2	262	3	US-09-261-767-4	Sequence 4, Appl
866	172.5	4.4	458	4	US-09-949-016-7238	Sequence 7238, Ap	939	167.5	4.2	262	3	US-09-261-767-4	Sequence 4, Appl
867	172.5	4.4	1448	3	US-08-882-046-6	Sequence 6, Appl	940	167	4.2	262	3	US-09-261-767-4	Sequence 4, Appl
868	172.5	4.4	1448	4	US-09-566-047-6	Sequence 6, Appl	941	166.5	4.2	103	3	US-09-583-638-2	Sequence 2, Appl
869	172	4.4	250	4	US-09-270-767-33709	Sequence 33709, A	942	166.5	4.2	520	3	US-09-374-135-5	Sequence 5, Appl
870	172	4.4	357	4	US-09-270-767-43564	Sequence 43564, A	943	166.5	4.2	520	3	US-09-068-740A-3	Sequence 3, Appl
871	172	4.4	357	4	US-09-270-767-58936	Sequence 58936, A	944	166.5	4.2	723	3	US-09-068-740A-9	Sequence 9, Appl
872	172	4.4	721	3	US-08-981-392-5	Sequence 5, Appl	945	166.5	4.2	723	3	US-09-423-753-27	Sequence 27, Appl
873	172	4.4	721	3	US-09-908-322-5	Sequence 5, Appl	946	166	4.2	723	3	US-09-641-612-6	Sequence 6, Appl
874	171.5	4.3	238	3	US-08-944-483-39	Sequence 39, Appl	947	166	4.2	124	6	5514582-38	Sequence 6, Appl
875	171.5	4.3	259	3	US-08-906-769-190	Sequence 190, App	948	166	4.2	124	6	5514582-38	Sequence 6, Appl
876	171.5	4.3	259	3	US-08-906-616-190	Sequence 190, App	949	166	4.2	237	3	US-08-768-859A-1	Sequence 1, Appl
877	171.5	4.3	259	3	US-08-639-075A-190	Sequence 190, App	950	166	4.2	237	3	US-08-767-820A-1	Sequence 1, Appl
878	171.5	4.3	259	3	US-09-004-731-85	Sequence 85, Appl	951	166	4.2	237	3	US-08-622-046B-7	Sequence 7, Appl
879	171.5	4.3	259	3	US-09-012-431-190	Sequence 190, App	952	166	4.2	237	3	US-08-944-483-38	Sequence 38, Appl
880	171.5	4.3	259	3	US-08-749-699-85	Sequence 85, Appl	953	166	4.2	237	3	US-09-100-264-3	Sequence 3, Appl
881	171.5	4.3	259	3	US-09-012-692-190	Sequence 190, App	954	166	4.2	237	4	US-09-303-339-2	Sequence 2, Appl
882	171.5	4.3	259	3	US-08-906-613-190	Sequence 190, App	955	166	4.2	237	4	US-08-843-076D-7	Sequence 7, Appl
883	171.5	4.3	259	4	US-09-004-729-85	Sequence 85, Appl	956	166	4.2	237	4	US-09-303-208-1	Sequence 1, Appl
884	171.5	4.3	262	2	US-08-790-137-1	Sequence 1, Appl	957	166	4.2	243	3	US-08-944-483-70	Sequence 70, Appl
885	171.5	4.3	262	2	US-08-790-137-3	Sequence 3, Appl	958	166	4.2	441	4	US-09-949-016-10792	Sequence 10792, A
886	171.5	4.3	262	2	US-08-681-151-4	Sequence 4, Appl	959	165.5	4.2	923	3	US-09-439-711C-2	Sequence 2, Appl
887	171.5	4.3	262	2	US-08-824-874-4	Sequence 4, Appl	960	165.5	4.2	240	1	US-08-472-228A-1	Sequence 1, Appl
888	171.5	4.3	262	3	US-08-807-151-4	Sequence 4, Appl	961	165.5	4.2	240	5	US-09-146-831-1	Sequence 1, Appl
889	171.5	4.3	262	3	US-09-210-084-4	Sequence 4, Appl	962	165.5	4.2	240	5	PCT-US96-09303-1	Sequence 1, Appl
890	171.5	4.3	262	3	US-09-478-957-4	Sequence 4, Appl	963	165.5	4.2	383	1	US-08-597-545-2	Sequence 2, Appl
891	171.5	4.3	262	4	US-09-764-762-4	Sequence 4, Appl	964	165	4.2	383	1	US-08-457-135-2	Sequence 2, Appl
892	171.5	4.3	262	4	US-09-618-259-9	Sequence 9, Appl	965	164	4.2	101	3	US-09-374-135-4	Sequence 4, Appl
893	171.5	4.3	666	3	US-09-341-587-1	Sequence 1, Appl	966	164	4.2	351	3	US-09-245-041-11	Sequence 11, Appl
894	171.5	4.3	1785	3	US-09-341-587-3	Sequence 3, Appl	967	164	4.2	351	4	US-09-358-055B-11	Sequence 11, Appl
895	171	4.3	262	3	US-09-025-059-4	Sequence 4, Appl	968	164	4.2	812	4	US-09-893-238-11	Sequence 11, Appl
896	171	4.3	262	4	US-09-755-100A-14	Sequence 14, Appl	969	163	4.1	441	4	US-09-192-012-9	Sequence 9, Appl
897	171	4.3	287	4	US-09-270-767-33263	Sequence 33263, A	970	163	4.1	441	4	US-09-949-016-11196	Sequence 11196, A
898	171	4.3	287	4	US-09-270-767-48480	Sequence 48480, A	971	163	4.1	607	4	US-09-907-794A-190	Sequence 190, App
899	171	4.3	290	4	US-09-949-016-8166	Sequence 8166, Ap	972	163	4.1	607	4	US-09-905-125A-190	Sequence 190, App
900	171	4.3	717	4	US-09-601-040A-2	Sequence 2, Appl	973	163	4.1	607	4	US-09-902-775A-190	Sequence 190, App
901	171	4.3	729	4	US-09-601-040A-2	Sequence 2, Appl	974	163	4.1	607	4	US-09-906-700-190	Sequence 190, App
902	171	4.3	737	4	US-09-866-028-15	Sequence 15, Appl	975	163	4.1	607	4	US-09-903-603A-190	Sequence 190, App
903	171	4.3	737	4	US-09-944-457-15	Sequence 15, Appl	976	163	4.1	607	4	US-09-904-920A-190	Sequence 190, App

977	163	4.1	607	4	US-09-905-381A-190	Sequence 190, App	1050	156	4.0	238	5	PCT-US95-06157-8	Sequence 8, Appli
978	163	4.1	607	4	US-09-906-618-190	Sequence 190, App	1051	156	4.0	244	3	US-08-768-859A-10	Sequence 10, Appl
979	162.5	4.1	1290	1	US-08-470-3508-2	Sequence 2, Appli	1052	156	4.0	244	3	US-08-767-820A-10	Sequence 10, Appl
980	161.5	4.1	251	3	US-08-944-483-28	Sequence 28, Appli	1053	156	4.0	244	3	US-08-622-046B-5	Sequence 5, Appli
981	161.5	4.1	832	3	US-08-981-392-6	Sequence 6, Appli	1054	156	4.0	244	3	US-08-622-046B-16	Sequence 16, Appli
982	161.5	4.1	832	4	US-09-908-322-6	Sequence 6, Appli	1055	156	4.0	244	3	US-09-100-264-5	Sequence 5, Appli
983	161.5	4.1	1025	4	US-09-834-309-5	Sequence 5, Appli	1056	156	4.0	244	3	US-08-843-076D-5	Sequence 5, Appli
984	161	4.1	207	4	US-09-949-016-7712	Sequence 7712, Ap	1057	156	4.0	244	5	PCT-US95-06157-10	Sequence 10, Appl
985	161	4.1	293	4	US-09-509-908-2	Sequence 2, Appli	1058	156	4.0	261	3	US-08-768-859A-6	Sequence 6, Appli
986	160.5	4.1	238	4	US-09-664-595A-15	Sequence 15, Appl	1059	156	4.0	261	3	US-08-768-859A-19	Sequence 19, Appl
987	160.5	4.1	263	4	US-09-949-016-9072	Sequence 9072, Ap	1060	156	4.0	261	3	US-08-767-820A-6	Sequence 6, Appli
988	160.5	4.1	319	4	US-09-270-767-42672	Sequence 42672, A	1061	156	4.0	261	3	US-08-767-820A-19	Sequence 19, Appl
989	160.5	4.1	661	4	US-09-949-016-6157	Sequence 6157, Ap	1062	156	4.0	261	3	US-08-622-046B-3	Sequence 3, Appli
990	160.5	4.1	665	4	US-09-949-016-10776	Sequence 10776, A	1063	156	4.0	261	3	US-08-622-046B-14	Sequence 14, Appl
991	160	4.1	207	4	US-10-000-489-54	Sequence 54, Appl	1064	156	4.0	261	3	US-09-100-264-7	Sequence 7, Appli
992	160	4.1	234	3	US-08-944-483-46	Sequence 46, Appl	1065	156	4.0	261	3	US-08-983-075D-7	Sequence 7, Appli
993	160	4.1	268	4	US-09-949-016-10712	Sequence 10712, A	1066	156	4.0	261	4	US-08-843-076D-3	Sequence 3, Appli
994	160	4.1	2871	4	US-09-538-092-1076	Sequence 1076, Ap	1067	156	4.0	261	5	PCT-US95-06157-6	Sequence 6, Appli
995	159.5	4.0	228	2	US-08-766-982-11	Sequence 11, Appl	1068	156	4.0	278	4	US-09-949-016-7711	Sequence 7711, Ap
996	159.5	4.0	228	3	US-09-296-219-11	Sequence 11, Appl	1069	155.5	3.9	247	2	US-08-851-974-1	Sequence 1, Appli
997	159.5	4.0	276	4	US-09-270-767-32048	Sequence 32048, A	1070	155.5	3.9	247	2	US-09-213-390-1	Sequence 1, Appli
998	159.5	4.0	276	4	US-09-270-767-47265	Sequence 47265, A	1071	155.5	3.9	830	3	US-08-872-855-11	Sequence 11, Appl
999	159	4.0	237	2	US-08-844-024-2	Sequence 2, Appli	1072	155	3.9	2489	4	US-09-911-842A-5	Sequence 5, Appli
1000	159	4.0	237	2	US-08-718-547-2	Sequence 2, Appli	1073	154.5	3.9	228	1	US-08-278-091-7	Sequence 7, Appli
1001	158.5	4.0	283	4	US-09-244-111-2	Sequence 2, Appli	1074	154.5	3.9	228	1	US-08-483-859-7	Sequence 7, Appli
1002	158.5	4.0	385	1	US-08-597-545-1	Sequence 1, Appli	1075	154.5	3.9	228	1	US-08-472-173-7	Sequence 7, Appli
1003	158.5	4.0	385	1	US-08-457-133-1	Sequence 1, Appli	1076	154.5	3.9	228	2	US-08-487-167-7	Sequence 7, Appli
1004	158.5	4.0	385	1	US-09-142-027A-10	Sequence 10, Appl	1077	154.5	3.9	228	2	US-08-482-816-7	Sequence 7, Appli
1005	158.5	4.0	833	1	US-08-264-534-6	Sequence 6, Appli	1078	154.5	3.9	228	2	US-08-296-149-7	Sequence 7, Appli
1006	158.5	4.0	833	1	US-08-083-590A-2	Sequence 2, Appli	1079	154.5	3.9	228	2	US-08-801-499-7	Sequence 7, Appli
1007	158.5	4.0	833	1	US-08-465-500-6	Sequence 6, Appli	1080	154.5	3.9	228	2	US-09-615-271-7	Sequence 7, Appli
1008	158.5	4.0	833	2	US-08-346-128-6	Sequence 6, Appli	1081	154.5	3.9	228	3	US-09-074-660-7	Sequence 7, Appli
1009	158.5	4.0	833	2	US-08-532-384-2	Sequence 2, Appli	1082	154.5	3.9	228	3	US-09-074-659-7	Sequence 7, Appli
1010	158.5	4.0	833	3	US-08-893-828-6	Sequence 6, Appli	1083	154.5	3.9	228	3	US-09-106-468-7	Sequence 7, Appli
1011	158.5	4.0	156	3	US-08-845-998-4	Sequence 4, Appli	1084	154.5	3.9	228	3	US-09-106-468-7	Sequence 7, Appli
1012	158	4.0	190	2	US-09-261-416-6	Sequence 6, Appli	1085	154.5	3.9	228	3	US-09-106-468-7	Sequence 7, Appli
1013	157.5	4.0	190	3	US-09-206-537-4	Sequence 4, Appli	1086	154	3.9	224	1	US-08-553-516-2	Sequence 7, Appli
1014	157.5	4.0	190	3	US-09-430-854-4	Sequence 4, Appli	1087	154	3.9	224	1	US-08-944-483-40	Sequence 40, Appl
1015	157.5	4.0	226	4	US-09-601-040A-28	Sequence 28, Appl	1088	154	3.9	227	3	US-08-238-130-2	Sequence 2, Appli
1016	157.5	4.0	228	3	US-08-944-483-55	Sequence 55, Appl	1089	154	3.9	248	1	US-08-921-426-4	Sequence 4, Appli
1017	157.5	4.0	255	3	US-08-906-769-91	Sequence 91, Appl	1090	154	3.9	248	3	US-08-816-915-4	Sequence 4, Appli
1018	157.5	4.0	255	3	US-08-906-616-91	Sequence 91, Appl	1091	154	3.9	248	3	PCT-US95-07743-4	Sequence 37, Appl
1019	157.5	4.0	255	3	US-08-817-795-91	Sequence 91, Appl	1092	154	3.9	248	5	US-09-032-215-37	Sequence 4, Appli
1020	157.5	4.0	255	3	US-08-639-075A-91	Sequence 91, Appl	1093	154	3.9	268	2	US-08-824-874-1	Sequence 1, Appli
1021	157.5	4.0	255	3	US-09-012-431-91	Sequence 91, Appl	1094	154	3.9	268	3	US-09-210-084-1	Sequence 1, Appli
1022	157.5	4.0	255	3	US-08-906-613-141	Sequence 91, Appl	1095	154	3.9	268	4	US-09-270-767-33762	Sequence 33762, A
1023	157.5	4.0	255	3	PCT-US95-14442A-91	Sequence 91, Appl	1096	154	3.9	321	4	US-09-270-767-48979	Sequence 48979, A
1024	157.5	4.0	255	5	US-08-906-613-91	Sequence 91, Appl	1097	154	3.9	321	4	US-09-270-767-48979	Sequence 48979, A
1025	157.5	4.0	185	3	US-08-906-769-141	Sequence 141, App	1098	154	3.9	321	4	US-09-270-767-48979	Sequence 48979, A
1026	157	4.0	185	3	US-08-906-616-141	Sequence 141, App	1099	154	3.9	1466	6	5256642-6	Patent No. 5256642
1027	157	4.0	185	3	US-08-906-616-141	Sequence 141, App	1100	154	3.9	1466	6	5472939-6	Patent No. 5472939
1028	157	4.0	185	3	US-08-639-075A-141	Sequence 141, App	1101	154	3.9	1466	6	5256642-6	Patent No. 5256642
1029	157	4.0	185	3	US-09-012-431-141	Sequence 141, App	1102	154	3.9	1466	6	5472939-6	Patent No. 5472939
1030	157	4.0	185	3	US-09-012-692-141	Sequence 141, App	1103	154	3.9	1537	6	5256642-5	Patent No. 5256642
1031	157	4.0	185	3	US-08-906-613-141	Sequence 141, App	1104	154	3.9	1537	6	5472939-5	Patent No. 5472939
1032	157	4.0	610	6	5217870-2	Patent No. 5217870	1105	154	3.9	1537	6	5256642-5	Patent No. 5256642
1033	157	4.0	610	6	5217870-2	Patent No. 5217870	1106	154	3.9	1537	6	5472939-5	Patent No. 5472939
1034	157	4.0	647	4	US-09-949-016-10272	Sequence 10272, A	1107	154	3.9	1847	6	5256642-10	Patent No. 5256642
1035	156.5	4.0	312	4	US-09-636-382A-15	Sequence 15, Appl	1108	154	3.9	1847	6	5472939-10	Patent No. 5472939
1036	156.5	4.0	3635	4	US-09-845-583A-2	Sequence 2, Appli	1109	154	3.9	1847	6	5256642-10	Patent No. 5256642
1037	156	4.0	237	3	US-08-768-859A-16	Sequence 16, Appl	1110	154	3.9	1847	6	5472939-10	Patent No. 5472939
1038	156	4.0	237	3	US-08-768-859A-21	Sequence 21, Appl	1111	154	3.9	1947	4	US-09-612-314A-52	Sequence 52, Appl
1039	156	4.0	237	3	US-08-767-820A-16	Sequence 16, Appl	1112	154	3.9	2039	6	5472939-2	Patent No. 5472939
1040	156	4.0	237	3	US-08-767-820A-21	Sequence 21, Appl	1113	154	3.9	2039	6	5256642-2	Patent No. 5256642
1041	156	4.0	237	3	US-08-622-046B-1	Sequence 1, Appli	1114	154	3.9	2039	6	5472939-2	Patent No. 5472939
1042	156	4.0	237	3	US-08-622-046B-12	Sequence 12, Appl	1115	154	3.9	2039	6	5256642-2	Patent No. 5256642
1043	156	4.0	237	3	US-08-944-483-37	Sequence 37, Appl	1116	153.5	3.9	185	3	US-08-705-875A-5	Sequence 5, Appli
1044	156	4.0	237	3	US-09-100-264-1	Sequence 1, Appli	1117	153.5	3.9	185	3	US-09-220-731-22	Sequence 22, Appl
1045	156	4.0	237	3	US-09-100-264-12	Sequence 12, Appl	1118	153.5	3.9	185	4	US-09-242-999-5	Sequence 5, Appli
1046	156	4.0	237	4	US-08-843-076D-1	Sequence 1, Appli	1119	153.5	3.9	190	2	US-08-845-998-6	Sequence 6, Appli
1047	156	4.0	237	4	US-08-843-076D-8	Sequence 8, Appli	1120	153.5	3.9	190	3	US-09-206-537-6	Sequence 6, Appli
1048	156	4.0	238	3	US-08-768-859A-8	Sequence 8, Appli	1121	153.5	3.9	190	3	US-09-430-854-6	Sequence 6, Appli
1049	156	4.0	238	3	US-08-767-820A-8	Sequence 8, Appli	1122	153.5	3.9	352	4	US-09-902-540-9796	Sequence 9796, Ap

1123	153.5	3.9	610	1	US-08-365-470-3	Sequence 3, Appli	1196	148.5	3.8	111	4	US-09-341-461-30	Sequence 30, Appli
1124	153.5	3.9	610	3	US-09-209-668-19	Sequence 19, Appli	1197	148	3.8	113	4	US-09-438-046-23	Sequence 23, Appli
1125	153.5	3.9	610	3	US-09-009-490A-89	Sequence 89, Appli	1198	148	3.8	218	4	US-09-578-303-3	Sequence 3, Appli
1126	153.5	3.9	610	4	US-09-949-016-5942	Sequence 5942, Ap	1199	148	3.8	242	3	US-09-032-215-47	Sequence 47, Appli
1127	153.5	3.9	1725	4	US-09-562-702A-20	Sequence 20, Appli	1200	148	3.8	657	4	US-09-949-016-11365	Sequence 11365, A
1128	153.5	3.9	1725	4	US-09-561-818A-20	Sequence 20, Appli	1201	148	3.8	657	4	US-09-949-016-11366	Sequence 11366, A
1129	153.5	3.9	1786	4	US-09-562-702A-18	Sequence 18, Appli	1202	148	3.8	657	4	US-09-949-016-11367	Sequence 11367, A
1130	153.5	3.9	1786	4	US-09-561-818A-18	Sequence 18, Appli	1203	148	3.8	657	4	US-09-949-016-11368	Sequence 11368, A
1131	153	3.9	158	3	US-09-374-135-2	Sequence 2, Appli	1204	148	3.8	1480	3	US-09-191-647-7	Sequence 7, Appli
1132	153	3.9	248	3	US-08-906-769-111	Sequence 111, App	1205	148	3.8	1480	3	US-09-540-245A-7	Sequence 7, Appli
1133	153	3.9	248	3	US-08-906-616-111	Sequence 111, App	1206	148	3.8	1480	3	US-09-540-153-7	Sequence 7, Appli
1134	153	3.9	248	3	US-08-817-795-111	Sequence 111, App	1207	148	3.8	1480	3	PCT-US91-09055-2	Sequence 2, Appli
1135	153	3.9	248	3	US-08-639-075A-111	Sequence 111, App	1208	147.5	3.7	197	1	US-08-456-840-48	Sequence 48, Appli
1136	153	3.9	248	3	US-09-012-431-111	Sequence 111, App	1209	147.5	3.7	197	2	US-08-266-407A-48	Sequence 48, Appli
1137	153	3.9	248	3	US-09-012-692-111	Sequence 111, App	1210	147.5	3.7	197	2	US-08-892-544-48	Sequence 48, Appli
1138	153	3.9	248	3	US-08-906-613-111	Sequence 111, App	1211	147.5	3.7	246	3	US-08-906-769-127	Sequence 127, App
1139	153	3.9	248	5	PCT-US95-14442A-111	Sequence 111, App	1212	147.5	3.7	246	3	US-08-906-616-127	Sequence 127, App
1140	153	3.9	254	3	US-09-578-303-5	Sequence 5, Appli	1213	147.5	3.7	246	3	US-08-639-075A-127	Sequence 127, App
1141	153	3.9	286	4	US-09-270-767-45162	Sequence 45162, A	1214	147.5	3.7	246	3	US-09-012-431-127	Sequence 127, App
1142	152.5	3.9	267	4	US-09-949-016-10711	Sequence 10711, A	1215	147.5	3.7	246	3	US-09-012-692-127	Sequence 127, App
1143	152.5	3.9	642	3	US-08-872-855-10	Sequence 10, Appli	1216	147.5	3.7	246	3	US-08-906-613-127	Sequence 127, App
1144	152	3.9	247	2	US-08-851-974-4	Sequence 4, Appli	1217	147.5	3.7	574	6	5378464-3	Patent No. 5378464
1145	152	3.9	247	2	US-09-313-390-4	Sequence 4, Appli	1218	147.5	3.7	574	6	5378464-3	Patent No. 5378464
1146	152	3.9	247	4	US-09-949-016-6457	Sequence 6457, Ap	1219	147.5	3.7	1765	4	US-09-562-702A-16	Sequence 16, Appli
1147	152	3.9	237	1	US-08-096-946-10	Sequence 10661, A	1220	147.5	3.7	1765	4	US-09-561-818A-16	Sequence 16, Appli
1148	152	3.9	1033	4	US-09-834-309-1	Sequence 1, Appli	1221	147.5	3.7	1786	4	US-09-562-702A-14	Sequence 14, Appli
1149	151.5	3.8	259	4	US-09-949-016-10954	Sequence 10954, A	1222	147.5	3.7	1786	4	US-09-561-818A-14	Sequence 14, Appli
1150	151.5	3.8	716	2	US-08-766-982-1	Sequence 1, Appli	1223	147.5	3.7	1786	4	US-09-561-709B-9	Sequence 9, Appli
1151	151.5	3.8	716	3	US-09-296-219-1	Sequence 1, Appli	1224	147.5	3.7	1786	4	US-09-538-092-869	Sequence 869, App
1152	151	3.8	110	4	US-09-341-461-27	Sequence 27, Appli	1225	147.5	3.7	4391	4	US-10-006-011A-2	Sequence 2, Appli
1153	151	3.8	237	1	US-08-096-946-10	Sequence 10, Appli	1226	147	3.7	239	3	US-09-004-731-44	Sequence 44, Appli
1154	151	3.8	237	5	PCT-US94-07323-10	Sequence 10, Appli	1227	147	3.7	239	3	US-08-749-699-44	Sequence 44, Appli
1155	151	3.8	237	5	PCT-US95-06157-16	Sequence 16, Appli	1228	147	3.7	239	3	US-09-004-729-44	Sequence 44, Appli
1156	150.5	3.8	277	1	US-08-024-868-2	Sequence 2, Appli	1229	147	3.7	242	3	US-09-004-731-41	Sequence 41, Appli
1157	150.5	3.8	277	2	US-08-242-097-2	Sequence 2, Appli	1230	147	3.7	242	3	US-08-749-699-41	Sequence 41, Appli
1158	150.5	3.8	277	3	US-09-206-695-2	Sequence 2, Appli	1231	147	3.7	242	4	US-09-004-729-41	Sequence 41, Appli
1159	150.5	3.8	277	3	US-09-000-179-1	Sequence 1, Appli	1232	147	3.7	476	4	US-09-949-016-11726	Sequence 11726, A
1160	150.5	3.8	277	5	PCT-US96-11995-1	Sequence 1, Appli	1233	146.5	3.7	223	1	US-08-278-091-13	Sequence 13, Appli
1161	150.5	3.8	277	5	PCT-US96-11995-1	Sequence 1, Appli	1234	146.5	3.7	223	1	US-08-483-859-13	Sequence 13, Appli
1162	150.5	3.8	500	4	US-09-423-753-2	Sequence 2, Appli	1235	146.5	3.7	223	1	US-08-472-173-13	Sequence 13, Appli
1163	150.5	3.8	659	4	US-09-423-753-3	Sequence 3, Appli	1236	146.5	3.7	223	2	US-08-487-167-13	Sequence 13, Appli
1164	150.5	3.8	685	3	US-08-872-855-2	Sequence 2, Appli	1237	146.5	3.7	223	2	US-08-482-816-13	Sequence 13, Appli
1165	150.5	3.8	685	4	US-09-423-753-25	Sequence 25, Appli	1238	146.5	3.7	223	2	US-08-296-149-13	Sequence 13, Appli
1166	150.5	3.8	685	4	US-09-641-612-7	Sequence 7, Appli	1239	146.5	3.7	223	2	US-08-801-499-13	Sequence 13, Appli
1167	150.5	3.8	1064	1	US-08-537-210A-3	Sequence 3, Appli	1240	146.5	3.7	223	2	US-08-615-271-13	Sequence 13, Appli
1168	150.5	3.8	1064	3	US-09-113-825-3	Sequence 3, Appli	1241	146.5	3.7	223	3	US-09-074-660-13	Sequence 13, Appli
1169	150	3.8	113	3	US-09-438-046-22	Sequence 22, Appli	1242	146.5	3.7	223	3	US-09-074-659-13	Sequence 13, Appli
1170	150	3.8	238	3	US-08-344-483-31	Sequence 31, Appli	1243	146.5	3.7	223	3	US-09-106-468-13	Sequence 13, Appli
1171	150	3.8	238	6	5180819-4	Patent No. 5180819	1244	146.5	3.7	223	3	US-09-106-466A-13	Sequence 13, Appli
1172	150	3.8	238	6	5180819-4	Patent No. 5180819	1245	146.5	3.7	223	3	US-09-106-467-13	Sequence 13, Appli
1173	150	3.8	263	4	US-09-653-813-2	Sequence 2, Appli	1246	146	3.7	143	4	US-10-067-422-32	Sequence 32, Appli
1174	150	3.8	267	2	US-08-378-404B-46	Sequence 46, Appli	1247	146	3.7	157	3	US-09-518-046-23	Sequence 23, Appli
1175	150	3.8	276	1	US-08-467-155A-1	Sequence 1, Appli	1248	146	3.7	263	4	US-09-653-813-4	Sequence 4, Appli
1176	150	3.8	276	2	US-08-628-198-1	Sequence 1, Appli	1249	146	3.7	263	4	US-09-653-813-6	Sequence 6, Appli
1177	150	3.8	276	3	US-09-201-038-1	Sequence 1, Appli	1250	145.5	3.7	108	4	US-09-341-461-22	Sequence 22, Appli
1178	150	3.8	276	5	PCT-US96-07343-1	Sequence 1, Appli	1251	145.5	3.7	252	3	US-08-906-769-103	Sequence 103, App
1179	150	3.8	276	4	US-09-949-016-11369	Sequence 11369, A	1252	145.5	3.7	252	3	US-08-906-616-103	Sequence 103, App
1180	150	3.8	677	4	US-09-949-016-11370	Sequence 11370, A	1253	145.5	3.7	252	3	US-08-817-795-103	Sequence 103, App
1181	150	3.8	677	4	US-09-949-016-11371	Sequence 11371, A	1254	145.5	3.7	252	3	US-08-639-075A-103	Sequence 103, App
1182	150	3.8	677	4	US-09-949-016-11372	Sequence 11372, A	1255	145.5	3.7	252	3	US-09-012-431-103	Sequence 103, App
1183	149.5	3.8	46	4	US-10-067-422-17	Sequence 17, Appli	1256	145.5	3.7	252	3	US-09-012-692-103	Sequence 103, App
1184	149.5	3.8	385	1	US-08-340-539A-2	Sequence 2, Appli	1257	145.5	3.7	252	3	US-08-906-613-103	Sequence 103, App
1185	149.5	3.8	385	2	US-08-461-592B-2	Sequence 2, Appli	1258	145.5	3.7	252	5	PCT-US95-14442A-103	Sequence 103, App
1186	149.5	3.8	1925	4	US-09-949-016-10403	Sequence 10403, A	1259	145	3.7	110	4	US-09-341-461-21	Sequence 21, Appli
1187	149	3.8	283	1	US-07-906-983-2	Sequence 2, Appli	1260	145	3.7	232	3	US-08-906-769-81	Sequence 81, Appli
1188	149	3.8	575	4	US-09-949-016-11264	Sequence 11264, A	1261	145	3.7	232	3	US-08-906-616-81	Sequence 81, Appli
1189	149	3.8	575	4	US-09-949-016-11265	Sequence 11265, A	1262	145	3.7	232	3	US-08-817-795-81	Sequence 81, Appli
1190	149	3.8	575	4	US-09-949-016-11266	Sequence 11266, A	1263	145	3.7	232	3	US-08-639-075A-81	Sequence 81, Appli
1191	149	3.8	575	4	US-09-949-016-11267	Sequence 11267, A	1264	145	3.7	232	3	US-09-012-431-81	Sequence 81, Appli
1192	149	3.8	806	4	US-09-949-016-11268	Sequence 11268, Ap	1265	145	3.7	232	3	US-09-012-692-81	Sequence 81, Appli
1193	149	3.8	1404	2	US-08-400-159-2	Sequence 2, Appli	1266	145	3.7	232	3	US-08-906-613-81	Sequence 81, Appli
1194	149	3.8	1404	3	US-08-611-729A-2	Sequence 2, Appli	1267	145	3.7	232	5	PCT-US95-14442A-81	Sequence 81, Appli
1195	149	3.8	1404	4	US-09-195-524-2	Sequence 2, Appli	1268	145	3.7	372	2	US-08-513-278-4	Sequence 4, Appli

1269	145	3.7	372	6	5514582-4	Patent No. 5514582	1342	136.5	3.5	224	1	US-08-483-859-12	Sequence 12, Appl
1270	145	3.7	272	6	5514582-4	Patent No. 5514582	1343	136.5	3.5	224	1	US-08-472-173-12	Sequence 12, Appl
1271	144.5	3.7	258	3	US-09-004-731-16	Sequence 16, Appl	1344	136.5	3.5	224	2	US-08-487-167-12	Sequence 12, Appl
1272	144.5	3.7	258	3	US-09-004-731-19	Sequence 19, Appl	1345	136.5	3.5	224	2	US-08-482-816-12	Sequence 12, Appl
1273	144.5	3.7	258	3	US-08-749-699-16	Sequence 16, Appl	1346	136.5	3.5	224	2	US-08-296-149-12	Sequence 12, Appl
1274	144.5	3.7	258	3	US-08-749-699-19	Sequence 19, Appl	1347	136.5	3.5	224	2	US-08-801-499-12	Sequence 12, Appl
1275	144.5	3.7	258	4	US-09-004-729-16	Sequence 16, Appl	1348	136.5	3.5	224	2	US-08-615-271-12	Sequence 12, Appl
1276	144.5	3.7	258	4	US-09-004-729-19	Sequence 19, Appl	1349	136.5	3.5	224	2	US-08-615-271-12	Sequence 12, Appl
1277	144	3.7	163	4	US-09-270-767-60652	Sequence 60652, A	1350	136.5	3.5	224	3	US-09-074-660-12	Sequence 12, Appl
1278	143	3.6	237	3	US-09-004-731-22	Sequence 22, Appl	1351	136.5	3.5	224	3	US-09-106-468-12	Sequence 12, Appl
1279	143	3.6	237	3	US-08-749-699-22	Sequence 22, Appl	1352	136.5	3.5	224	3	US-09-106-468A-12	Sequence 12, Appl
1280	143	3.6	237	4	US-09-004-729-22	Sequence 22, Appl	1353	136.5	3.5	224	3	US-09-106-467-12	Sequence 12, Appl
1281	143	3.6	549	3	US-09-245-041-9	Sequence 9, Appl	1354	136.5	3.5	226	1	US-07-929-198-4	Sequence 4, Appl
1282	143	3.6	549	4	US-09-358-055B-9	Sequence 9, Appl	1355	136.5	3.5	247	2	US-08-978-404B-47	Sequence 1, Appl
1283	143	3.6	549	4	US-09-893-238-9	Sequence 9, Appl	1356	136	3.4	326	2	US-08-640-977-1	Sequence 1, Appl
1284	143	3.6	1260	3	US-09-245-041-2	Sequence 2, Appl	1357	136	3.4	345	4	US-09-976-594-458	Sequence 458, App
1285	143	3.6	1260	4	US-09-358-055B-2	Sequence 2, Appl	1358	135.5	3.4	256	3	US-08-906-769-89	Sequence 89, Appl
1286	143	3.6	1260	4	US-09-893-238-2	Sequence 2, Appl	1359	135.5	3.4	256	3	US-08-906-616-89	Sequence 89, Appl
1287	143	3.6	3075	2	US-08-460-309-5	Sequence 5, Appl	1360	135.5	3.4	256	3	US-08-817-795-89	Sequence 89, Appl
1288	143	3.6	3075	2	US-08-125-077-5	Sequence 5, Appl	1361	135.5	3.4	256	3	US-08-639-075A-89	Sequence 89, Appl
1289	142.5	3.6	226	1	US-07-929-198-6	Sequence 6, Appl	1362	135.5	3.4	256	3	US-09-012-431-89	Sequence 89, Appl
1290	142	3.6	240	2	US-08-824-692-23	Sequence 23, Appl	1363	135.5	3.4	256	3	US-09-012-692-89	Sequence 89, Appl
1291	142	3.6	577	2	US-08-435-149-3	Sequence 3, Appl	1364	135.5	3.4	256	3	US-08-906-613-89	Sequence 89, Appl
1292	142	3.6	611	3	US-09-475-460A-32	Sequence 32, Appl	1365	135.5	3.4	313	4	PCT-US95-1442A-89	Sequence 89, Appl
1293	142	3.6	611	4	US-09-748-061A-32	Sequence 32, Appl	1366	135.5	3.4	313	4	US-09-270-767-44375	Sequence 44375, A
1294	142	3.6	168	1	US-08-537-210A-2	Sequence 2, Appl	1367	135.5	3.4	372	2	US-08-513-278-2	Sequence 2, Appl
1295	142	3.6	168	3	US-09-113-825-2	Sequence 2, Appl	1368	135.5	3.4	372	6	5514582-2	Patent No. 5514582
1296	142	3.6	1480	3	US-09-182-024A-5	Sequence 5, Appl	1369	135.5	3.4	372	6	5514582-2	Patent No. 5514582
1297	141	3.5	226	3	US-08-944-283-41	Sequence 41, Appl	1370	135	3.4	233	2	US-08-738-413B-9	Sequence 9, Appl
1298	140	3.5	148	4	US-09-618-259-2	Sequence 2, Appl	1371	135	3.4	735	3	US-09-191-647-9	Sequence 9, Appl
1299	140	3.5	154	3	US-09-261-416-7	Sequence 7, Appl	1372	135	3.4	735	3	US-09-540-245A-9	Sequence 9, Appl
1300	140	3.5	578	3	US-08-981-392-13	Sequence 13, Appl	1373	135	3.4	735	3	US-09-540-153-9	Sequence 9, Appl
1301	140	3.5	578	4	US-09-508-322-13	Sequence 13, Appl	1374	134.5	3.4	113	4	US-09-341-461-24	Sequence 24, Appl
1302	140	3.5	297	4	US-09-747-371-3	Sequence 3, Appl	1375	134.5	3.4	223	1	US-07-956-848A-41	Sequence 41, Appl
1303	139.5	3.5	207	4	US-09-244-111-4	Sequence 4, Appl	1376	134.5	3.4	223	1	US-08-471-956-41	Sequence 41, Appl
1304	139.5	3.5	214	4	US-09-380-683-57	Sequence 57, Appl	1377	134.5	3.4	304	3	US-09-088-651-2	Sequence 2, Appl
1305	139.5	3.5	256	3	US-09-032-215-32	Sequence 32, Appl	1378	134.5	3.4	1525	3	US-09-191-647-2	Sequence 2, Appl
1306	139	3.5	267	3	US-08-906-769-145	Sequence 145, App	1379	134.5	3.4	1525	3	US-09-540-245A-2	Sequence 2, Appl
1307	139	3.5	267	3	US-08-906-616-145	Sequence 145, App	1380	134.5	3.4	1525	2	US-09-540-153-2	Sequence 2, Appl
1308	139	3.5	267	3	US-08-639-075A-145	Sequence 145, App	1381	134	3.4	266	2	US-08-640-977-4	Sequence 4, Appl
1309	139	3.5	267	3	US-09-004-731-67	Sequence 67, Appl	1382	134	3.4	1656	4	US-09-949-016-7247	Sequence 7247, App
1310	139	3.5	267	3	US-09-012-431-145	Sequence 145, App	1383	134	3.4	1821	4	US-09-949-016-5938	Sequence 5938, App
1311	139	3.5	267	3	US-08-749-699-67	Sequence 67, Appl	1384	133.5	3.4	290	2	US-08-824-692-29	Sequence 29, Appl
1312	139	3.5	267	3	US-09-012-692-145	Sequence 145, App	1385	133	3.4	248	3	US-08-640-977-2	Sequence 2, Appl
1313	139	3.5	267	3	US-08-906-613-145	Sequence 145, App	1386	132	3.3	110	4	US-09-341-461-26	Sequence 26, Appl
1314	139	3.5	267	4	US-09-004-729-67	Sequence 67, Appl	1387	132	3.3	112	4	US-09-341-461-34	Sequence 34, Appl
1315	139	3.5	495	4	US-10-006-011A-4	Sequence 4, Appl	1388	132	3.3	119	4	US-09-438-046-24	Sequence 24, Appl
1316	139	3.5	705	4	US-10-006-011A-3	Sequence 3, Appl	1389	132	3.3	159	3	US-09-020-956-172	Sequence 172, App
1317	139	3.5	1139	1	US-08-537-210A-4	Sequence 4, Appl	1390	132	3.3	159	3	US-09-030-607-172	Sequence 172, App
1318	139	3.5	1139	3	US-09-113-825-4	Sequence 4, Appl	1391	132	3.3	159	3	US-09-439-313-172	Sequence 172, App
1319	138.5	3.5	1139	3	US-09-518-046-22	Sequence 22, Appl	1392	132	3.3	159	3	US-09-352-616A-172	Sequence 172, App
1320	138.5	3.5	226	1	US-07-929-198-2	Sequence 2, Appl	1393	132	3.3	159	4	US-09-232-149A-172	Sequence 172, App
1321	138.5	3.5	226	2	US-08-557-146-15	Sequence 15, Appl	1394	132	3.3	159	4	US-09-159-812-172	Sequence 172, App
1322	138.5	3.5	226	2	US-09-154-344-15	Sequence 15, Appl	1395	132	3.3	159	4	US-09-636-215-172	Sequence 172, App
1323	138.5	3.5	226	3	US-08-944-483-43	Sequence 43, Appl	1396	132	3.3	159	4	US-09-685-166A-172	Sequence 172, App
1324	138.5	3.5	260	3	US-08-983-075D-9	Sequence 9, Appl	1397	132	3.3	159	4	US-09-115-453-172	Sequence 172, App
1325	138	3.5	182	4	US-09-328-925-12	Sequence 12, Appl	1398	132	3.3	159	4	US-09-688-489-172	Sequence 172, App
1326	138	3.5	216	3	US-08-824-692-24	Sequence 24, Appl	1399	132	3.3	159	4	US-09-679-426-172	Sequence 172, App
1327	138	3.5	249	3	US-09-578-303-2	Sequence 2, Appl	1400	132	3.3	159	4	US-09-759-143-172	Sequence 172, App
1328	138	3.5	253	3	US-08-906-769-131	Sequence 131, App	1401	132	3.3	159	4	US-09-651-236-838	Sequence 838, App
1329	138	3.5	253	3	US-08-906-616-131	Sequence 131, App	1402	132	3.3	166	4	US-09-636-215-838	Sequence 838, App
1330	138	3.5	253	3	US-08-639-075A-131	Sequence 131, App	1403	132	3.3	166	4	US-09-685-166A-838	Sequence 838, App
1331	138	3.5	253	3	US-09-012-431-131	Sequence 131, App	1404	132	3.3	166	4	US-09-679-426-838	Sequence 838, App
1332	138	3.5	253	3	US-09-012-692-131	Sequence 131, App	1405	132	3.3	166	4	US-09-759-143-838	Sequence 838, App
1333	138	3.5	253	3	US-08-906-613-131	Sequence 131, App	1406	132	3.3	166	4	US-09-651-236-838	Sequence 838, App
1334	138	3.5	291	1	US-08-467-155A-11	Sequence 11, Appl	1407	131.5	3.3	215	4	US-09-612-314A-33	Sequence 33, Appl
1335	138	3.5	291	2	US-08-628-198-11	Sequence 11, Appl	1408	131.5	3.3	810	2	US-08-820-170A-34	Sequence 34, Appl
1336	138	3.5	291	3	US-09-301-038-11	Sequence 11, Appl	1409	131.5	3.3	810	3	US-09-055-699-34	Sequence 34, Appl
1337	138	3.5	291	5	PCT-US96-07343-11	Sequence 11, Appl	1410	131.5	3.3	810	3	US-09-273-565-34	Sequence 34, Appl
1338	138	3.5	345	4	US-09-000-489-106	Sequence 106, App	1411	131.5	3.3	810	3	US-09-565-538-34	Sequence 34, Appl
1339	138	3.5	583	4	US-09-641-612-2	Sequence 2, Appl	1412	131.5	3.3	810	3	US-09-661-468-34	Sequence 34, Appl
1340	136.5	3.5	109	4	US-09-341-461-33	Sequence 33, Appl	1413	131.5	3.3	810	3	US-09-976-165-34	Sequence 34, Appl
1341	136.5	3.5	224	1	US-08-278-091-12	Sequence 12, Appl	1414	131	3.3	219	2	US-08-925-708-2	Sequence 2, Appl


```
451 NITAPKTQGLRWPQAAIYRRTSGVHDSGLHGKAMFLVCSGALVNRVTVAACHCVDLIG 510
|||||
301 NITAPKTQGLRWPQAAIYRRTSGVHDSGLHGKAMFLVCSGALVNRVTVAACHCVDLIG 360
|||||
511 KVTMIKTADLVKVLGKFRDDEKTIQSLQISAILLHPNYDPILLDDADIAILLKLLDKA 570
|||||
361 KVTMIKTADLVKVLGKFRDDEKTIQSLQISAILLHPNYDPILLDDADIAILLKLLDKA 420
|||||
571 RISTRVQPICLAASRDLSFQESHITVAGWNLADVRSPGKNDTLRSVVVDSLLC 630
|||||
421 RISTRVQPICLAASRDLSFQESHITVAGWNLADVRSPGKNDTLRSVVVDSLLR 480
|||||
631 EQHEDHGIPVSDTNMFCASWEPTAPSDICTAETGGIAAVFPGRASPEPRWHLMLGLVS 690
|||||
481 EQHEDHGIPVSDTNMFCASWEPTAPSDICTAETGGIAAVFPGRASPEPRWHLMLGLVS 540
|||||
691 WSYDKTCSHRLSTAPTKVLPFKDWIERNMK 720
|||||
541 WSYDKTCSHRLSTAPTKVLPFKDWIERNMK 570
|||||

RESULT 2
US-08-296-014A-4
; Sequence 4, Application US/08296014A
; Patent No. 5716834
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: Ho, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,014A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1019 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-296-014A-4

Query Match 16.9%; Score 665; DB 1; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.7e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

34 PGAEWIMCECEYDQIECVCFGKEE-----VVGYYTIPCCRNEENECDSCLIH 82
184 PNGQWNPFPKICR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCDS----- 229
83 PGCTIFENCKSCR-NGSWGCTL----- 103
```

```
Db 230 PYYLIGQETLTCQNGQWNGQIPQCKNLVFCPLDLPVNAHAEHKVIGVEQKYGFQPGTE 289
|||||
QY 104 -----DQFYVKGFCACR--AGMYGG--DCMR-----CGQVLR-- 133
|||||
Db 290 VYTTCGNYFLMGFTLCKNPDGSGSGSQPSCVKVADREVCDCSKAVDFLDDVGEVRIH 349
|||||
QY 134 APKGQILLSE-----YPLNAHCEWTHA-----KPGFVI----- 162
|||||
Db 350 CPAGCSLITAGTWGTATYHELSSVCEAAIHACKLPNSGGAVHVNNPGVSDFLGSLNGI 409
|||||
QY 163 ---QURFVMLSLEFDYM-----COYDYVEVRD-----GDNRDGQIIKRVCGN--E 202
|||||
Db 410 KSEELKSLARSFRFDYVRSSTAGKSGCPDGMFEVDENCYVVTSKORAWERAQGVCTNMAA 469
|||||
QY 203 RAPATQS--IGSSLHVLPHSDG--SKNFDGFF-----AIYEETIACSS 241
|||||
Db 470 RLAVLDKDVIPNSLTETLRLGKGLTTTWIGLHRLDAEKPIWELMDORSNVVLDNLTFWAS 529
|||||
QY 242 SPCFHDGTCVL---DKAGS--YKCAACLAGYTGQRCENLLEERN---CSDPGGPGVNGYQKI 293
|||||
Db 530 GEPGNETCVYMDIQDQLQSVWTKSCFPQSSPACWMDLSDRNKAACDDPGSLENGHATL 589
|||||
QY 294 TCGPGLINGRHAIGITVVSFFCNNSYVLGSGNKRKTCQNGEWSGKQPICIK--ACREPKI 351
|||||
Db 590 HGQS--IDGFYA--GSSIRYSCVHLHSLGTETVTCTTGTWSAPKPRCIVKITCONPPV 645
|||||
QY 352 SDLVRRRLPMQVQSRRETPHLQLYSAAFSKQLQ---SAPTKKPALPFGD----- 398
|||||
Db 646 PYSGSVEIKP---PSRTNSISRVGPFLLRPLPLPLARAAPPPKPRSSQSTVDLASK 702
|||||
QY 399 --LPMGYQHLHTQLOVEICISPFYRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455
|||||
Db 703 VKLPEGHYVGSRAIYTCESRYEYELLGSGQRCDSNGNWSGRAPASCIPVCGRSDSPSPF 762
|||||
QY 456 -----KTOGLRWPQAAIYRRTSGVHDSGLHGKAMFLVCSGALVNRVTVAACHCVDLIG 510
|||||
Db 763 IWNNGNSTEIGQWPQAGISRWLA-----DHNMFQCGGSLNKEKWIATAHCVTYSA 815
|||||
QY 511 KVTMIKTADLVKVLGKFRDDEKTIQSLQISAILLHPNYDPILLDDADIAILLKLLDKA 570
|||||
Db 816 TAEIIDPNQFKYGLGYNDSDRDDDYQVRRSALEIHNPNPDGPNLNFDAIQLKTPV 875
|||||
QY 571 RISTRVQPICLAASRDLSFQESHITVAGWNLADVRSPGKNDTLRSVVV 624
|||||
Db 876 TLITTRVQPICLPT--DITF---REHLKEGTAVVTGAG---LNENNTYSETIQQAVLPV 926
|||||
QY 625 VDSLICEQEHEDHGIPVSDTNMFCASWEPTAPSDICTAETGGIAAVFPGRASPEPRWH 684
|||||
Db 927 VAASTCEGYKEADLPITVTENNFCAGYK--KGRYDACSGLSGG--PLVFADDSRTERRWV 983
|||||
QY 685 LMGLYSWSYDKTCSH--RLSTAPTKVLPFKDWIER 717
|||||
Db 984 LEGIVSWGSPSGCGKANQYGGFTKVNFLSWIRQ 1017
|||||

RESULT 3
US-08-596-405-4
; Sequence 4, Application US/08596405
; Patent No. 5858706
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: Ho, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
```


ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,405
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1781-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-596-405-4

Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.7e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAENIMCECEVDQIECVCPGKRE-----VGYTIPCCRNNEECDSCLIH 82
DB 184 PNGQSNFPKICR-----ECAMVSPHEGKVNALSGDMIEGATL-----RFSCHS---- 229
QY 83 PCTIFENCKSCR-NGSWGTL----- 103
DB 230 PYLIGQETLTCOGNGMGQIPQCKNLVCPDLPDVPNHAHKVIGVEKYGQFPQGT 289
QY 104 -----DPFVVGFGCAECR--AGMYGG--DCWR-----CGQVLR-- 133
DB 290 VYTCGNYVFLMGFTLCKNPDGWSGQSCVKVADREVDCDSKAVDFLDDVGSPVRIH 349
QY 134 APKQILLES-----YPLNAHCETIHA-----KPGFVI----- 162
DB 350 CPAGCSLTAGTGWGTATVHELSSVCRAAHAGKLPNSGGAVHVNNGPYSDPLGSLNGI 409
QY 163 ---QLRFVNLSEEDYM-----COYDYVEVRD-----GDNRDQIIRKVCN--E 202
DB 410 KSEELKSLARSPRFYVRSSTAGKCGCPDGWFVEVDENVYVTSKORAMERAGQVCTNMAA 469
QY 203 RPAIQS--IGSSLHVLPHSDG-SKNFDGFH-----AIYEEITACSS 241
DB 470 RLAVLDKQVINSLTETLGGKLTWTWGLRLDAEKPIWELMDRSNVVLDNLTFFAS 529
QY 242 SPCPHDGTCLV---DKAGS--YKACLAGYTQRCENLLEERN---CSDPGGPVNGYQKI 293
DB 530 GEPGNETNCVYMDIQDQLQSVKTKSCFQPSFACWMDLSRDKAKCDDPGSLENGHATL 589
QY 294 TCGPGLINGRHAKIGTIVSFFCWNYSVLGNKERTCOQNGEWSGKPICIK--ACREPKI 351
DB 590 HQQS--IDGFYA--GSSIRYSCEVLHLSGTETVCTTGTWTSAPKPCIKVITCONPPV 645
QY 352 SDLVRRRLPMQVQSRPTPLHLYSAAFSKQLQ---SAPTKKPALPFGD----- 398
DB 646 PSYGVEIKP---PRTNSIRVGPFPLRLPLPLPLAARAPPPKPRSSQSTVDLASK 702
QY 399 ---LPMGYQHLHTQLOYEICISPFYRLGSSRRTLRTGKWSGRAPSCIPICGKIENITAP- 455
DB 703 VKLPEGHYRVGSRAIYTCESRYELLGSGRRCDNSGNWSGRPASCIPVCGRSDSPSPF 762
QY 456 -----KTQGLRWPQAAIYRRTSGVHDGSLHKGANFLVCSGALVNERVTVAHCVTDLG 510
DB 763 IWNNGNSTIGWPQWQAGISRWLA-----DHNMFLOCGGSLLEKRWITVAHCVTYS 815

QY 511 KVTMIKTADLVKVLGKYRDDDRDEKTIQSLQISAIILHPNYDPILLDADIALKLDKA 570
DB 816 TAEIIDPNQFKMYLGGYRDDSDDDYVQVREALEIHVNPNDPGNLFNFDIALIQLKTPV 875
QY 571 RISTRVOPICLAASRDLSFQESH-----TVAGWVNLADVRSPGFKNDILRSQVSV 624
DB 876 TLTRVQPICLPT--DITT---REHLKEGTLAVVTGWMG---LNENNTYSETIQQAVLPV 926
QY 625 VDSLLCEEQHEHDGIPVSVTDNMFCASWEPTAPSDICTAETGIAAIVSPFGRASPEPRWH 684
DB 927 VAASTCEEGYKADPLTWTENNFCAGYK-KGRYDACSDSG--PLVFADDSRTERRWV 983
QY 685 LMGLVSWSYDKTCSH-RLSTAFTKVLPFKDWIER 717
DB 984 LEGIVSWGSPSGCGKANQYGGFTKVNVLFWIRQ 1017

RESULT 4
US-08-877-620-4
Sequence 4, Application US/08877620
Patent No. 5985590
GENERAL INFORMATION:
APPLICANT: Ding, Jeak Ling
APPLICANT: HO, Bow
TITLE OF INVENTION: The Cloned Factor C cDNA of the
TITLE OF INVENTION: Singapore Horshoe Crab, Carinoscorpius
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Birch, Stewart, Kolasch & Birch
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/877,620
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/596,405
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1781-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-877-620-4

Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.7e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAENIMCECEVDQIECVCPGKRE-----VGYTIPCCRNNEECDSCLIH 82
DB 184 PNGQSNFPKICR-----ECAMVSPHEGKVNALSGDMIEGATL-----RFSCHS---- 229
QY 83 PCTIFENCKSCR-NGSWGTL----- 103


```
Db 984 LEGIVSWGSPSCGKXANQYGGTKVNFVLSWIRQ 1017

RESULT 6
US-09-626-795-4
; Sequence 4, Application US/09626795
; Patent No. 6719973
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: HO, Bow
; TITLE OF INVENTION: Use of Recombinant Factor C to Induce Bacteriostasis
; FILE REFERENCE: 4810-61737
; CURRENT APPLICATION NUMBER: US/09/626,795
; CURRENT FILING DATE: 2000-07-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Carcinoscopus rotundicauda
US-09-626-795-4

Query Match 16.9%; Score 665; DB 4; Length 1019;
Best Local Similarity 25.4%; Pred No. 1.7e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGEAWNIMRECCEYDQIECVCPGKRE-----VVGTYIPCCRNNEECDSCLTH 82
Db 184 PNGQSNPPPKCIR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCHS-----229
QY 83 PCTIFENCKSCR-NGSWGGLT-----103
Db 230 PYLLIGQETLTCQGNQWNGQIPQCKNLVFCPLDPVNAEHKVKIGVEQKYQFPQGTG 289
QY 104 -----DPPYKGFYCAECR--AGWYGG--DCMR-----CGQVLR--133
Db 290 VTYTCGNYFLMGFTLCKNPDGWSGSPQSCVKVADREVDCDSKAVDFLDDVGPVRIH 349
QY 134 APKGOILLES-----YPLNAHCEWTIHA-----KPGFVI-----162
Db 350 CPAGCSLTAGTGWGTATYHVELSSVCRAAHAGKLPNSGGAVHVNNPVSDPLGSLDNGI 409
QY 163 ---QLRFVLSLEFDYM-----CQDYVEVRD-----GDRDQGIKRVCGN--E 202
Db 410 KSEELKSLARSFRFVRSSTAGSKGCPDGMFEVDENVYVTSKQAWERAQGVCTNMAA 469
QY 203 RPAPIQS--IGSSLVHLFHSFG-SKNFDGFH-----AIVEEITACSS 241
Db 470 RLAVLDKQVLPNSLTETLKGGLTTTWIGLHRLDAEKPIWELMDRSNVVLDNLTFFAS 529
QY 242 SPCHFHDGTCVL-----DKAGS-YKACLAGYTCQRCENLLEERN-----CSDPGGPNVNGYQKI 293
Db 530 GEPGNETCVYMDIQDQLSQVWTKSCFPQSPSFACWMDLSDRNKAACDDPGSLENGHATL 589
QY 294 TGGPGLNGRHAKIGTVVSFFPCNNYSVLGSGNEKRTCOQNGEWSGKQPCIK--ACREPKI 351
Db 590 HQQS--IDGFYA--GSSIRYSEVLHLSGTETVCTTNGTWSAPKRCIKVITCQNPV 645
QY 352 SDLVRRRLPMQVQSRPTPLHLYSAFSSKQKLO--SAPTKKPALPFGD-----398
Db 646 PSYGVEIKP---PRTSISVSGPFFLRPLPLPLARAAKPPKPRSSQBSTVDLASK 702
QY 399 --LPMGYOHLHTQLOECISPPYRRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455
Db 703 VKLPGHYRVGSRAIYTCESRYELLGSGRCDSNGNWSGRPASCIPVCGRSDSPRPF 762
QY 456 -----KTQGLRWPQAAIYRRTSGVHDSGLHGAWFLVCSGALVNERTVVAHCVTDLG 510
Db 763 IWNNGNSTEIGWPQWQAGISRLA-----DHNMFLOCGSLLNEKMWIVTAAHCVTYS 815
QY 511 KVTMIKTADLVKLVKFRDDEKTKTQSLQISAILHPNYDPIILLADTALIKLLDKA 570
Db 816 TABIIDPNQFKMYLKGKYYRDRDDYVQVREALEIHVNPNDYDGNLNFIALIQLKTPV 875

QY 571 RISTRVQPICLAASRLSTSFQESH-----TVAGMNVLADVRSPGPKNDLTRSGVSV 624
Db 876 TLTRTRVQPICLPT--DITT---REHLKEGTLAAVVTGWM---LNENNTYSETIQAVLPV 926
QY 625 VDSLCEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGCGIAAVSPGRASPEPRWH 684
Db 927 VAASTCEBGYKEADLPLVTENMFCAGYK-KGRYDACSGDSGG--PLVFADDSRTERRW 983
QY 685 LMGLVSWSYDKTCSH-RLSTAFTKVLPFKDWIER 717
Db 984 LEGIVSWGSPSCGKXANQYGGTKVNFVLSWIRQ 1017

RESULT 7
US-08-296-014A-2
; Sequence 2, Application US/08296014A
; Patent No. 5716834
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: HO, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horsehoe Crab, Carcinoscopus
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,014A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1083 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-296-014A-2

Query Match 16.9%; Score 665; DB 1; Length 1083;
Best Local Similarity 25.4%; Pred No. 1.8e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGEAWNIMRECCEYDQIECVCPGKRE-----VVGTYIPCCRNNEECDSCLTH 82
Db 248 PNGQSNPPPKCIR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCHS-----293
QY 83 PCTIFENCKSCR-NGSWGGLT-----103
Db 294 PYLLIGQETLTCQGNQWNGQIPQCKNLVFCPLDPVNAEHKVKIGVEQKYQFPQGTG 353
QY 104 -----DPPYKGFYCAECR--AGWYGG--DCMR-----CGQVLR--133
Db 354 VTYTCGNYFLMGFTLCKNPDGWSGSPQSCVKVADREVDCDSKAVDFLDDVGPVRIH 413
```

```
QY' 134 APKGQILLES-----YPLNAHCEWTHA---KPGFVI----- 162
Db 414 CPAGCSLTAGTWGTAIYHELSSVCRAAHAGKLPNSGAVHVNNGPYSDFLGLDLNGI 473
QY 163 ---QLRFVMSLEFDYM-----CQDYVEVRD-----GDNRDGQI1KRVCN--E 202
Db 474 KSEELKSLARSFRFDYSSSTAGKSCPDGWFEDVENCYVVTSKQRAWERAQGVCTNMAA 533
QY 203 RPAPQOS--IGSSLHVLPHSDG-SKNFDGFH-----AIYEETACSS 241
Db 534 RLAVLDKQVIPNSLTETLKGKGLTTWIGLHRLDAEKPFIWELMDRNVVLDNLTFWAS 593
QY 242 SPCFHDGTCVL---DKAGS--YKACLAGYTCQRCENLLEERN---CSDPGGPNVGYQKI 293
Db 594 GEPGNETNCVYMDIQDLQSVWMTKSCFQPSFACMMDLSDRNKAACDDPGSLENGHATL 653
QY 294 TCGPGLINGRHAKIGTVVSFFCNNSYVLGSGNEKRTCCQNGEWSGKQPICIK--ACREPRI 351
Db 654 HQQS--IDGFYA--GSSIRYCEVLHYLSTGTETVCTTGTWSAPKRCIKVITCONPPV 709
QY 352 SDLVRRRLPMQVQSRRETPHOLYSAAFSKQKLO---SAPTKKPALPFGD----- 398
Db 710 PSYGSVEIKP---PRTNSISRVGSPFLRLPLPLARAAKPPPKPRSSQPSSTDVLDASK 766
QY 399 --LPMGYOHLHTQLOVEICISPFYRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455
Db 767 VKLPEGHYRVGSRATYTCESRYELLGSGRRCDNSNGNWSGRPASCPVCGRSDSPRSPF 826
QY 456 -----KTQGLRWPQAAIYRRTSGVHDGSLHKGAMFLVCSGALVNERTVVVAACHVTDLG 510
Db 827 IWNNGNSTEIGQWPQAGISRWLA-----DHNMFQCGGSLLEKWIIVTAACHVTVSA 879
QY 511 KYTMKTADLKVLGKFRDDEKTIQSLQISAILHPNYDPILLDADIALKLLDKA 570
Db 880 THAIEDPNQFMYLGYKYRDDSDDDYVQVREALEIHNPNYDPGNLNFADIALIQLKTPV 939
QY 571 RISTRVQPICLAASRDLSFQESH1-----TVAGNVLADVRSFGKNDLRSQVSV 624
Db 1048 LEGIVSWGSPSGCGKANQYGGFTKVNVLFWIRQ 1081
```

RESULT 8

```
US-08-596-405-2
; Sequence 2, Application US/08596405
; Patent No. 5858706
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 810 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

Db 940 TLTRVQPICLPT--DITT--REHLKEGTAVVTCWG-----LNENNTYSETIQAVLPV 990
QY 625 VDSLCEQHEHDGIPVSVTDNMFCASWEPTAPSDICTAETGCGIAAVSPGGRASPEPRWH 684
Db 991 VAASTCEGKYKADPLPLTVTENMFCAGYK-KGRYDACSDDSG--PLVFADDSRTERRVW 1047
QY 685 LMLVSWSYDKTCSH-RLSTATKVLPPFKDWIER 717
Db 1048 LEGIVSWGSPSGCGKANQYGGFTKVNFLSWIRQ 1081

RESULT 9
US-08-877-620-2
; Sequence 2, Application US/08877620
; Patent No. 5985590
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: Ho, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,620
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/596,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1083 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-877-620-2

Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.8e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PCAEWNIMCRECEYDQIECVCGKRE-----VVGYTIPCCRNEECDSCLTH 82
Db 248 PNGQSNPPPKCIR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RSCDS----- 293
QY 83 PCTTFENCKSCR-NGSWGGLT----- 103
Db 294 PYLLIGQETLTCCQGNQWGOIPQCKNLVFCPLDVPVNHAEHKVIGVEQKYQPQGTG 353
QY 104 -----DPPYKGFYCAECR--AGWYGG--DCWR-----CGQVLR-- 133
Db 354 VTYTCGNYFLMGFTLCKNPGSWGSGQSPCKVADREVDCDSKAVDFLDDVGSPVRIH 413

QY 134 APKQIILLES-----YPLNAHCEWTIHA-----KPGFVI----- 162
Db 414 CPAGSLTAGTVMGTAIYHELSSVCRAAHAGKLPNSGAVHVNPNPGYSDFLGLSLNGI 473
QY 163 ---QLRFVWLSLEFDVM-----CQDYVVEVRD-----GDNRDGOIKRVCGN--E 202
Db 474 KSEELKSLARSFRFDYVSSSTAGKSGCPDGFVEVDCNVCYVTSKQRAWERAQVCTNMAA 533
QY 203 RPAPIQS--IGSSLHLVPHSDG-SKNFDGFH-----AIYEETPACSS 241
Db 534 RLAVLDKDVIPNSLTETLRGKGLTTTWIGLHRLDAEKPFIMELMDRSNVVLDNLTFWAS 593
QY 242 SPCFHDGTCVL-----DKAGS-YKACLAGYTCQRCENLEERN-----CSPGPGPVNGYQKI 293
Db 594 GEPGNETNCVYMDIQDLQSVNMTKSCFCQSSSFACMMDLSRDKAKACDIPGSLNGHATL 653
QY 294 TGGPGLINGRAKIGTVVSVFCNNSVLSGNKRTCOQNGEWSGKQPICIK--ACREPKI 351
Db 654 HGQS--IDGFYA--GSSRYSCVHLHLSGTVTCTTNGTWSAPKPRCIKIVTCQNPV 709
QY 352 SDLVRRVRLPMQVQSRQETPLHQLYSAAFSKQLQ---SAPTKKPALPFGD----- 398
Db 710 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLPLABAAKPPPKPRSSQSPSTVDLASK 766
QY 399 ---LPMGYOHLHTQLOEYCISPPYRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455
Db 767 VKLPEGHYRVGSRATYTCESRYEYELGSGRRCDNSGNMWSGRPASCIPVCGRSDSPSPF 826
QY 456 -----KTQGLRWPQAAIYRRTSGVHDGSLHKGANFLVCSGALVNERTVVAAHCVTDLG 510
Db 827 IWNGSTIEIGMPWQAGISWLA-----DHNMFQCGGSLLEKWIIVTAHCVTYSA 879
QY 511 KVTMIKTADLVKLVKPYRDDDRDEKTIQSLQISAIILHPNYDPIILLDDAIALLKLDKA 570
Db 880 TAEIIDPNQFKMYLGYRDDSDDDYVQVREALSHVNPVNDPGLNLFADIALIQLKTPV 939
QY 571 RISTRVQPICLAAASRDLSTSFQESHI-----TVAGNVLADVRSFGKNDTLRSQVSV 624
Db 940 TLTRVQPICLPT--DITT--REHLKEGTAVVTCWG-----LNENNTYSETIQAVLPV 990
QY 625 VDSLCEQHEHDGIPVSVTDNMFCASWEPTAPSDICTAETGCGIAAVSPGGRASPEPRWH 684
Db 991 VAASTCEGKYKADPLPLTVTENMFCAGYK-KGRYDACSDDSG--PLVFADDSRTERRVW 1047
QY 685 LMLVSWSYDKTCSH-RLSTATKVLPPFKDWIER 717
Db 1048 LEGIVSWGSPSGCGKANQYGGFTKVNFLSWIRQ 1081

RESULT 10
US-09-287-368-2
; Sequence 2, Application US/09287368A
; Patent No. 6645724
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: Ho, Bow
; TITLE OF INVENTION: Assays for Endotoxin and Methods for Removal of Endotoxin
; TITLE OF INVENTION: from a Sample Using Recombinant Factor C
; FILE REFERENCE: 1781-0165P
; CURRENT APPLICATION NUMBER: US/09/287,368A
; CURRENT FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: 09/201,786
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/081,767
; EARLIER FILING DATE: 1998-05-21
; EARLIER APPLICATION NUMBER: 60/058,816
; EARLIER FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Carinoscorpius rotundicauda

FEATURE:
; OTHER INFORMATION: any n or Xaa = Unknown
US-09-287-368-2

Query Match 16.9%; Score 665; DB 4; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.8e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;
QY 34 PGAENINMRECEVDQIECVCPGKRE-----VVGTYIPCCRNEECDSCLIH 82
DB 248 PNGQNSNPPKIR-----ECAMVSPHEGKVNALSGDMIEGATL-----RFSCHS----- 293
QY 83 PGCTIFENCKSCR-NGSWGTL-----VPLNAHCEWTHA-----KPGFVI----- 103
DB 294 PYLIGQETLTCQNGQWNGQIPQCKNLVFCPLDLPVNAHAEKVKIGVEQKYQPPQGT 353
QY 104 -----DDPYVKGFCYCAECR--AGWYGG--DCMR-----CGQVLR-- 133
DB 354 VTYTCGNYFLMGFTLCKNPDGWSGQSPCKVADREVDCDSKAVDFLDDVGPVRIH 413
QY 134 APKQIILLES-----YPLNAHCEWTHA-----KPGFVI----- 162
DB 414 CPAGCSLTAAGTWGTAIYHELSSVCRAAHAGKLPNSGGAHVNVNPGYDFLGLSLNGI 473
QY 163 ---QLRFVMLSLEEDYM-----CQDYVVEVRD-----GDNRDGQIIKRVCGN--E 202
DB 474 KSEELKSLARSFRFDYVSSSTAGKSGCPDGWEFVENCYVVTSKORAWERAQGVCTNMAA 533
QY 203 RPAPQOS--IGSSLHVLPHSDG-SKNFDGFH-----AIYEETACSS 241
DB 534 RLAVLDKDVIPNSLTETLKGKLTITWIGLRLDAEKPFIMELMDRSNVVLDNLTFWAS 593
QY 242 SPCHDGTGCVL---DKAGS--YKACLAGYTCQRCENLLEERN---CSDPGGPVNGYQKI 293
DB 594 GEPGNETNCVYMDIQDQLQSVWTKSCFPSPSFACWMDLSRDKAKCDDPGSLENGHATL 653
QY 294 TGGPGLINGRAHAKIGTVVSVFFCNNSYVLSGNEKRTCCQNGEWSGKQIPCIK--ACREPKI 351
DB 654 HQQS--IDGFYA--GSSIRYSEVLHLSGTETVTCTTNGTWSAPKPRCIVKITCQNPV 709
QY 352 SDLVRRRVLPQVQSRPETHLYSAAFSKQKIQ---SAPTKKPALPFGD----- 398
DB 710 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLPLARAAKPPPKPRSSQSPSTVDLASK 766
QY 399 ---LPMGYQHLHQLQVEICISPFYRLGSSRRCLRTGKWSGRAPSCIPICGKIENITAP- 455
DB 767 VKLPEGHYRVSRAIYTCESRYEYELLSQGRCDNSGNWSGRAPASCIPIVCGRSDSPSPF 826
QY 456 ----KTOGLRWPQWQAGISRWLA-----DHNMFQCGGSLNKKWIVTAACHVITYSA 879
DB 827 IWNGNSTEIGQWQWQAGISRWLA-----DHNMFQCGGSLNKKWIVTAACHVITYSA 879
QY 511 KYTMIKTADLKVVLGKFRYDDDRDEKTIQSLQISAILHPNYDPIILLDADIALKLLDKA 570
DB 880 TAEIIDPNQFKYLGKRYDDSDDDYVQVREALEIHVNPNDPGLNFDIALIQLKTPV 939
QY 571 RISTRVQPICLAASRDLSFQESH-----TVAGNVLDVRSFGKNDTLRSQVSV 624
DB 940 TLTRVQPICLPT--DITT---REHLKEGTAVVTGCG---LNENNTYSETIQAVL 990
QY 625 VDSLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGIIAAVSPGGRASPRVH 684
DB 991 VAASTCEEGKEADLPLTVTENMFCAGYK-KGRYDACSQSGS--PLVFADDSRTERRV 1047
QY 685 LMLGVSSDKTCSH-RLSTAFTKVLFPKDWIER 717
DB 1048 LEGIVSGSPSGCKANQYGFTKVNVFLSWIRQ 1081

RESULT 11
US-09-626-795-2
; Sequence 2, Application US/09626795
; Patent No. 6719973

GENERAL INFORMATION:
; APPLICANT: DING, Jeak Ling
; TITLE OF INVENTION: Use of Recombinant Factor C to Induce Bacteriostasis
; FILE REFERENCE: 4810-61737
; CURRENT APPLICATION NUMBER: US/09/626,795
; CURRENT FILING DATE: 2000-07-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Carinoscorpius rotundicauda
US-09-626-795-2

Query Match 16.9%; Score 665; DB 4; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.8e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;
QY 34 PGAENINMRECEVDQIECVCPGKRE-----VVGTYIPCCRNEECDSCLIH 82
DB 248 PNGQNSNPPKIR-----ECAMVSPHEGKVNALSGDMIEGATL-----RFSCHS----- 293
QY 83 PGCTIFENCKSCR-NGSWGTL-----VPLNAHCEWTHA-----KPGFVI----- 103
DB 294 PYLIGQETLTCQNGQWNGQIPQCKNLVFCPLDLPVNAHAEKVKIGVEQKYQPPQGT 353
QY 104 -----DDPYVKGFCYCAECR--AGWYGG--DCMR-----CGQVLR-- 133
DB 354 VTYTCGNYFLMGFTLCKNPDGWSGQSPCKVADREVDCDSKAVDFLDDVGPVRIH 413
QY 134 APKQIILLES-----YPLNAHCEWTHA-----KPGFVI----- 162
DB 414 CPAGCSLTAAGTWGTAIYHELSSVCRAAHAGKLPNSGGAHVNVNPGYDFLGLSLNGI 473
QY 163 ---QLRFVMLSLEEDYM-----CQDYVVEVRD-----GDNRDGQIIKRVCGN--E 202
DB 474 KSEELKSLARSFRFDYVSSSTAGKSGCPDGWEFVENCYVVTSKORAWERAQGVCTNMAA 533
QY 203 RPAPQOS--IGSSLHVLPHSDG-SKNFDGFH-----AIYEETACSS 241
DB 534 RLAVLDKDVIPNSLTETLKGKLTITWIGLRLDAEKPFIMELMDRSNVVLDNLTFWAS 593
QY 242 SPCHDGTGCVL---DKAGS--YKACLAGYTCQRCENLLEERN---CSDPGGPVNGYQKI 293
DB 594 GEPGNETNCVYMDIQDQLQSVWTKSCFPSPSFACWMDLSRDKAKCDDPGSLENGHATL 653
QY 294 TGGPGLINGRAHAKIGTVVSVFFCNNSYVLSGNEKRTCCQNGEWSGKQIPCIK--ACREPKI 351
DB 654 HQQS--IDGFYA--GSSIRYSEVLHLSGTETVTCTTNGTWSAPKPRCIVKITCQNPV 709
QY 352 SDLVRRRVLPQVQSRPETHLYSAAFSKQKIQ---SAPTKKPALPFGD----- 398
DB 710 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLPLARAAKPPPKPRSSQSPSTVDLASK 766
QY 399 ---LPMGYQHLHQLQVEICISPFYRLGSSRRCLRTGKWSGRAPSCIPICGKIENITAP- 455
DB 767 VKLPEGHYRVSRAIYTCESRYEYELLSQGRCDNSGNWSGRAPASCIPIVCGRSDSPSPF 826
QY 456 ----KTOGLRWPQWQAGISRWLA-----DHNMFQCGGSLNKKWIVTAACHVITYSA 879
DB 827 IWNGNSTEIGQWQWQAGISRWLA-----DHNMFQCGGSLNKKWIVTAACHVITYSA 879
QY 511 KYTMIKTADLKVVLGKFRYDDDRDEKTIQSLQISAILHPNYDPIILLDADIALKLLDKA 570
DB 880 TAEIIDPNQFKYLGKRYDDSDDDYVQVREALEIHVNPNDPGLNFDIALIQLKTPV 939
QY 571 RISTRVQPICLAASRDLSFQESH-----TVAGNVLDVRSFGKNDTLRSQVSV 624
DB 940 TLTRVQPICLPT--DITT---REHLKEGTAVVTGCG---LNENNTYSETIQAVL 990
QY 625 VDSLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGIIAAVSPGGRASPRVH 684

```
Db 991 VAASCEGKYKADLPLVTENMFCAGYK-KGRYDACSDDSGG--PLVFADDSRTERRVW 1047
Qy 685 LMLGVSWSYDKTCSH-RLSTAFTKVLFPKDWIER 717
Db 1048 LEGIVSWGSPSGCGKANQYGGFTKVNFLSWIRQ 1081

RESULT 12
US-09-949-016-6138
; Sequence 6138, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6138
; LENGTH: 699
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6138

Query Match 12.2%; Score 482; DB 4; Length 699;
Best Local Similarity 24.9%; Pred. No. 1.7e-31;
Matches 178; Conservative 93; Mismatches 215; Indels 228; Gaps 39;

Qy 69 CRNEECDSLIHPCGCTIFENCKSCRNCSWGGLDDFVYKGFYCAECRAGWY----GGD 124
Db 143 CKEREDEELSCDHY-----CHN-----YIGGYCS-CRFGYLHTDNR 180
Qy 125 C-MRCQVLRAPKGOILL-----ESYPLNAHCWTIHAKPGFVIQLRFVWLSLEFDY-- 176
Db 181 CRVCSNDLFTORTGVITSPDPNPPYKSSSECLYIELEGFWNLQFEDI---FDIQH 237
Qy 177 ----COYDYVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNFDGFHAI 232
Db 238 PEVPCPYDIKIKVGP----KVLGPFCEKAPPEPSTQSHSVLLFPHSDNSAENRGWRL- 292
Qy 233 YBEITACSSSPCFHDGTCVLDKAGSYKACLAGYTCQRCENLEERNCSDDPGGPNVGYQK 292
Db 293 -----SYRAA-----GNECPHEL-----QP--PVH----- 309
Qy 293 ITGGPGLINGRAHAKIGTVVSPF-----CNNSY-VLSGNEKR-----TCQNGEWSGKQ 339
Db 310 -----GKIEPSQAKY-----FFKDQVLVSCDTGYKVLKDNVEMDTFQIECLKDGTSNKI 359
Qy 340 PIC-ICACREPKISDLVRRRLVPMQVQSRETFPLHQLYSAAFSKQKLSAPTKKPALPFGD 398
Db 360 PTCIKVDCRAP----- 372
Qy 399 LPMGQVHLHT-----OLOYECISPPYRRLGSSR--RTCLRTGKWS-----GRA-PSC 442
Db 373 LEHGLITFTSRNLATYKSEIKYSCOEPPYKMLNNNTGIYTCSAQWMNMKVLGRSLPTC 432
Qy 443 IPICG-----KIENITAPKTQGLRWPMQAAIYRTSGVHDGSLHKGAWFLVCSGA 492
Db 433 LPVCGLPKPSRKLMAIRFN-GRPAQKGT-PMIAML-----SHLNGQPF--CGGS 478
Qy 493 LVNERTVVAACHV---TDLGKVT-----MIKADLKVVLGKFYRDDDKTIQSLQIS 544
Db 479 LLGSSWIVTAACHLQSLDGPDTLRDSDLSFSDFKILGKHW--LRSDNEHQHGVK 536
Qy 545 AIIHPNVDPIILLADIATILKLDKARISTRVQPICLAASDLSTSFQF-SHITVAGMNV 603
```

```
Db 537 HTTLHPQYDNTFENDVALVELLESFVTLNAFVMPICLPEGPQ-----QEGAMVIVSGWK 591
Qy 604 LADVRSPGFKNDTLRSVVSVVDSLLCERHEDHGIPVSVTONMFCASDEPTAPSICTA 663
Db 592 QFLQRP-----ETLMEIPIVDHSTCQKAYAP--LKKVTRDMICAG-EKEGKDACAG 644
Qy 664 ETGGIAAVSPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLFPKDWIER 717
Db 645 DSGGPMVTLNRERG-----QWYLVTGTVSGDDCGCKDRYG-VYSYIHHNKDWIOR 693

RESULT 13
US-09-949-016-11182
; Sequence 11182, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11182
; LENGTH: 717
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11182

Query Match 12.0%; Score 475; DB 4; Length 717;
Best Local Similarity 24.6%; Pred. No. 6.9e-31;
Matches 176; Conservative 93; Mismatches 217; Indels 228; Gaps 38;

Qy 69 CRNEECDSLIHPCGCTIFENCKSCRNCSWGGLDDFVYKGFYCAECRAGWY----GGD 124
Db 161 CKEREDEELSCDHY-----CHN-----YIGGYCS-CRFGYLHTDNR 198
Qy 125 C-MRCQVLRAPKGOILL-----ESYPLNAHCWTIHAKPGFVIQLRFVWLSLEFD- 174
Db 199 CRVCSNDLFTORTGVITSPDPNPPYKSSSECLYIELEGFWNLQFEDI---FDIEDH 255
Qy 175 --YMCQDYVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNFDGFHAI 232
Db 256 PEVPCPYDIKIKVGP----KVLGPFCEKAPPEPSTQSHSVLLFPHSDNSGENRGWRL- 310
Qy 233 YBEITACSSSPCFHDGTCVLDKAGSYKACLAGYTCQRCENLEERNCSDDPGGPNVGYQK 292
Db 311 -----SYRAA-----GNECPHEL-----QP--PVH----- 327
Qy 293 ITGGPGLINGRAHAKIGTVVSPF-----CNNSY-VLSGNEKR-----TCQNGEWSGKQ 339
Db 328 -----GKIEPSQAKY-----FFKDQVLVSCDTGYKVLKDNVEMDTFQIECLKDGTSNKI 377
Qy 340 PIC-ICACREPKISDLVRRRLVPMQVQSRETFPLHQLYSAAFSKQKLSAPTKKPALPFGD 398
Db 378 PTCIKVDCRAP----- 390
Qy 399 LPMGQVHLHT-----OLOYECISPPYRRLGSSR--RTCLRTGKWS-----GRA-PSC 442
Db 391 LEHGLITFTSRNLATYKSEIKYSCOEPPYKMLNNNTGIYTCSAQWMNMKVLGRSLPTC 450
Qy 443 IPICG-----KIENITAPKTQGLRWPMQAAIYRTSGVHDGSLHKGAWFLVCSGA 492
Db 451 LPVCGLPKPSRKLMAIRFN-GRPAQKGT-PMIAML-----SHLNGQPF--CGGS 496
```

```
QY 493 LVNERTVVAAHC-----TDLGKVTMIKTADLVKLVGFYRDDDRDEKTIQSLOIS 544
Db 497 LIGSWIVTAACHLQSDPEPTLRDSDLLSPDFKIILGKHW--LRSDENEQHLGVK 554
QY 545 AILHPNYPDILLDADIAILKLLDKARISTRVQPICLAASRDLS*SQB-SHITVAGMNV 603
Db 555 HTLHPQYDNTFENDVALVELLESFVLNAFVMPICLPEGPQ-----QEGAMVIVSGWK 609
QY 604 LADVSPGFKNITLRSVVVDSLLCEQHEHEDHGIPVSTNNMFCASHEPTAPSDICTA 663
Db 610 QFLQRP-----ETLMEIEIPIVDHSTCQKAYAP--LKKKVTDRDMICAG-EKEGGKDACAG 662
QY 664 ETGGIAAVSFPCRASPEPHLMGLVSWSYDKTCSHRLSTAFKVLPPFKDWIER 717
Db 663 DSGGPMVTLNRBG-----QWILVGVISWGGDCGKKDRIY-VYSYIHNKDWIQR 711

RESULT 14
US-09-949-016-7775
; Sequence 7775, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7775
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7775

Query Match 10.1%; Score 399.5; DB 4; Length 691;
Best Local Similarity 22.6%; Pred. No. 1.3e-24;
Matches 173; Conservative 79; Mismatches 243; Indels 269; Gaps 34;

QY 128 CGQVLR--APK-----GQILLESYP-----LNAHCETWTHAKPGFVIQLRFVMLSLEFDY 175
Db 16 CGSVATPLGPKWPEPVFGRSLASPGPEYANDQERRWTLTAPGYRLRLYFTHFDLELSH 75
QY 176 MCQYDYVEVRDGNRDGQIIKRVCGNE-----RPAP-----IQIGSSLHLVLFHSDGS--KN 225
Db 76 LCEYDFVKLSG-----AKVLATLCQGESTDERAPGKDTFYSLGSSLDITFRSDYSNEKP 131
QY 226 FDGEHAIV--EETACSSSP-----CFHDGTCLVDKAGSYKACACLAGYTGQR-----CENL 274
Db 132 FTGFEAFYAEDIDECQVAPGEAPTCDHH---CHNHLGGFYCSCRAGYVLRNKRKTSAL 188
QY 275 -----LEE----- 277
Db 189 CSGQVFTQSGELSSPEYPRYPKLSCTYSISLEBGSFVILDVFBESFDVETHPTLCYP 248
QY 278 -----RNCSDP 283
Db 249 DFLKIQTDRREHGPPCGKTLPHRIETKSNVTITFTVDSGDHTGWKIHYTSTAQPCYP 308
QY 284 GGPVNGYQKITGPGGLNGRHAQ--IGTVVSPFCNNYS-VLSG-----NEKRTCCQNGEW 335
Db 309 MAPPNHG-----VSPVQAKYILKDSFSLFCETGYELLQHLPLKSFYAVCQKXGWS 359
QY 336 SGKQPTC-IKACREPKISDLVRRRLPM-QVOSRETPHLQLYSAAFSKLOSAPTKKPA 393
Db 360 DRMPACSI VDCGPPD-----YLPFSGRVEITGFGVTYKAV----- 396
```

```
QY 394 LPFGDLPMGYQHHLTQLOVEICISPFY-RRLGSSRRRTCLRTGKWSG-----RAPSCIPICG 447
Db 397 -----IOYSCEETFTWKVNDGKVCADGFWTSSKGEKSLPVCEPVC 440
QY 448 KIENITAPKTOGLR-----WPWQAAYRRTSGVHDGSLHKGAMFLVCSGALVNERTVVV 501
Db 441 LSRATTGGRIYGGQAKPGDFPQVLLGGTT-----AAGALLYDNWVLT 485
QY 502 AAHCVTDLGKVTMIKTADLVKLVGFYRDDDRDEKTIQSLO-----ISAILLHPNY-D 553
Db 486 AAHAYVE-----QKHDAASALDIRMG-----TLKRLSPHYTQAWSEAVFIHEGYTH 530
QY 554 PILLDADIAILKLLDKARISTRVQPICLAASRDLS*SQB-SHITVAGMNVLADVSPGFK 613
Db 531 DAGFONDIALIKLVNKVINSNITPICLPRKEAESFMRTDDICTAGWG---LTQRGFL 586
QY 614 NDTLRSVVVDSLLCEQHEHEDHGIP-VSVTDNMFCAWSEPTAPSDICTAETGGIAAVS 672
Db 587 ARNLAMYVDIPIVDHQKCTAAAYEKPPYPRGSVTANMLCAGLE-SGGKDSCRGDSGG--ALV 643
QY 673 PFCRASPEPHLMGLVSWSYDKTCSHRLSTAFKVLPPFKDWIE 716
Db 644 F--LDSETERWFVGIVSGWGMNCGEAGQYGVYTKVINYIPWIE 685

RESULT 15
US-09-027-337-2
; Sequence 2, Application US/09027337B
; Patent No. 5972616
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirofushi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
; Breast and Ovarian Carcinomas
; FILE REFERENCE: D6064
; CURRENT APPLICATION NUMBER: US/09/027,337B
; CURRENT FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of TADG-15 encoded by nucleotides
; OTHER INFORMATION: 23 to 2589 of Sequence 1
; Patent No. 5972616
US-09-027-337-2

Query Match 8.3%; Score 327; DB 2; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.8e-18;
Matches 144; Conservative 69; Mismatches 224; Indels 230; Gaps 27;

QY 128 CGQVLRAPKGOI-----LLESYFLNAHCEWTHAKPGFVIQLRFVMLSLEFDY----- 176
Db 340 CGGLRKAQGTSPSPYPGHYFPNIDCTWNIE-----VNNQHVKVSPKFFVLLPEGVPA 394
QY 177 --CQYDYVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSLHLVLFHSDGSKNFDGFHAIYE 234
Db 395 GTCPKDYVEING-----EKYCGRSQFVVTNSNKITVRFHSDQSYTDTGFLAEY- 444
QY 235 EITACSSSPCFHDGTC-----VLDKAGSYKACACLAGY----- 266
Db 445 -LSYDSSDPCPGQFTCRGTCIRKELRCDGWADCTDHSDELNCSDAGHQFTCKNFKCP 503
QY 267 -----TGQRCNLLERNCSDPGGPVNGYQKITGPGGLNGRHAQIGTVVSPFCNNYSV 320
Db 504 LFWVCDSVNDCDNGSDQGCSCP-----AQTFRCSNGKC 537
QY 321 LSG-----NEKRTCCQNGEWSGKQPIKACREPKISDLVRRRLPMQVOSRETPHLQLYS 376
Db 538 LSKSQOCNCKDDCGDGSDEASCPKVNVTVC----- 567
```



```
QY, 377 AAFSKQLQSAPTKPALPFGDLPNGYQHLHTLOQYECISPFYRRLGSSRRTCLRTGKWS 436
Db 568 -----TK-----HT---YRCLNGL-----CLSKGN-- 584
QY 437 GRAPCIPICGKIENITAPKTQ-----GLR-----WPMQAAIYVRTS 473
Db 585 -----PCDCGKEDCSGSDKDCDGLRSTRQARVVGGTTDADEGEWPMQVSLHALQ 637
QY 474 GYHDSLHKGAWFLVCSGALVNERTVVAACHCVTDLGKVTMIKTADLKVVLGKFYRDDDR 533
Db 638 G-----H-----ICGASLISPNMLVSAACHVYIDDRGFYSDPTQWTAFLG-LHDQSOR 684
QY 534 DEKTIQSLQISAIILHPNYDPILLADIAILKLLDKARISTVOPICLAASRDLSTSPQE 593
Db 685 SAPGVQERLKRILISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLP---DASHVPPA 741
QY 594 SH-ITVAGNVLADVRSQGFKNDTLRSQVSVVDSLLCEEQHEHGGIPVSVTDNMFCASW 652
Db 742 GKAIWVTH---GHTQYGGTGALILQKGEIRVINQTTENL-----LPQOITPRMVCVGF 793
QY 653 EPTAPSDICTAETGG-IAAVSPFGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLPP 711
Db 794 -LSGGVDSQCGSGGFLSSVEADGRI-----FQAGVVSNG-DGCAQRNKGVTYTRPLPLF 845
QY 712 KDWIERN 718
Db 846 RDWIKEN 852
```

Search completed: May 8, 2005, 16:06:10
Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 9, 2005, 21:04:33 ; Search time 320 Seconds
(without alignments)
3681.623 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 3945

Sequence: 1 MELGCWTLGLTLQLLLIS.....LSTAFKVLFPKDWIERNMK 720

Scoring table:

BLOSUM62	Xgapop 10.0 , Xgapext 0.5
-O=/cgn2_1/USPTO.spool/US10063692/runat.09052005.122255.4878/app.query.fasta_1.903	
-DB=Issued Patents NA_QFIX=fastap_SUFFIX=p2n.rni-MINMATCH=0.1-LOOPCL=0	
-LOOPEXT=0-UNITS=bits-START=1-END=1-MATRIX=blomsum62-TRANS=human40.cdi	
-LIST=1500-DOCAI=500-OUTPMT=200-NORM=ext-HEAPSIZE=500-MINLEN=0-ALIGN=15	
-MODE=LOCAL-OUTPMT=200-NORM=ext-HEAPSIZE=500-MINLEN=0-MAXLEN=2000000000	
-USER=US10063692_@CEN.1.184@runat.09052005.122255.4878-NCPU=6-ICPU=3	
-NO MAP-LARGEQUERY-NEG_SCORES=0-WAIT-DSPBLOCK=100-LONGLOG	
-DRV_TIMEOUT=120-WARN_TIMEOUT=30-THREADS=1-XGAPOP=10-XGAPEXT=0.5-FGAPOP=6	
-FGAPEXT=7-XGAPOP=10-XGAPEXT=0.5-DELOP=6-DELEXT=7	

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh
-O=/cgn2_1/USPTO.spool/US10063692/runat.09052005.122255.4878/app.query.fasta_1.903
-DB=Issued Patents NA_QFIX=fastap_SUFFIX=p2n.rni-MINMATCH=0.1-LOOPCL=0
-LOOPEXT=0-UNITS=bits-START=1-END=1-MATRIX=blomsum62-TRANS=human40.cdi
-LIST=1500-DOCAI=500-OUTPMT=200-NORM=ext-HEAPSIZE=500-MINLEN=0-ALIGN=15
-MODE=LOCAL-OUTPMT=200-NORM=ext-HEAPSIZE=500-MINLEN=0-MAXLEN=2000000000
-USER=US10063692_@CEN.1.184@runat.09052005.122255.4878-NCPU=6-ICPU=3
-NO MAP-LARGEQUERY-NEG_SCORES=0-WAIT-DSPBLOCK=100-LONGLOG
-DRV_TIMEOUT=120-WARN_TIMEOUT=30-THREADS=1-XGAPOP=10-XGAPEXT=0.5-FGAPOP=6
-FGAPEXT=7-XGAPOP=10-XGAPEXT=0.5-DELOP=6-DELEXT=7

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3450.5	87.5	2886	3	US-09-280-116-104
2	2946.5	74.7	2259	4	US-10-067-422-2
3	2678.5	67.9	2142	4	US-09-620-312D-1006
4	2678.5	67.9	2144	4	US-09-620-312D-1006
5	893	22.6	505	3	US-09-280-116-169
6	665	16.9	3448	1	US-08-296-014A-3
7	665	16.9	3448	2	US-08-596-405-3
8	665	16.9	3448	4	US-08-877-620-3
9	665	16.9	3448	4	US-09-287-368-3
10	665	16.9	3448	4	US-09-626-795-3
11	665	16.9	4182	4	US-08-296-014A-1
12	665	16.9	4182	2	US-08-596-405-1
13	665	16.9	4182	2	US-08-877-620-1
14	665	16.9	4182	4	US-09-287-368-1
15	665	16.9	4182	4	US-09-626-795-1
16	482	12.2	2787	4	US-09-949-016-267
17	475	12.0	2752	4	US-09-949-016-5311
18	403.5	10.2	2492	3	US-09-381-779-1
19	403.5	10.2	2492	4	US-09-712-018-1
20	399.5	10.1	2439	4	US-09-949-016-1904
21	335.5	8.5	3147	3	US-09-027-337-1
22	335.5	8.5	3147	3	US-09-644-600-1
23	335.5	8.5	3147	3	US-09-644-600-18
24	335.5	8.5	3147	4	US-09-654-600A-1
25	335.5	8.5	3147	4	US-09-654-600A-18
26	324	8.2	2900	3	US-09-027-337-9
27	324	8.2	2900	3	US-09-644-600-9
28	317.5	8.0	2581	1	US-08-200-900A-9
29	317.5	8.0	2581	4	US-08-794-042-1
30	317.5	8.0	2581	5	PCT-US94-00616-1
31	317.5	8.0	2581	5	PCT-US94-00616-1
32	312.5	7.9	1843	4	US-09-328-925-49
33	312.5	7.9	1843	4	US-09-949-016-50
34	310.5	7.9	1260	4	US-10-182-263-7
35	310.5	7.9	1386	2	US-08-756-506-3
36	310.5	7.9	1386	4	US-10-182-263-8
37	310.5	7.9	1755	6	5225537-1
38	310.5	7.9	1755	6	5225537-1
39	310.5	7.9	1755	6	5225537-1
40	310	7.9	1386	4	US-09-949-016-5011
41	310	7.9	1386	4	US-10-182-263-11
42	309	7.8	1386	4	US-10-182-263-9
43	308	7.8	1386	4	US-10-182-263-10
44	296.5	7.5	1387	6	5270178-1
45	296.5	7.5	1387	6	5270178-1
46	295.5	7.5	1554	2	US-08-469-486-1
47	295.5	7.5	1554	2	US-08-469-658-1
48	290.5	7.4	2521	3	US-09-949-016-5630
49	289.5	7.3	1848	3	US-08-814-412-10
50	289.5	7.3	2162	1	US-08-119-512-3
51	289.5	7.3	2162	1	US-08-488-015B-3
52	289.5	7.3	2162	1	US-08-488-015B-25
53	289.5	7.3	2544	4	US-09-703-695A-3
54	289.5	7.3	2544	4	US-10-443-701-3
55	289	7.3	7360	5	PCT-US95-09576-1
56	289	7.3	7360	5	PCT-US95-09576-1
57	288.5	7.3	3547	4	US-09-959-392-3
58	287.5	7.3	1366	4	US-09-054-272-17
59	286	7.2	1738	6	5200340-1
60	286	7.2	1738	6	5200340-1
61	286	7.2	1955	2	US-08-883-795A-39
62	286	7.2	1974	2	US-08-811-949-38
63	286	7.2	2101	2	US-08-811-949-42
64	286	7.2	2457	6	5344773-1
65	286	7.2	2457	6	5344773-1
66	281	7.1	1467	4	US-09-367-777-43
67	281	7.1	1467	4	US-09-367-791A-26
68	281	7.1	1605	6	5244676-1
69	281	7.1	1605	6	5244676-1
70	280.5	7.1	1164	4	US-09-949-016-3704
71	278.5	7.1	1440	1	US-07-882-202A-3
72	278.5	7.1	1440	1	US-08-021-615A-3
73	278.5	7.1	1440	1	US-08-321-777-3
74	278.5	7.1	1440	3	US-09-009-217-13
75	278.5	7.1	1440	3	US-09-009-656-13
76	278.5	7.1	1440	5	PCT-US93-04493-3
77	278.5	7.1	2462	3	US-08-479-733A-25
78	278.5	7.1	2462	3	US-08-487-427-25
79	278.5	7.1	2462	3	US-08-479-727A-25
80	278.5	7.1	2462	3	US-08-482-369A-25
81	278.5	7.1	2462	5	PCT-US95-07439-25
82	278.5	7.1	2475	4	US-09-949-016-3652
83	278	7.0	1502	4	US-09-949-016-3653
84	277	7.0	1338	4	US-09-782-587B-2
85	277	7.0	1357	4	US-09-782-587B-4

86	276.5	7.0	1727	6	5244676-4	Patent No. 5244676	159	255	6.5	3552	4	US-09-949-016-819	Sequence 819, App
87	276.5	7.0	1727	6	5244676-4	Patent No. 5244676	160	254	6.4	1372	6	5219569-1	Patent No. 5219569
88	276.5	7.0	2033	1	US-08-148-910-14	Sequence 14, Appl	161	254	6.4	1372	6	5219569-1	Sequence 1, Appl
89	276.5	7.0	2033	1	US-08-448-937A-14	Sequence 14, Appl	162	253.5	6.4	2487	1	US-08-377-292-1	Sequence 12009, A
90	275.5	7.0	2409	4	US-09-949-016-2968	Sequence 2968, Ap	163	253.5	6.4	76221	4	US-09-949-016-17053	Sequence 17053, A
91	275.5	7.0	2422	1	US-08-475-845-1	Sequence 1, Appl	164	253.5	6.4	76221	4	US-09-023-655-157	Sequence 157, App
92	275.5	7.0	2422	1	US-08-327-690-1	Sequence 1, Appl	165	251	6.4	2152	4	US-09-880-503-15	Sequence 15, Appl
93	275.5	7.0	2422	2	US-08-660-289-1	Sequence 1, Appl	166	249.5	6.3	1212	4	US-09-880-503-15	Sequence 1, Appl
94	275.5	7.0	2422	2	US-08-537-807-1	Sequence 1, Appl	167	249	6.3	2483	2	US-08-177-109A-1	Sequence 1, Appl
95	275.5	7.0	2422	2	US-08-871-003-1	Sequence 1, Appl	168	249	6.3	2483	2	US-08-687-706-1	Sequence 1, Appl
96	275.5	7.0	2422	3	US-08-464-203-1	Sequence 1, Appl	169	249	6.3	2733	4	US-09-976-594-517	Sequence 517, App
97	275.5	7.0	2422	3	US-09-189-607-1	Sequence 1, Appl	170	248.5	6.3	1314	2	US-08-811-949-48	Sequence 48, Appl
98	275.5	7.0	2422	3	US-09-378-907-1	Sequence 1, Appl	171	248.5	6.3	1314	2	US-08-811-949-50	Sequence 50, Appl
99	275.5	7.0	2422	5	PCT-US94-05779-1	Sequence 1, Appl	172	248.5	6.3	1314	2	US-08-811-949-54	Sequence 54, Appl
100	275	7.0	1683	4	US-09-912-559-1	Sequence 2, Appl	173	248.5	6.3	1314	2	US-08-811-949-56	Sequence 56, Appl
101	275	7.0	1683	4	US-09-912-559-1	Sequence 2, Appl	174	248.5	6.3	2879	4	US-09-949-016-5150	Sequence 5150, Ap
102	275	7.0	3008	4	US-09-949-016-587	Sequence 587, App	175	248	6.3	1419	2	US-08-811-949-62	Sequence 62, Appl
103	271.5	6.9	732	1	US-08-361-395-2	Sequence 2, Appl	176	246.5	6.2	885	3	US-08-338-368-1	Sequence 1, Appl
104	271.5	6.9	1506	4	US-09-949-016-1842	Sequence 1842, Ap	177	246.5	6.2	1139	2	US-08-558-269-9	Sequence 9, Appl
105	267.5	6.8	1404	3	US-09-202-101-15	Sequence 15, Appl	178	246.5	6.2	1139	2	US-09-410-882-9	Sequence 9, Appl
106	267	6.8	1437	2	US-08-479-733A-26	Sequence 26, Appl	179	246.5	6.2	1869	3	US-08-952-967-7	Sequence 7, Appl
107	267	6.8	1437	3	US-08-487-427-26	Sequence 26, Appl	180	246.5	6.2	1947	1	US-07-998-972A-2	Sequence 2, Appl
108	267	6.8	1437	3	US-08-479-727A-26	Sequence 26, Appl	181	246.5	6.2	1947	1	US-08-463-953-2	Sequence 2, Appl
109	267	6.8	1437	3	US-08-482-369A-26	Sequence 26, Appl	182	246.5	6.2	1947	1	US-08-462-261-2	Sequence 2, Appl
110	267	6.8	1437	5	PCT-US95-07439-26	Sequence 26, Appl	183	246.5	6.2	1947	1	US-08-479-733A-24	Sequence 24, Appl
c 111	265	6.7	5532	3	US-08-651-472-72	Sequence 72, Appl	184	246.5	6.2	1947	3	US-08-487-427-24	Sequence 24, Appl
c 112	265	6.7	5532	3	US-08-358-928-72	Sequence 72, Appl	185	246.5	6.2	1947	3	US-08-479-727A-24	Sequence 24, Appl
113	264.5	6.7	2497	6	5185259-2	Patent No. 5185259	186	246.5	6.2	1947	3	US-08-482-369A-24	Sequence 24, Appl
114	264.5	6.7	2497	6	5185259-2	Patent No. 5185259	187	246.5	6.2	1947	5	PCT-US92-11357-2	Sequence 2, Appl
115	263.5	6.7	3013	4	US-09-949-016-4921	Sequence 4921, Ap	188	246.5	6.2	1947	5	PCT-US95-07439-24	Sequence 24, Appl
116	263	6.7	1475	3	US-09-643-597-122	Sequence 122, App	189	246.5	6.2	1988	1	US-07-750-080A-15	Sequence 15, Appl
117	263	6.7	1475	4	US-09-480-884A-122	Sequence 122, App	190	246.5	6.2	1988	3	US-08-651-472-15	Sequence 15, Appl
118	263	6.7	1475	4	US-09-542-615A-122	Sequence 122, App	191	246.5	6.2	1988	3	US-08-651-472-15	Sequence 15, Appl
119	263	6.7	1475	4	US-09-606-421B-122	Sequence 122, App	192	244.5	6.2	807	3	US-08-358-928-15	Sequence 15, Appl
120	263	6.7	1475	4	US-09-321-107-122	Sequence 122, App	193	244.5	6.2	1739	3	US-09-715-994-1	Sequence 1, Appl
121	263	6.7	1475	4	US-09-466-396A-122	Sequence 122, App	194	243	6.2	5021	4	US-08-681-151-2	Sequence 2, Appl
122	263	6.7	1475	4	US-09-476-496A-122	Sequence 122, App	195	242.5	6.1	1068	1	US-09-285-385C-1	Sequence 1, Appl
123	263	6.7	1475	4	US-09-630-940B-122	Sequence 122, App	196	242.5	6.1	1605	2	US-08-427-640-7	Sequence 7, Appl
124	263	6.7	1475	4	US-09-285-479-122	Sequence 122, App	197	242.5	6.1	2457	3	US-09-000-846-1	Sequence 1, Appl
125	263	6.7	2294	3	US-09-643-597-123	Sequence 123, App	198	242.5	6.1	2457	4	US-08-872-757-1	Sequence 1, Appl
126	263	6.7	2294	4	US-09-480-884A-123	Sequence 123, App	199	241	6.1	1065	2	US-09-850-048A-1	Sequence 1, Appl
127	263	6.7	2294	4	US-09-542-615A-123	Sequence 123, App	200	241	6.1	3546	3	US-08-872-757-3	Sequence 3, Appl
128	263	6.7	2294	4	US-09-606-421B-123	Sequence 123, App	201	241	6.1	3546	4	US-09-850-048A-3	Sequence 3, Appl
129	263	6.7	2294	4	US-09-023-655-1217	Sequence 1217, Ap	202	240.5	6.1	1068	6	5223256-3	Patent No. 5223256
130	263	6.7	2294	4	US-09-221-107-123	Sequence 1217, Ap	203	240.5	6.1	1068	6	5223256-3	Patent No. 5223256
131	263	6.7	2294	4	US-09-466-396A-123	Sequence 123, App	204	240.5	6.1	1233	1	US-08-254-922-1	Sequence 1, Appl
132	263	6.7	2294	4	US-09-476-496A-123	Sequence 123, App	205	240.5	6.1	1233	1	US-08-286-748B-1	Sequence 1, Appl
133	263	6.7	2294	4	US-09-630-940B-123	Sequence 123, App	206	240.5	6.1	10878	4	US-09-911-842A-1	Sequence 1, Appl
134	263	6.7	2294	4	US-09-285-479-123	Sequence 123, App	207	239.5	6.1	11230	4	US-09-911-842A-3	Sequence 3, Appl
135	263	6.7	2301	6	5188829-2	Patent No. 5188829	208	239	6.1	1170	2	US-08-811-949-66	Sequence 66, Appl
136	263	6.7	2301	6	5188829-2	Patent No. 5188829	209	238	6.0	2625	3	US-09-245-041-18	Sequence 18, Appl
137	262.5	6.7	1389	6	5521070-1	Sequence 16, Appl	210	238	6.0	2625	4	US-09-358-055B-18	Sequence 18, Appl
138	262.5	6.7	1389	6	5521070-1	APPLICANT: MEU	211	238	6.0	2625	3	US-09-893-238-18	Sequence 18, Appl
139	262.5	6.7	1389	6	5521070-1	APPLICANT: MEU	212	238	6.0	4072	3	US-09-245-041-16	Sequence 16, Appl
140	262.5	6.7	1548	2	US-08-484-891-6	Sequence 6, Appl	213	238	6.0	4072	4	US-09-358-055B-16	Sequence 16, Appl
141	262.5	6.7	1548	4	US-09-150-811-6	Sequence 6, Appl	214	238	6.0	4072	4	US-09-893-238-16	Sequence 16, Appl
142	262.5	6.7	1610	1	US-08-209-846A-6	Sequence 6, Appl	215	238	6.0	8589	3	US-09-245-041-14	Sequence 14, Appl
143	262.5	6.7	1610	2	US-08-472-809B-6	Sequence 6, Appl	216	238	6.0	8589	4	US-09-358-055B-14	Sequence 14, Appl
144	262.5	6.7	1610	3	US-08-438-265-6	Sequence 6, Appl	217	238	6.0	8589	4	US-09-893-238-18	Sequence 18, Appl
145	262.5	6.7	2775	3	US-09-053-871A-22	Sequence 22, Appl	218	237	6.0	4771	2	US-08-866-650-2	Sequence 2, Appl
146	262.5	6.7	2802	3	US-08-742-877-1	Sequence 1, Appl	219	237	6.0	4771	3	US-09-021-287-2	Sequence 2, Appl
147	262.5	6.7	2804	4	US-10-133-907-2	Sequence 2, Appl	220	237	6.0	4771	3	US-09-420-473-2	Sequence 2, Appl
148	262.5	6.7	2833	4	US-09-949-016-5252	Sequence 5252, Ap	221	236.5	6.0	1065	1	US-08-427-640-5	Sequence 5, Appl
149	262.5	6.7	4933	4	US-09-959-392-1	Sequence 1, Appl	222	236.5	6.0	1068	1	US-08-427-640-3	Sequence 3, Appl
150	261.5	6.6	2792	4	US-09-118-748-1	Sequence 1, Appl	223	236.5	6.0	1068	1	US-08-137-116-2	Sequence 2, Appl
151	259	6.6	2505	4	US-09-799-451-179	Sequence 179, App	224	236.5	6.0	1068	2	US-08-811-949-44	Sequence 44, Appl
152	258.5	6.6	1236	1	US-07-957-039A-7	Sequence 7, Appl	225	236.5	6.0	1068	2	US-08-811-949-46	Sequence 46, Appl
153	258.5	6.6	1236	4	US-08-153-799-17	Sequence 17, Appl	226	236.5	6.0	1068	2	US-08-811-949-58	Sequence 58, Appl
154	258.5	6.6	1236	4	US-09-023-655-927	Sequence 927, App	227	236.5	6.0	1068	2	US-08-811-949-58	Sequence 4, Appl
155	258.5	6.6	1236	4	US-08-106-503-12	Sequence 12, Appl	228	236.5	6.0	1137	3	US-09-553-498-9	Sequence 9, Appl
156	258.5	6.6	1548	1	US-08-106-078-15	Sequence 15, Appl	229	236.5	6.0	1137	3	US-09-553-498-9	Sequence 9, Appl
157	258.5	6.6	1548	1	US-08-591-492-21	Sequence 21, Appl	230	236.5	6.0	1137	3	US-09-618-869-9	Sequence 9, Appl
158	256.5	6.5	1335	1	US-07-942-157A-2	Sequence 2, Appl	231	236.5	6.0	1724	6	5200340-5	Patent No. 5200340

232	236.5	6.0	1724	6	5200340-5	Patent No. 5200340	305	224	5.7	2440	4	US-09-949-016-5212	Sequence 5212, Ap
233	236	6.0	1068	2	US-08-811-949-52	Sequence 52, Appl	306	223.5	5.7	1042	4	US-09-949-016-3129	Sequence 3129, Ap
234	235.5	6.0	1103	2	US-09-016-366A-24	Sequence 24, Appl	307	222.5	5.6	1783	3	US-09-510-738A-188	Sequence 188, App
235	235.5	6.0	2730	3	US-08-936-135-17	Sequence 17, Appl	308	222.5	5.6	1783	4	US-09-861-966-188	Sequence 188, App
236	235.5	6.0	2730	4	US-09-439-711C-17	Sequence 17, Appl	309	222.5	5.6	1783	4	US-09-919-048-188	Sequence 188, App
237	235.5	6.0	2781	3	US-08-936-135-19	Sequence 19, Appl	310	222.5	5.6	1783	4	US-09-949-016-1311	Sequence 1311, Ap
238	235.5	6.0	2781	4	US-08-939-711C-19	Sequence 19, Appl	311	222	5.6	1128	2	US-09-016-366A-20	Sequence 20, Appl
239	235.5	6.0	3404	4	US-09-583-638-3	Sequence 3, Appl	312	222	5.6	1128	2	US-08-978-404B-15	Sequence 15, Appl
240	235	6.0	1219	2	US-08-978-404B-7	Sequence 7, Appl	313	222	5.6	1615	3	US-09-820-002-1	Sequence 1, Appl
241	233.5	5.9	1163	2	US-08-558-269-5	Sequence 5, Appl	314	221.5	5.6	2413	3	US-09-518-046-1	Sequence 1, Appl
242	233.5	5.9	1163	3	US-09-410-882-5	Sequence 5, Appl	315	221	5.6	943	3	US-08-705-875A-3	Sequence 3, Appl
243	233.5	5.9	2363	3	US-09-742-703-3	Sequence 3, Appl	316	221	5.6	943	3	US-09-242-999-3	Sequence 3, Appl
244	233	5.9	1077	4	US-08-949-016-1108	Sequence 1108, Ap	317	220.5	5.6	1169	3	US-09-386-642-7	Sequence 7, Appl
245	232.5	5.9	1500	1	US-08-487-037-4	Sequence 4, Appl	318	220.5	5.6	11725	2	US-08-756-506-1	Sequence 1, Appl
246	232.5	5.9	3919	2	US-08-866-650-4	Sequence 4, Appl	319	220.5	5.6	11725	4	US-09-328-925-50	Sequence 50, Appl
247	232.5	5.9	3919	2	US-09-021-287-4	Sequence 4, Appl	320	220.5	5.6	11725	4	US-09-054-272-31	Sequence 31, Appl
248	232.5	5.9	3919	3	US-09-240-473-4	Sequence 4, Appl	321	220	5.6	1137	2	US-09-016-366A-18	Sequence 18, Appl
249	232.5	5.9	5145	3	US-08-991-408-1	Sequence 1, Appl	322	220	5.6	1137	2	US-08-978-404B-13	Sequence 13, Appl
250	232.5	5.9	5145	3	US-09-432-473-1	Sequence 1, Appl	323	218.5	5.5	735	3	US-09-079-970A-1	Sequence 1, Appl
251	231.5	5.9	1170	2	US-08-811-949-64	Sequence 64, Appl	324	218.5	5.5	771	3	US-09-079-970A-4	Sequence 4, Appl
252	231	5.9	4661	4	US-09-285-385C-3	Sequence 3, Appl	325	218.5	5.5	1189	4	US-09-607-745-8	Sequence 8, Appl
253	230.5	5.8	780	4	US-10-165-442-6	Sequence 6, Appl	326	218	5.5	2430	4	US-09-192-012-4	Sequence 4, Appl
254	230.5	5.8	888	4	US-10-165-442-5	Sequence 5, Appl	327	218	5.5	2679	6	5200340-7	Patent No. 5200340
255	230.5	5.8	967	4	US-09-242-999-21	Sequence 21, Appl	328	218	5.5	2679	6	5200340-7	Patent No. 5200340
256	230	5.8	1161	3	US-09-032-215-9	Sequence 9, Appl	329	218	5.5	2753	1	US-07-854-603-1	Sequence 1, Appl
c 257	230	5.8	1161	3	US-09-032-215-10	Sequence 10, Appl	330	217.5	5.5	1142	3	US-09-386-642-8	Sequence 8, Appl
258	230	5.8	1161	3	US-09-032-215-15	Sequence 15, Appl	331	217.5	5.5	8091	4	US-09-230-652-1	Sequence 1, Appl
c 259	230	5.8	1161	3	US-09-032-215-16	Sequence 16, Appl	332	217.5	5.5	8257	3	US-09-484-970B-65	Sequence 65, Appl
260	230	5.8	1175	3	US-09-032-215-12	Sequence 12, Appl	333	217	5.5	807	2	US-08-270-584A-1	Sequence 1, Appl
c 261	230	5.8	1175	3	US-09-032-215-14	Sequence 14, Appl	334	217	5.5	807	2	US-08-765-192-1	Sequence 1, Appl
262	230	5.8	1373	3	US-09-032-215-6	Sequence 6, Appl	335	217	5.5	807	3	US-09-199-793-1	Sequence 1, Appl
c 263	230	5.8	1373	3	US-09-032-215-7	Sequence 7, Appl	336	217	5.5	807	4	US-09-613-822B-1	Sequence 1, Appl
264	230	5.8	1434	4	US-10-177-661-1	Sequence 11, Appl	337	217	5.5	1031	2	US-08-978-404B-1	Sequence 1, Appl
265	230	5.8	1748	4	US-09-879-792-11	Sequence 11, Appl	338	217	5.5	1378	4	US-09-907-794A-262	Sequence 262, App
266	229	5.8	726	3	US-09-004-731-35	Sequence 35, Appl	339	217	5.5	1378	4	US-09-905-125A-262	Sequence 262, App
267	229	5.8	726	3	US-08-749-699-35	Sequence 35, Appl	340	217	5.5	1378	4	US-09-902-775A-262	Sequence 262, App
268	229	5.8	726	3	US-09-004-729-35	Sequence 35, Appl	341	217	5.5	1378	4	US-09-906-700-262	Sequence 262, App
269	229	5.8	1200	3	US-09-004-731-32	Sequence 32, Appl	342	217	5.5	1378	4	US-09-903-603A-262	Sequence 262, App
c 270	229	5.8	1200	3	US-09-004-731-34	Sequence 34, Appl	343	217	5.5	1378	4	US-09-904-920A-262	Sequence 262, App
c 271	229	5.8	1200	3	US-08-749-699-32	Sequence 32, Appl	344	217	5.5	1378	4	US-09-909-064-262	Sequence 262, App
c 272	229	5.8	1200	3	US-08-749-699-34	Sequence 34, Appl	345	217	5.5	1378	4	US-09-905-381A-262	Sequence 262, App
273	229	5.8	1200	3	US-09-004-729-32	Sequence 32, Appl	346	217	5.5	1378	4	US-09-906-618-262	Sequence 262, App
c 274	229	5.8	1200	3	US-09-004-729-34	Sequence 34, Appl	347	217	5.5	1430	3	US-09-386-629-1	Sequence 1, Appl
275	229	5.8	1894	3	US-09-004-731-29	Sequence 29, Appl	348	217	5.5	2497	2	US-08-643-219-12	Sequence 12, Appl
c 276	229	5.8	1894	3	US-09-004-731-31	Sequence 31, Appl	349	217	5.5	2497	2	US-09-131-995-12	Sequence 12, Appl
c 277	229	5.8	1894	3	US-09-032-215-3	Sequence 3, Appl	350	217	5.5	2497	2	US-08-832-087B-12	Sequence 12, Appl
278	229	5.8	1894	3	US-08-749-699-29	Sequence 29, Appl	351	217	5.5	2497	3	US-08-851-350-12	Sequence 12, Appl
c 279	229	5.8	1894	3	US-08-749-699-31	Sequence 31, Appl	352	217	5.5	2497	3	US-09-132-154-12	Sequence 12, Appl
280	229	5.8	1894	3	US-09-004-729-29	Sequence 29, Appl	353	217	5.5	2497	4	US-08-924-287A-12	Sequence 12, Appl
c 281	229	5.8	1894	3	US-09-004-729-31	Sequence 31, Appl	354	217	5.5	2732	4	US-09-949-016-4112	Sequence 4112, App
282	228	5.8	3690	3	US-08-991-408-3	Sequence 3, Appl	355	216.5	5.5	1292	4	US-09-205-258-189	Sequence 189, App
283	228	5.8	3690	3	US-09-432-473-3	Sequence 3, Appl	356	216	5.5	833	2	US-08-790-137-2	Sequence 2, Appl
284	227	5.8	726	4	US-09-657-986B-1	Sequence 1, Appl	357	216	5.5	959	1	US-08-568-031-1	Sequence 1, Appl
285	227	5.8	959	4	US-09-023-942A-25	Sequence 25, Appl	358	216	5.5	959	2	US-08-966-319-1	Sequence 1, Appl
286	227	5.8	968	3	US-08-705-875A-9	Sequence 9, Appl	359	216	5.5	959	3	US-09-153-304-1	Sequence 1, Appl
287	227	5.8	968	4	US-09-242-999-9	Sequence 9, Appl	360	216	5.5	1081	2	US-09-016-366A-22	Sequence 22, Appl
288	226.5	5.7	3579	4	US-09-949-016-4627	Sequence 4627, Ap	361	216	5.5	1081	2	US-08-978-404B-17	Sequence 17, Appl
289	226	5.7	2038	4	US-09-008-271A-18	Sequence 18, Appl	362	216	5.5	1081	4	US-09-917-254-50	Sequence 50, Appl
290	226	5.7	2037	4	US-09-949-016-3367	Sequence 3367, Ap	363	216	5.5	1130	4	US-09-387-375-8	Sequence 8, Appl
291	226	5.7	2037	4	US-09-949-016-3368	Sequence 3368, Ap	364	216	5.5	1130	4	US-10-041-400A-8	Sequence 8, Appl
292	226	5.7	2079	3	US-09-656-002-1	Sequence 1, Appl	365	216	5.5	1130	4	US-10-042-091A-8	Sequence 8, Appl
293	226	5.7	2079	4	US-09-851-588-5	Sequence 5, Appl	366	215	5.4	1166	3	US-09-386-629-2	Sequence 2, Appl
294	226	5.7	2091	4	US-09-851-588-7	Sequence 7, Appl	367	215	5.4	2296	1	US-07-750-080A-18	Sequence 18, Appl
295	226	5.7	2217	4	US-09-949-016-5667	Sequence 5667, Ap	368	215	5.4	2296	3	US-08-651-472-18	Sequence 18, Appl
296	226	5.7	2217	4	US-09-949-016-5668	Sequence 5668, Ap	369	215	5.4	2296	3	US-08-358-928-18	Sequence 18, Appl
297	225	5.7	24735	4	US-09-949-016-12850	Sequence 12850, A	370	215	5.4	14802	4	US-09-949-016-16753	Sequence 16753, A
298	224	5.7	831	4	US-09-880-503-14	Sequence 14, Appl	371	214	5.4	1314	3	US-09-025-059-2	Sequence 2, Appl
299	224	5.7	972	4	US-09-880-503-16	Sequence 16, Appl	372	212.5	5.4	1052	3	US-09-386-642-10	Sequence 10, Appl
300	224	5.7	1154	2	US-09-016-366A-16	Sequence 16, Appl	373	212.5	5.4	1192	3	US-08-944-483-8	Sequence 8, Appl
301	224	5.7	1154	2	US-08-978-404B-11	Sequence 11, Appl	374	211.5	5.4	696	1	US-08-508-448C-24	Sequence 24, Appl
302	224	5.7	2121	4	US-09-607-745-1	Sequence 1, Appl	375	211.5	5.4	901	1	US-08-508-448C-9	Sequence 9, Appl
303	224	5.7	2440	4	US-09-949-016-5210	Sequence 5210, Ap	376	211.5	5.4	1166	3	US-08-944-483-7	Sequence 7, Appl
304	224	5.7	2440	4	US-09-949-016-5211	Sequence 5211, Ap	377	211.5	5.4	1160	3	US-09-370-838-80	Sequence 80, Appl

378	211.5	5.4	1460	4	US-09-854-133-80	Sequence 80, Appl	451	203.5	5.2	802	4	US-09-949-016-2899	Sequence 2899, Ap
379	211.5	5.4	1517	1	US-08-508-448C-15	Sequence 15, Appl	452	203.5	5.2	1979	1	US-08-392-828C-3	Sequence 3, Appli
380	211.5	5.4	2790	3	US-09-370-838-79	Sequence 79, Appl	453	203.5	5.2	1979	3	US-09-330-945-3	Sequence 1, Appli
381	211.5	5.4	2790	4	US-09-854-133-79	Sequence 79, Appl	454	203.5	5.2	11272	4	US-09-341-461-1	Sequence 1, Appli
382	211	5.3	943	3	US-08-705-875A-1	Sequence 1, Appli	455	203	5.1	933	4	US-09-023-942A-29	Sequence 431, App
383	211	5.3	943	4	US-09-242-979A-1	Sequence 14, Appl	456	203	5.1	1212	4	US-09-620-942A-29	Sequence 7, Appli
384	211	5.3	1108	2	US-09-016-366A-14	Sequence 10, Appl	457	203	5.1	3539	3	US-08-936-135-7	Sequence 7, Appli
385	211	5.3	1108	2	US-08-978-404B-20	Sequence 10, Appl	458	203	5.1	3539	4	US-09-439-711C-7	Sequence 3, Appli
386	211	5.3	1553	3	US-09-280-116-10	Sequence 10, Appl	459	203	5.1	3846	4	US-09-755-100A-3	Sequence 9, Appli
387	211	5.3	1605	3	US-09-949-016-2349	Sequence 1349, Ap	460	203	5.1	4718	3	US-08-936-135-9	Sequence 9, Appli
388	211	5.3	3201	4	US-09-579-536C-17	Sequence 17, Appl	461	203	5.1	4718	4	US-09-439-711C-9	Sequence 9, Appli
389	211	5.3	3657	4	US-09-579-536C-2	Sequence 2, Appli	462	203	5.1	4733	3	US-08-936-135-11	Sequence 11, Appl
390	211	5.3	4208	3	US-09-214-278-6	Sequence 6, Appli	463	203	5.1	4733	4	US-09-439-711C-11	Sequence 11, Appl
391	211	5.3	4208	3	US-09-068-740A-10	Sequence 10, Appl	464	203	5.1	4765	3	US-08-936-135-21	Sequence 21, Appl
392	211	5.3	4208	4	US-09-855-722-6	Sequence 6, Appli	465	203	5.1	4765	4	US-09-439-711C-21	Sequence 21, Appl
393	211	5.3	4855	4	US-09-917-254-34	Sequence 34, Appl	466	203	5.1	4769	3	US-08-936-135-13	Sequence 13, Appl
394	211	5.3	5458	3	US-09-199-865-2	Sequence 2, Appli	467	203	5.1	4769	4	US-09-439-711C-13	Sequence 13, Appl
395	211	5.3	5458	4	US-10-213-329-2	Sequence 2, Appli	468	203	5.1	4780	3	US-08-936-135-23	Sequence 23, Appl
396	211	5.3	5590	3	US-08-882-046-1	Sequence 1, Appli	469	203	5.1	4780	4	US-09-439-711C-23	Sequence 23, Appl
397	211	5.3	5590	4	US-09-566-047-1	Sequence 1, Appli	470	203	5.1	4784	3	US-08-936-135-15	Sequence 15, Appl
398	211	5.3	5885	4	US-09-949-016-4426	Sequence 4426, Ap	471	203	5.1	4784	4	US-09-439-711C-15	Sequence 15, Appl
399	211	5.3	5896	4	US-09-949-016-31	Sequence 31, Appl	472	203	5.1	16520	4	US-09-949-016-14710	Sequence 14710, A
400	211	5.3	6464	2	US-08-400-159-5	Sequence 5, Appli	473	203	5.1	16520	4	US-09-949-016-15394	Sequence 3, Appli
401	211	5.3	6464	3	US-08-611-729A-5	Sequence 5, Appli	474	202	5.1	2544	3	US-09-518-046-3	Sequence 13646, A
402	211	5.3	6464	4	US-09-195-524-5	Sequence 5, Appli	475	202	5.1	23640	4	US-09-949-016-13646	Sequence 1, Appli
403	211	5.3	7191	4	US-08-949-016-14871	Sequence 14871, A	476	200.5	5.1	734	1	US-08-650-129-1	Sequence 1, Appli
404	210.5	5.3	866	1	US-08-650-129-3	Sequence 3, Appli	477	200.5	5.1	734	2	US-08-984-417-1	Sequence 1, Appli
405	210.5	5.3	866	3	US-08-984-417-3	Sequence 3, Appli	478	200.5	5.1	897	2	US-08-956-267A-1	Sequence 1, Appli
406	210.5	5.3	1462	3	US-09-370-838-55	Sequence 55, Appl	479	200.5	5.1	1154	3	US-09-636-382A-1	Sequence 1, Appli
407	210.5	5.3	1462	4	US-09-854-133-55	Sequence 55, Appl	480	200	5.1	1154	4	US-09-163-951-15	Sequence 15, Appl
408	210	5.3	1341	4	US-10-177-661-3	Sequence 3, Appli	481	200	5.1	1155	4	US-09-345-881-15	Sequence 15, Appl
409	210	5.3	2771	4	US-09-949-016-5148	Sequence 5148, Ap	482	200	5.1	1240	3	US-09-163-951-14	Sequence 14, Appl
410	210	5.3	2821	4	US-09-620-312B-179	Sequence 179, App	483	200	5.1	1240	4	US-09-345-881-14	Sequence 14, Appl
411	209.5	5.3	1479	3	US-09-642-749-1	Sequence 1, Appli	484	200	5.1	9723	1	US-08-083-590A-21	Sequence 21, Appl
412	209.5	5.3	1479	3	US-09-691-840-1	Sequence 1, Appli	485	200	5.1	9723	2	US-08-532-384-21	Sequence 21, Appl
413	209	5.3	1230	4	US-09-879-792-35	Sequence 35, Appl	486	199	5.0	994	3	US-09-008-271A-19	Sequence 19, Appl
414	208.5	5.3	2479	3	US-09-342-749-29	Sequence 29, Appl	487	199	5.0	1068	4	US-09-949-016-2280	Sequence 1, Appli
415	208.5	5.3	2479	3	US-09-691-840-29	Sequence 29, Appl	488	198.5	5.0	825	3	US-09-120-582-1	Sequence 1, Appli
416	208.5	5.3	2479	4	US-09-685-166A-894	Sequence 894, App	489	198.5	5.0	3399	2	US-09-949-016-4400	Sequence 27, Appl
417	208.5	5.3	2479	4	US-09-679-426-894	Sequence 894, App	490	198	5.0	1126	2	US-08-479-733A-27	Sequence 27, Appl
418	208.5	5.3	2479	4	US-09-759-143-894	Sequence 894, App	491	198	5.0	1126	3	US-08-487-427-27	Sequence 27, Appl
419	207.5	5.3	1077	3	US-08-807-151-2	Sequence 2, Appli	492	198	5.0	1126	3	US-08-479-727A-27	Sequence 27, Appl
420	207.5	5.3	1077	3	US-09-478-957-2	Sequence 2, Appli	493	198	5.0	1126	3	US-08-482-369A-27	Sequence 27, Appl
421	207.5	5.3	1146	4	US-08-205-258-247	Sequence 247, App	494	198	5.0	1126	5	PCT-US95-07439-27	Sequence 2, Appli
422	207.5	5.3	1476	4	US-09-759-143-931	Sequence 931, App	495	197.5	5.0	871	1	US-08-744-026-2	Sequence 2, Appli
423	207.5	5.3	1476	4	US-09-759-143-930	Sequence 930, App	496	197.5	5.0	871	2	US-09-102-732-2	Sequence 2, Appli
424	207.5	5.3	2026	4	US-09-907-794A-103	Sequence 103, App	497	197.5	5.0	871	3	US-09-261-767-2	Sequence 7, Appli
425	207.5	5.3	2026	4	US-09-905-125A-103	Sequence 103, App	498	197.5	5.0	871	3	US-08-969-987-7	Sequence 7, Appli
426	207.5	5.3	2026	4	US-09-902-775A-103	Sequence 103, App	499	197.5	5.0	1074	4	US-09-949-016-1077	Sequence 1077, Ap
427	207.5	5.3	2026	4	US-09-906-700-103	Sequence 103, App	500	196.5	5.0	970	1	US-08-148-910-3	Sequence 3, Appli
428	207.5	5.3	2026	4	US-09-903-603A-103	Sequence 103, App	501	196.5	5.0	970	1	US-08-448-937A-3	Sequence 3, Appli
429	207.5	5.3	2026	4	US-09-904-920A-103	Sequence 103, App	502	195.5	5.0	2340	3	US-08-742-877-3	Sequence 3, Appli
430	207.5	5.3	2026	4	US-09-909-064-103	Sequence 103, App	503	195.5	5.0	6677	3	US-08-939-366-27	Sequence 27, Appl
431	207.5	5.3	2026	4	US-09-905-381A-103	Sequence 103, App	504	195.5	5.0	6677	3	US-09-467-997-6	Sequence 6, Appli
432	207.5	5.3	2026	4	US-09-906-618-103	Sequence 103, App	505	194.5	4.9	1802	3	US-09-032-523-5	Sequence 5, Appli
433	207.5	5.3	2448	4	US-09-949-016-5203	Sequence 5203, Ap	506	194.5	4.9	1802	4	US-09-802-633-5	Sequence 5, Appli
434	207.5	5.3	3245	4	US-09-759-143-929	Sequence 929, App	507	194	4.9	1093	6	5223425-3	Patent No. 5223425
435	206.5	5.2	821	1	US-08-650-129-2	Sequence 2, Appli	508	194	4.9	1093	6	5223425-3	Patent No. 5223425
436	206.5	5.2	821	3	US-08-984-417-2	Sequence 2, Appli	509	194	4.9	1167	3	US-09-020-956-175	Sequence 175, App
437	206.5	5.2	1613	4	US-09-387-375-1	Sequence 1, Appli	510	194	4.9	1167	3	US-09-030-607-175	Sequence 175, App
438	206.5	5.2	1613	4	US-10-041-400A-1	Sequence 1, Appli	511	194	4.9	1167	3	US-09-439-313-175	Sequence 175, App
439	206.5	5.2	1613	4	US-10-042-091A-1	Sequence 1, Appli	512	194	4.9	1167	3	US-09-352-616A-175	Sequence 175, App
440	205.5	5.2	1049	3	US-09-386-642-9	Sequence 9, Appli	513	194	4.9	1167	3	US-09-232-149A-175	Sequence 175, App
441	205.5	5.2	1095	2	US-08-978-404B-9	Sequence 9, Appli	514	194	4.9	1167	4	US-09-159-812-175	Sequence 175, App
442	205.5	5.2	1165	4	US-09-023-942A-28	Sequence 28, Appl	515	194	4.9	1167	4	US-09-636-215-175	Sequence 175, App
443	204.5	5.2	1322	4	US-09-949-016-3389	Sequence 3389, Ap	516	194	4.9	1167	4	US-09-685-166A-175	Sequence 175, App
444	204.5	5.2	3582	2	US-08-400-159-9	Sequence 9, Appli	517	194	4.9	1167	4	US-09-115-453-175	Sequence 175, App
445	204.5	5.2	3582	4	US-08-611-729A-9	Sequence 9, Appli	518	194	4.9	1167	4	US-09-688-489-175	Sequence 175, App
446	204.5	5.2	3582	4	US-09-195-524-9	Sequence 9, Appli	519	194	4.9	1167	4	US-09-679-426-175	Sequence 175, App
447	204	5.2	944	3	US-09-070-526-1	Sequence 1, Appli	520	194	4.9	1167	4	US-09-759-143-175	Sequence 175, App
448	204	5.2	1343	4	US-09-618-259-72	Sequence 72, Appl	521	194	4.9	1167	4	US-09-651-236-175	Sequence 175, App
449	204	5.2	1360	4	US-09-618-259-6	Sequence 6, Appli	522	193.5	4.9	1806	4	US-09-800-729-75	Sequence 75, Appl
450	204	5.2	7244	4	US-09-774-528-143	Sequence 143, App	523	193.5	4.9	1806	4	US-10-067-422-5	Sequence 5, Appli

524	193	4.9	804	3	US-09-032-215-44	Sequence 44, Appl	597	186.5	4.7	796	3	US-09-280-116-107	Sequence 107, App
525	193	4.9	804	3	US-09-032-215-45	Sequence 45, Appl	598	186	4.7	1130	3	US-09-386-653A-8	Sequence 8, Appl
526	193	4.9	835	6	5223425-7	Patent No. 5223425	599	186	4.7	2508	3	US-08-981-392-1	Sequence 1, Appl
527	193	4.9	835	6	5223425-7	Patent No. 5223425	600	186	4.7	2508	3	US-09-908-322-1	Sequence 1, Appl
528	193	4.9	933	3	US-09-032-215-41	Sequence 41, Appl	601	186	4.7	2883	3	US-08-981-392-3	Sequence 3, Appl
529	193	4.9	933	3	US-09-032-215-43	Sequence 43, Appl	602	186	4.7	2883	3	US-09-908-322-3	Sequence 3, Appl
530	193	4.9	1266	4	US-09-800-729-15	Sequence 15, Appl	603	186	4.7	3471	3	US-09-116-473-3	Sequence 3, Appl
531	192	4.9	944	3	US-08-906-769-82	Sequence 82, Appl	604	185.5	4.7	768	3	US-09-032-215-29	Sequence 29, Appl
532	192	4.9	944	3	US-08-906-616-82	Sequence 82, Appl	605	185.5	4.7	768	3	US-09-032-215-30	Sequence 30, Appl
533	192	4.9	944	3	US-08-817-795-82	Sequence 82, Appl	606	185.5	4.7	1059	3	US-08-163-919A-1	Sequence 1, Appl
534	192	4.9	944	3	US-08-639-075A-82	Sequence 82, Appl	607	185.5	4.7	1059	3	US-08-462-515-1	Sequence 1, Appl
535	192	4.9	944	3	US-09-012-431-82	Sequence 82, Appl	608	185.5	4.7	1059	3	PCT-US94-14073-1	Sequence 1, Appl
536	192	4.9	944	3	US-09-012-692-82	Sequence 82, Appl	609	185.5	4.7	1103	3	US-09-386-642-59	Sequence 59, Appl
537	192	4.9	944	3	US-08-906-613-82	Sequence 82, Appl	610	185.5	4.7	2216	2	US-08-666-082B-2	Sequence 2, Appl
538	192	4.9	944	5	PCT-US95-14442A-82	Sequence 82, Appl	611	185.5	4.7	2219	1	US-07-882-925A-1	Sequence 1, Appl
539	192	4.9	2419	3	US-09-245-041-8	Sequence 8, Appl	612	185.5	4.7	2219	1	US-08-184-012C-1	Sequence 1, Appl
540	192	4.9	2419	3	US-09-358-055B-8	Sequence 8, Appl	613	185.5	4.7	2232	1	US-08-334-177-1	Sequence 1, Appl
541	192	4.9	2419	3	US-09-893-238-8	Sequence 8, Appl	614	185.5	4.7	2232	5	PCT-US95-13830-1	Sequence 1, Appl
542	192	4.9	8827	3	US-09-245-041-1	Sequence 1, Appl	615	185.5	4.7	2262	1	US-07-882-925A-7	Sequence 7, Appl
543	192	4.9	8827	3	US-09-358-055B-1	Sequence 1, Appl	616	185.5	4.7	2262	1	US-08-184-012C-7	Sequence 7, Appl
544	192	4.9	8827	3	US-09-893-238-1	Sequence 1, Appl	617	185	4.7	1100	4	US-09-023-942A-5	Sequence 5, Appl
545	191.5	4.9	3142	1	US-08-110-158-3	Sequence 3, Appl	618	184.5	4.7	992	1	US-08-358-782D-13	Sequence 13, Appl
546	191.5	4.9	3142	4	US-09-023-655-1090	Sequence 1090, Ap	619	184.5	4.7	992	2	US-08-764-527A-13	Sequence 13, Appl
547	191.5	4.9	3144	5	PCT-US91-05059-1	Sequence 1, Appl	620	184	4.7	1081	3	US-09-008-271A-15	Sequence 15, Appl
548	191	4.8	765	3	US-09-439-313-524	Sequence 524, App	621	184	4.7	1100	4	US-09-307-794A-256	Sequence 256, App
549	191	4.8	765	4	US-09-636-215-524	Sequence 524, App	622	184	4.7	1100	4	US-09-905-125A-256	Sequence 256, App
550	191	4.8	765	4	US-09-685-166A-524	Sequence 524, App	623	184	4.7	1100	4	US-09-902-775A-256	Sequence 256, App
551	191	4.8	765	4	US-09-679-426-524	Sequence 524, App	624	184	4.7	1100	4	US-09-906-700-256	Sequence 256, App
552	191	4.8	765	4	US-09-759-143-524	Sequence 524, App	625	184	4.7	1100	4	US-09-903-603A-256	Sequence 256, App
553	191	4.8	765	4	US-09-651-236-524	Sequence 524, App	626	184	4.7	1100	4	US-09-904-920A-256	Sequence 256, App
554	191	4.8	2416	3	US-09-261-416-1	Sequence 1, Appl	627	184	4.7	1100	4	US-09-909-064-256	Sequence 256, App
555	191	4.8	3371	3	US-09-116-473-1	Sequence 1, Appl	628	184	4.7	1100	4	US-09-905-381A-256	Sequence 256, App
556	190	4.8	945	3	US-09-032-215-26	Sequence 26, Appl	629	184	4.7	1100	4	US-09-906-618-256	Sequence 256, App
557	190	4.8	945	3	US-09-032-215-28	Sequence 28, Appl	630	184	4.7	1248	3	US-09-020-956-171	Sequence 171, App
558	190	4.8	1037	3	US-09-386-642-60	Sequence 60, Appl	631	184	4.7	1248	3	US-09-030-607-171	Sequence 171, App
559	190	4.8	2185	4	US-09-270-767-12720	Sequence 12720, A	632	184	4.7	1248	3	US-09-439-313-171	Sequence 171, App
560	189.5	4.8	1110	3	US-09-386-653A-1	Sequence 1, Appl	633	184	4.7	1248	3	US-09-352-616A-171	Sequence 171, App
561	189	4.8	969	3	US-09-502-600-30	Sequence 30, Appl	634	184	4.7	1248	3	US-09-232-149A-171	Sequence 171, App
562	189	4.8	969	3	US-09-918-243-30	Sequence 30, Appl	635	184	4.7	1248	3	US-09-159-812-171	Sequence 171, App
563	189	4.8	986	2	US-08-557-146-1	Sequence 1, Appl	636	184	4.7	1248	4	US-09-636-215-171	Sequence 171, App
564	189	4.8	986	2	US-09-154-344-1	Sequence 1, Appl	637	184	4.7	1248	4	US-09-685-166A-171	Sequence 171, App
565	189	4.8	986	2	US-09-949-016-1845	Sequence 1845, Ap	638	184	4.7	1248	4	US-09-115-453-171	Sequence 171, App
566	189	4.8	1089	3	US-08-930-188-1	Sequence 1, Appl	639	184	4.7	1248	4	US-09-688-489-171	Sequence 171, App
567	189	4.8	1089	3	US-08-930-188-3	Sequence 3, Appl	640	184	4.7	1248	4	US-09-679-426-171	Sequence 171, App
568	189	4.8	1089	5	PCT-US96-04294-1	Sequence 1, Appl	641	184	4.7	1248	4	US-09-759-143-171	Sequence 171, App
569	189	4.8	1089	5	PCT-US96-04294-3	Sequence 3, Appl	642	184	4.7	1248	4	US-09-651-236-171	Sequence 171, App
570	189	4.8	1094	4	US-09-023-942A-3	Sequence 3, Appl	643	184	4.7	3955	3	US-09-214-278-4	Sequence 4, Appl
571	189	4.8	1214	3	US-09-439-313-225	Sequence 225, App	644	184	4.7	3955	4	US-09-855-722-4	Sequence 7, Appl
572	189	4.8	1214	3	US-09-352-616A-225	Sequence 225, App	645	184	4.7	4483	2	US-08-400-159-7	Sequence 7, Appl
573	189	4.8	1214	3	US-09-232-149A-225	Sequence 225, App	646	184	4.7	4483	3	US-08-611-729A-7	Sequence 7, Appl
574	189	4.8	1214	4	US-09-159-812-225	Sequence 225, App	647	184	4.7	4483	4	US-09-195-524-7	Sequence 7, Appl
575	189	4.8	1214	4	US-09-636-215-225	Sequence 225, App	648	183.5	4.7	2136	4	US-09-600-991-19	Sequence 19, Appl
576	189	4.8	1214	4	US-09-685-166A-225	Sequence 225, App	649	183.5	4.7	2136	4	US-09-601-040A-11	Sequence 11, Appl
577	189	4.8	1214	4	US-09-115-453-225	Sequence 225, App	650	183.5	4.7	2219	4	US-09-949-016-1110	Sequence 1110, Ap
578	189	4.8	1214	4	US-09-688-489-225	Sequence 225, App	651	183.5	4.7	2692	3	US-08-981-392-11	Sequence 11, Appl
579	189	4.8	1214	4	US-09-679-426-225	Sequence 225, App	652	183.5	4.7	2692	4	US-09-908-322-11	Sequence 11, Appl
580	189	4.8	1214	4	US-09-759-143-225	Sequence 225, App	653	183.5	4.7	3652	3	US-08-936-135-5	Sequence 5, Appl
581	189	4.8	1214	4	US-09-651-236-225	Sequence 225, App	654	183.5	4.7	3652	4	US-09-439-711C-5	Sequence 5, Appl
582	189	4.8	1215	3	US-09-439-313-326	Sequence 326, App	655	182.5	4.6	799	4	US-09-023-942A-7	Sequence 7, Appl
583	189	4.8	1215	3	US-09-352-616A-326	Sequence 326, App	656	182.5	4.6	980	4	US-09-023-942A-30	Sequence 30, Appl
584	189	4.8	1215	3	US-09-232-149A-326	Sequence 326, App	657	182.5	4.6	1592	2	US-08-252-493C-1	Sequence 1, Appl
585	189	4.8	1215	4	US-09-636-215-326	Sequence 326, App	658	182.5	4.6	1592	3	US-09-276-197-1	Sequence 1, Appl
586	189	4.8	1215	4	US-09-685-166A-326	Sequence 326, App	659	182	4.6	1225	3	US-09-734-675-1	Sequence 1, Appl
587	189	4.8	1215	4	US-09-688-489-326	Sequence 326, App	660	182	4.6	1386	2	US-08-897-340-1	Sequence 1, Appl
588	189	4.8	1215	4	US-09-679-426-326	Sequence 326, App	661	182	4.6	1386	3	US-09-252-329-1	Sequence 1, Appl
589	189	4.8	1215	4	US-09-759-143-326	Sequence 326, App	662	181.5	4.6	867	1	US-07-590-301A-1	Sequence 1, Appl
590	189	4.8	1215	4	US-09-651-236-326	Sequence 326, App	663	181.5	4.6	1556	1	US-08-597-545-3	Sequence 3, Appl
591	189	4.8	1350	4	US-09-636-215-616	Sequence 616, App	664	181.5	4.6	1556	1	US-08-457-135-3	Sequence 3, Appl
592	189	4.8	1350	4	US-09-685-166A-616	Sequence 616, App	665	181.5	4.6	3231	4	US-09-866-028-14	Sequence 14, Appl
593	189	4.8	1350	4	US-09-679-426-616	Sequence 616, App	666	181.5	4.6	3231	4	US-09-944-457-14	Sequence 14, Appl
594	189	4.8	1350	4	US-09-759-143-616	Sequence 616, App	667	181.5	4.6	3757	2	US-09-016-366A-13	Sequence 13, Appl
595	189	4.8	1350	4	US-09-651-236-616	Sequence 616, App	668	181.5	4.6	3757	2	US-08-578-404B-19	Sequence 19, Appl
596	188	4.8	855	4	US-09-044-604-1	Sequence 1, Appl	669	180.5	4.6	917	4	US-09-669-751-101	Sequence 101, App

670	180.5	4.6	2219	1	US-07-882-925A-2	Sequence 2, Appli	743	170	4.3	641	3	US-08-906-616-148	Sequence 148, App
671	180.5	4.6	2219	1	US-08-184-012C-2	Sequence 2, Appli	744	170	4.3	641	3	US-08-639-075A-148	Sequence 148, App
672	179.5	4.6	863	6	5223425-9	Sequence 2, Appli	745	170	4.3	641	3	US-09-012-431-148	Sequence 148, App
673	179.5	4.6	863	6	5223425-9	Patent No. 5223425	746	170	4.3	641	3	US-09-012-692-148	Sequence 148, App
674	179.5	4.6	925	1	US-07-990-301A-3	Sequence 3, Appli	747	170	4.3	641	3	US-08-906-613-148	Sequence 10, Appl
675	179	4.5	690	1	US-08-379-621-1	Sequence 1, Appli	748	170	4.3	1051	4	US-09-245-041-10	Sequence 10, Appl
676	179	4.5	690	2	US-08-889-078-1	Sequence 1, Appli	749	170	4.3	1051	4	US-09-358-058B-10	Sequence 10, Appl
677	179	4.5	1152	2	US-09-032-215-24	Sequence 24, Appl	750	170	4.3	1051	4	US-09-893-238-10	Sequence 7, Appli
c 678	179	4.5	1152	3	US-09-032-215-25	Sequence 25, Appl	751	170	4.3	2154	4	US-09-601-040A-7	Sequence 3, Appli
679	179	4.5	1303	3	US-09-032-215-21	Sequence 21, Appl	752	170	4.3	2190	4	US-09-601-040A-3	Sequence 3, Appli
c 680	179	4.5	1303	3	US-09-032-215-23	Sequence 23, Appl	753	170	4.3	2772	3	US-08-936-135-1	Sequence 1, Appli
681	179	4.5	1828	3	US-09-280-116-108	Sequence 108, App	754	170	4.3	2772	4	US-09-439-711C-1	Sequence 1, Appli
682	178.5	4.5	1506	2	US-08-839-008-4	Sequence 4, Appli	755	169.5	4.3	11009	4	US-09-845-583A-1	Sequence 11, Appl
683	178.5	4.5	1506	2	US-08-839-008-6	Sequence 6, Appli	756	169.5	4.3	25621	4	US-09-902-540-1253	Sequence 1253, Ap
684	178.5	4.5	2766	3	US-08-936-135-3	Sequence 3, Appli	757	169	4.3	1158	4	US-09-142-027A-11	Sequence 11, Appl
685	178.5	4.5	2766	3	US-09-439-711C-3	Sequence 3, Appli	758	169	4.3	1158	4	US-09-142-027A-13	Sequence 13, Appl
686	178	4.5	700	4	US-09-270-767-14199	Sequence 14199, A	759	169	4.3	1573	1	US-08-597-545-4	Sequence 4, Appli
687	178	4.5	13863	4	US-09-814-915A-83	Sequence 83, Appl	760	169	4.3	1573	1	US-08-457-135-4	Sequence 4, Appli
688	176.5	4.5	859	3	US-09-044-604-2	Sequence 2, Appli	761	169	4.3	3423	4	US-09-755-100A-5	Sequence 5, Appli
c 689	176	4.5	699	3	US-09-004-731-26	Sequence 26, Appl	762	168.5	4.3	2270	4	US-09-229-151C-13	Sequence 13, Appl
c 690	176	4.5	699	3	US-09-004-731-28	Sequence 28, Appl	763	168.5	4.3	4661	4	US-09-755-100A-2	Sequence 2, Appli
691	176	4.5	699	3	US-08-749-699-26	Sequence 26, Appl	764	168.5	4.3	4661	4	US-09-755-100A-2	Sequence 2, Appli
c 692	176	4.5	699	3	US-08-749-699-28	Sequence 28, Appl	765	168	4.3	806	3	US-08-906-769-120	Sequence 120, App
693	176	4.5	699	3	US-09-004-729-26	Sequence 26, Appl	766	168	4.3	806	3	US-08-906-616-120	Sequence 120, App
c 694	176	4.5	699	3	US-09-004-729-28	Sequence 28, Appl	767	168	4.3	806	3	US-08-639-075A-120	Sequence 120, App
695	176	4.5	924	3	US-09-004-731-23	Sequence 23, Appl	768	168	4.3	806	3	US-09-012-431-120	Sequence 120, App
c 696	176	4.5	924	3	US-09-004-731-25	Sequence 25, Appl	769	168	4.3	806	3	US-09-012-692-120	Sequence 120, App
697	176	4.5	924	3	US-08-749-699-23	Sequence 23, Appl	770	168	4.3	806	3	US-08-906-613-120	Sequence 120, App
c 698	176	4.5	924	3	US-08-749-699-25	Sequence 25, Appl	771	167.5	4.2	1462	1	US-08-358-782D-14	Sequence 14, Appl
699	176	4.5	924	3	US-09-004-729-23	Sequence 23, Appl	772	167.5	4.2	1462	1	US-08-764-527A-14	Sequence 14, Appl
c 700	176	4.5	924	3	US-09-004-729-25	Sequence 25, Appl	773	167	4.2	2183	4	US-09-641-612-9	Sequence 9, Appli
701	175.5	4.4	1431	3	US-09-495-050A-249	Sequence 249, App	774	167	4.2	2989	6	5378464-1	Patent No. 5378464
702	174.5	4.4	4315	3	US-08-882-046-3	Sequence 3, Appli	775	167	4.2	2989	6	5378464-1	Patent No. 5378464
703	174.5	4.4	4315	3	US-09-566-047-3	Sequence 3, Appli	776	167	4.2	2989	6	5378464-1	Patent No. 5378464
704	174	4.4	2001	3	US-09-341-587-2	Sequence 2, Appli	c 777	166	4.2	14484	4	US-09-902-540-1108	Sequence 1108, Ap
705	174	4.4	2663	3	US-09-068-740A-8	Sequence 8, Appli	778	166	4.2	711	3	US-09-100-264-4	Sequence 4, Appli
706	174	4.4	2663	3	US-09-423-753-8	Sequence 8, Appli	779	165	4.2	1454	1	US-08-843-076D-23	Sequence 23, Appl
707	174	4.4	5802	3	US-09-341-587-4	Sequence 4, Appli	780	165	4.2	1454	1	US-08-467-155A-22	Sequence 2, Appli
708	174	4.4	5943	4	US-09-976-594-272	Sequence 272, App	781	165	4.2	1454	2	US-08-628-198-2	Sequence 2, Appli
709	173.5	4.4	1245	4	US-09-270-767-17860	Sequence 17860, A	782	165	4.2	1454	2	US-09-201-038-2	Sequence 2, Appli
710	173	4.4	633	4	US-09-242-999-19	Sequence 19, Appl	783	165	4.2	1454	4	US-09-771-357-94	Sequence 94, Appl
711	172.5	4.4	863	6	5223425-1	Patent No. 5223425	784	165	4.2	1454	5	US-10-059-579A-94	Sequence 94, Appl
712	172.5	4.4	863	6	5223425-1	Patent No. 5223425	785	164.5	4.2	903	4	US-09-902-540-2069	Sequence 2, Appli
713	172.5	4.4	1480	2	US-08-839-008-8	Sequence 8, Appli	786	164.5	4.2	916	4	US-09-902-540-2069	Sequence 2069, App
714	172.5	4.4	1480	2	US-09-919-497-39	Sequence 39, Appli	787	164.5	4.2	9668	4	US-09-949-016-4532	Sequence 4532, App
715	172.5	4.4	1508	4	US-09-949-016-1367	Sequence 1367, App	788	164	4.2	696	3	US-09-280-116-180	Sequence 180, Appl
716	172.5	4.4	1537	2	US-08-839-008-1	Sequence 1, Appli	789	164	4.2	2570	4	US-09-229-151C-14	Sequence 14, Appl
717	172.5	4.4	1820	4	US-09-799-451-885	Sequence 885, App	c 790	163.5	4.1	12270	4	US-09-949-016-16891	Sequence 16891, A
c 718	172	4.4	828	4	US-09-270-767-2080	Sequence 2080, App	791	163.5	4.1	16541	4	US-09-949-016-16891	Sequence 16890, A
c 719	172	4.4	828	4	US-09-270-767-17362	Sequence 17362, A	c 792	163.5	4.1	22089	4	US-09-949-016-16890	Sequence 1, Appli
720	172	4.4	1452	4	US-09-270-767-27664	Sequence 27664, A	793	163	4.1	1752	4	US-09-641-612-1	Sequence 1, Appli
721	172	4.4	2039	4	US-09-270-767-11981	Sequence 11981, A	794	163	4.1	2917	4	US-09-907-794A-189	Sequence 189, App
722	172	4.4	5653	4	US-09-583-638-1	Sequence 1, Appli	795	163	4.1	2917	4	US-09-905-125A-189	Sequence 189, App
723	172	4.4	8374	4	US-09-639-207-11	Sequence 11, Appl	796	163	4.1	2917	4	US-09-902-775A-189	Sequence 189, App
724	171.5	4.3	682	3	US-09-163-951-13	Sequence 13, Appl	797	163	4.1	2917	4	US-09-906-700-189	Sequence 189, App
725	171.5	4.3	682	3	US-09-345-881-13	Sequence 13, Appl	798	163	4.1	2917	4	US-09-903-603A-189	Sequence 189, App
726	171.5	4.3	778	3	US-08-906-769-189	Sequence 189, App	799	163	4.1	2917	4	US-09-904-920A-189	Sequence 189, App
727	171.5	4.3	778	3	US-08-906-616-189	Sequence 189, App	800	163	4.1	2917	4	US-09-909-064-189	Sequence 189, App
728	171.5	4.3	778	3	US-08-639-075A-189	Sequence 189, App	801	163	4.1	2917	4	US-09-905-381A-189	Sequence 189, App
729	171.5	4.3	778	3	US-09-004-731-84	Sequence 84, Appl	802	163	4.1	2917	4	US-09-906-618-189	Sequence 189, App
730	171.5	4.3	778	3	US-09-012-431-189	Sequence 189, App	803	162.5	4.1	873	4	US-09-949-016-3201	Sequence 3201, App
731	171.5	4.3	778	3	US-08-749-699-84	Sequence 84, Appl	804	162.5	4.1	4360	1	US-08-470-350B-1	Sequence 1, Appli
732	171.5	4.3	778	3	US-09-012-692-189	Sequence 189, App	805	162	4.1	2055	3	US-08-872-855-3	Sequence 3, Appli
733	171.5	4.3	778	3	US-08-906-613-189	Sequence 189, App	806	162	4.1	2055	4	US-09-641-612-10	Sequence 10, Appl
734	171.5	4.3	778	3	US-09-004-729-84	Sequence 84, Appl	807	162	4.1	2800	3	US-08-872-855-1	Sequence 1, Appli
735	171.5	4.3	6289	4	US-09-949-016-15446	Sequence 15446, A	808	162	4.1	3339	4	US-09-423-753-4	Sequence 4, Appli
736	171	4.3	864	4	US-09-270-767-1634	Sequence 1634, Ap	809	161.5	4.1	884	2	US-08-851-974-2	Sequence 2, Appli
737	171	4.3	864	4	US-09-270-767-16916	Sequence 16916, A	810	161.5	4.1	884	2	US-09-213-390-2	Sequence 2, Appli
738	171	4.3	1253	3	US-09-949-016-2295	Sequence 2295, Ap	811	161.5	4.1	1265	3	US-09-020-956-173	Sequence 173, App
739	171	4.3	1406	4	US-09-949-016-5325	Sequence 5325, App	812	161.5	4.1	1265	3	US-09-030-607-173	Sequence 173, App
740	171	4.3	2154	4	US-09-601-040A-5	Sequence 5, Appli	813	161.5	4.1	1265	3	US-09-439-313-173	Sequence 173, App
741	171	4.3	2190	4	US-09-601-040A-1	Sequence 1, Appli	814	161.5	4.1	1265	3	US-09-352-616A-173	Sequence 173, App
742	170	4.3	641	3	US-08-906-769-148	Sequence 148, App	815	161.5	4.1	1265	3	US-09-232-149A-173	Sequence 173, App

816	161.5	4.1	1265	4	US-09-159-812-173	Sequence 173, App	889	157	4.0	610	3	US-09-012-692-140	Sequence 140, App
817	161.5	4.1	1265	4	US-09-636-215-173	Sequence 173, App	890	157	4.0	610	3	US-08-906-613-140	Sequence 140, App
818	161.5	4.1	1265	4	US-09-685-166A-173	Sequence 173, App	891	157	4.0	1148	4	US-09-270-767-13591	Sequence 13591, A
819	161.5	4.1	1265	4	US-09-115-453-173	Sequence 173, App	892	157	4.0	3862	4	US-09-949-016-4401	Sequence 4401, App
820	161.5	4.1	1265	4	US-09-688-489-173	Sequence 173, App	893	157	4.0	3863	4	US-08-482-073-1	Sequence 1, Appli
821	161.5	4.1	1265	4	US-09-679-426-173	Sequence 173, App	894	157	4.0	3863	6	5217870-1	Patent No. 5217870
822	161.5	4.1	1265	4	US-09-759-143-173	Sequence 173, App	895	157	4.0	3863	6	5217870-1	Patent No. 5217870
823	161.5	4.1	1265	4	US-09-651-236-173	Sequence 173, App	896	156.5	4.0	796	4	US-09-902-540-1941	Sequence 1941, Ap
824	161.5	4.1	1462	4	US-09-270-767-11082	Sequence 173, App	897	156.5	4.0	807	3	US-09-715-994-3	Sequence 3, Appli
825	161.5	4.1	1729	2	US-08-844-024-1	Sequence 11082, A	898	156.5	4.0	1171	4	US-09-636-382A-14	Sequence 14, Appli
826	161.5	4.1	1729	2	US-08-718-547-1	Sequence 1, Appli	899	156.5	4.0	2438	4	US-09-949-016-5393	Sequence 5393, Ap
827	161	4.1	1143	4	US-09-949-016-1841	Sequence 1, Appli	900	156.5	4.0	2438	4	US-09-949-016-5394	Sequence 5394, Ap
828	161	4.1	1499	4	US-09-509-908-1	Sequence 1, Appli	901	156.5	4.0	2438	4	US-09-949-016-5395	Sequence 5395, Ap
829	161	4.1	1907	3	US-10-000-489-53	Sequence 53, Appli	902	156.5	4.0	2438	4	US-09-949-016-5396	Sequence 5396, Ap
830	160.5	4.1	725	3	US-09-197-801-12	Sequence 12, Appli	903	156	4.0	711	3	US-08-622-046B-13	Sequence 13, Appli
831	160.5	4.1	725	3	US-09-551-028-12	Sequence 12, Appli	904	156	4.0	711	3	US-08-622-046B-13	Sequence 13, Appli
832	160.5	4.1	725	3	US-09-664-595A-12	Sequence 12, Appli	905	156	4.0	711	3	US-09-100-264-2	Sequence 2, Appli
833	160.5	4.1	2186	4	US-09-949-016-4905	Sequence 4905, Ap	906	156	4.0	711	4	US-08-843-076D-2	Sequence 2, Appli
834	160.5	4.1	2208	4	US-09-949-016-286	Sequence 286, App	907	156	4.0	760	3	US-08-768-859A-7	Sequence 7, Appli
835	160.5	4.1	3042	4	US-09-919-039-100	Sequence 100, App	908	156	4.0	760	3	US-08-767-820A-7	Sequence 7, Appli
836	160	4.1	900	4	US-09-949-016-4841	Sequence 4841, App	909	156	4.0	760	5	PCT-US95-06157-7	Sequence 7, Appli
837	159.5	4.0	875	4	US-09-270-767-419	Sequence 419, App	910	156	4.0	766	3	US-08-768-859A-9	Sequence 9, Appli
838	159.5	4.0	875	4	US-09-270-767-15701	Sequence 15701, A	911	156	4.0	766	3	US-08-767-820A-9	Sequence 9, Appli
839	159.5	4.0	12183	4	US-09-902-540-1066	Sequence 1066, Ap	912	156	4.0	766	3	US-08-622-046B-6	Sequence 6, Appli
840	159	4.0	1082	4	US-09-244-111-1	Sequence 1, Appli	913	156	4.0	766	3	US-08-622-046B-17	Sequence 17, Appli
841	159	4.0	1507	4	US-09-949-016-1840	Sequence 1840, Ap	914	156	4.0	766	3	US-09-100-264-6	Sequence 6, Appli
842	159	4.0	1981	3	US-08-981-392-26	Sequence 26, Appli	915	156	4.0	766	3	US-08-843-076D-6	Sequence 6, Appli
843	159	4.0	1981	4	US-09-908-322-26	Sequence 26, Appli	916	156	4.0	766	5	PCT-US95-06157-7	Sequence 7, Appli
844	159	4.0	2188	1	US-07-882-925A-4	Sequence 4, Appli	917	156	4.0	766	5	PCT-US95-06157-7	Sequence 7, Appli
845	159	4.0	2188	1	US-08-184-012C-4	Sequence 4, Appli	918	156	4.0	35100	2	US-08-770-379-17	Sequence 17, Appli
846	159	4.0	2857	3	US-08-981-392-4	Sequence 4, Appli	919	156	4.0	35100	2	US-08-757-669A-17	Sequence 17, Appli
847	159	4.0	2857	4	US-09-908-322-4	Sequence 4, Appli	920	155.5	3.9	6951	4	US-09-230-371A-17	Sequence 17, Appli
848	159	4.0	2892	1	US-08-264-534-5	Sequence 5, Appli	921	155.5	3.9	7313	4	US-09-023-655-1265	Sequence 1265, Ap
849	159	4.0	2892	1	US-08-083-590A-1	Sequence 1, Appli	922	154.5	3.9	998	1	US-09-620-312D-259	Sequence 259, App
850	159	4.0	2892	1	US-08-465-500-5	Sequence 5, Appli	923	154.5	3.9	998	1	US-08-553-516-1	Sequence 1, Appli
851	159	4.0	2892	2	US-08-346-126-5	Sequence 5, Appli	924	154.5	3.9	998	2	US-08-238-130-1	Sequence 1, Appli
852	159	4.0	2892	2	US-08-346-128-5	Sequence 5, Appli	925	154.5	3.9	998	3	US-08-821-426-3	Sequence 3, Appli
853	159	4.0	2892	3	US-08-532-384-1	Sequence 1, Appli	926	154.5	3.9	998	5	PCT-US95-07743-3	Sequence 3, Appli
854	159	4.0	2892	3	US-08-893-828-5	Sequence 5, Appli	927	154.5	3.9	1498	5	PCT-US95-07743-3	Sequence 3, Appli
855	158	4.0	832	3	US-09-100-264-8	Sequence 8, Appli	928	154.5	3.9	6951	6	5256642-1	Patent No. 5256642
856	158	4.0	832	3	US-08-768-859A-5	Sequence 5, Appli	929	154.5	3.9	6951	6	5472939-1	Patent No. 5472939
857	158	4.0	832	3	US-08-768-859A-20	Sequence 20, Appli	930	154.5	3.9	6951	6	5256642-1	Patent No. 5256642
858	158	4.0	832	3	US-08-767-820A-5	Sequence 5, Appli	931	154.5	3.9	6951	6	5472939-1	Patent No. 5472939
859	158	4.0	832	3	US-08-767-820A-20	Sequence 20, Appli	932	154	3.9	744	3	US-09-032-215-39	Sequence 39, Appli
860	158	4.0	832	3	US-08-622-046B-4	Sequence 4, Appli	933	154	3.9	744	3	US-09-032-215-40	Sequence 40, Appli
861	158	4.0	832	3	US-08-622-046B-15	Sequence 15, Appli	934	154	3.9	782	4	US-09-229-151C-9	Sequence 9, Appli
862	158	4.0	832	4	US-08-843-076D-4	Sequence 4, Appli	935	154	3.9	833	4	US-09-229-151C-10	Sequence 10, Appli
863	158	4.0	832	5	PCT-US95-06157-5	Sequence 5, Appli	936	154	3.9	839	4	US-09-229-151C-8	Sequence 8, Appli
864	158	4.0	1341	3	US-08-983-075D-6	Sequence 6, Appli	937	154	3.9	841	3	US-09-032-215-36	Sequence 36, Appli
865	158	4.0	2639	3	US-09-374-135-1	Sequence 1, Appli	938	154	3.9	841	3	US-09-032-215-38	Sequence 38, Appli
866	158	4.0	5329	4	US-09-562-702A-19	Sequence 19, Appli	939	154	3.9	896	4	US-09-023-655-1309	Sequence 1309, Ap
867	158	4.0	5329	4	US-09-561-818A-19	Sequence 19, Appli	940	154	3.9	967	4	US-09-270-767-2133	Sequence 2133, Ap
868	158	4.0	5689	4	US-09-562-702A-17	Sequence 17, Appli	941	154	3.9	967	4	US-09-270-767-17415	Sequence 17415, A
869	158	4.0	5689	4	US-09-561-818A-17	Sequence 17, Appli	942	154	3.9	1476	2	US-08-824-874-2	Sequence 2, Appli
870	157.5	4.0	894	3	US-08-906-769-90	Sequence 90, Appli	943	154	3.9	1476	3	US-09-210-084-2	Sequence 2, Appli
871	157.5	4.0	894	3	US-08-906-616-90	Sequence 90, Appli	944	154	3.9	1476	3	US-09-210-084-2	Sequence 2, Appli
872	157.5	4.0	894	3	US-08-617-795-90	Sequence 90, Appli	945	153.5	3.9	599	3	US-08-705-875A-2	Sequence 2, Appli
873	157.5	4.0	894	3	US-08-639-075A-90	Sequence 90, Appli	946	153.5	3.9	599	3	US-09-242-999-2	Sequence 2, Appli
874	157.5	4.0	894	3	US-09-012-431-90	Sequence 90, Appli	947	153.5	3.9	1059	4	US-09-902-540-2450	Sequence 2450, Ap
875	157.5	4.0	894	3	US-09-012-431-90	Sequence 90, Appli	948	153.5	3.9	1364	3	US-09-280-116-20	Sequence 20, Appli
876	157.5	4.0	894	3	PCT-US95-14442A-90	Sequence 90, Appli	949	153.5	3.9	1833	1	US-08-365-470-2	Sequence 2, Appli
877	157.5	4.0	894	5	US-08-906-613-90	Sequence 90, Appli	950	153.5	3.9	2218	3	US-08-845-998-5	Sequence 5, Appli
878	157.5	4.0	2259	3	US-08-845-998-3	Sequence 3, Appli	951	153.5	3.9	2218	3	US-09-206-537-5	Sequence 5, Appli
879	157.5	4.0	2259	3	US-09-206-537-3	Sequence 3, Appli	952	153.5	3.9	2218	3	US-09-430-854-5	Sequence 5, Appli
880	157.5	4.0	2259	3	US-09-430-854-3	Sequence 3, Appli	953	153.5	3.9	3034	3	US-09-209-668-18	Sequence 18, Appli
881	157.5	4.0	5420	6	5256642-3	Patent No. 5256642	954	153.5	3.9	3834	4	US-09-949-016-71	Sequence 71, Appli
882	157.5	4.0	5420	6	5472939-3	Patent No. 5472939	955	153.5	3.9	3854	1	US-08-365-470-1	Sequence 1, Appli
883	157.5	4.0	5420	6	5256642-3	Patent No. 5256642	956	153.5	3.9	3858	4	US-08-344-155C-98	Sequence 98, Appli
884	157.5	4.0	5420	6	5472939-3	Patent No. 5472939	957	153.5	3.9	3858	3	US-09-009-490A-88	Sequence 88, Appli
885	157	4.0	610	3	US-08-906-769-140	Sequence 140, App	958	153.5	3.9	30371	4	US-09-949-016-15395	Sequence 15395, A
886	157	4.0	610	3	US-08-906-616-140	Sequence 140, App	959	153	3.9	1358	3	US-08-983-075D-8	Sequence 8, Appli
887	157	4.0	610	3	US-09-639-075A-140	Sequence 140, App	960	153	3.9	5561	1	US-08-400-159-1	Sequence 1, Appli
888	157	4.0	610	3	US-09-012-431-140	Sequence 140, App	961	153	3.9	5561	3	US-08-611-729A-1	Sequence 1, Appli

962	153	3.9	5561	4	US-09-195-524-1	Sequence 1, Appli	1035	147.5	3.7	758	3	US-09-012-692-126	Sequence 126, App
963	152.5	3.9	1040	4	US-09-023-655-1487	Sequence 1487, Ap	1036	147.5	3.7	758	3	US-08-906-613-126	Sequence 126, App
964	152.5	3.9	1040	4	US-09-949-016-4840	Sequence 4840, Ap	1037	147.5	3.7	493	3	US-09-392-184-20	Sequence 20, Appl
965	152.5	3.9	2272	4	US-09-949-016-5498	Sequence 5498, Ap	1038	147.5	3.7	1361	3	US-09-578-303-1	Sequence 1, Appli
966	152.5	3.9	2272	4	US-09-949-016-5499	Sequence 5499, Ap	1039	147.5	3.7	1786	4	US-09-949-016-5855	Sequence 5855, Ap
967	152.5	3.9	2272	4	US-09-949-016-5500	Sequence 5500, Ap	1040	147.5	3.7	11220	4	US-09-949-016-5061	Sequence 5061, Ap
968	152.5	3.9	2272	4	US-09-949-016-5501	Sequence 5501, Ap	1041	146.5	3.7	1734	3	US-09-484-970B-63	Sequence 63, Appl
969	152	3.9	841	3	US-08-906-769-110	Sequence 110, App	1042	146	3.7	779	3	US-08-906-769-80	Sequence 80, Appl
970	152	3.9	841	3	US-08-906-616-110	Sequence 110, App	1043	146	3.7	779	3	US-08-906-616-80	Sequence 80, Appl
971	152	3.9	841	3	US-08-817-795-110	Sequence 110, App	1044	146	3.7	779	3	US-08-817-795-80	Sequence 80, Appl
972	152	3.9	841	3	US-08-639-075A-110	Sequence 110, App	1045	146	3.7	779	3	US-08-639-075A-80	Sequence 80, Appl
973	152	3.9	841	3	US-09-012-431-110	Sequence 110, App	1046	146	3.7	779	3	US-09-012-431-80	Sequence 80, Appl
974	152	3.9	841	3	US-09-012-692-110	Sequence 110, App	1047	146	3.7	779	3	US-09-012-692-80	Sequence 80, Appl
975	152	3.9	841	3	US-08-906-613-110	Sequence 110, App	1048	146	3.7	779	3	US-08-906-613-80	Sequence 80, Appl
976	152	3.9	841	3	PCT-US95-14442A-110	Sequence 110, App	1049	146	3.7	779	3	PCT-US95-14442A-80	Sequence 80, Appl
977	152	3.9	882	4	US-09-949-016-4790	Sequence 4790, Ap	1050	146	3.7	789	4	US-09-653-813-3	Sequence 3, Appli
978	152	3.9	882	4	US-09-023-655-1150	Sequence 1150, Ap	1051	146	3.7	789	4	US-09-653-813-5	Sequence 5, Appli
979	152	3.9	920	4	US-09-949-016-586	Sequence 586, App	1052	145.5	3.7	850	3	US-08-906-769-102	Sequence 102, App
980	152	3.9	3934	4	US-09-023-655-1066	Sequence 1066, Ap	1053	145.5	3.7	850	3	US-08-906-616-102	Sequence 102, App
981	151.5	3.8	5433	4	US-09-949-016-5083	Sequence 5083, Ap	1054	145.5	3.7	850	3	US-08-817-795-102	Sequence 102, App
982	151.5	3.8	5433	4	US-09-562-702A-15	Sequence 15, Appl	1055	145.5	3.7	850	3	US-08-639-075A-102	Sequence 102, App
983	151.5	3.8	5433	4	US-09-561-818A-15	Sequence 15, Appl	1056	145.5	3.7	850	3	US-09-012-431-102	Sequence 102, App
984	151.5	3.8	5613	4	US-09-562-702A-13	Sequence 13, Appl	1057	145.5	3.7	850	3	US-09-012-692-102	Sequence 102, App
985	151.5	3.8	5613	4	US-09-561-818A-13	Sequence 13, Appl	1058	145.5	3.7	850	3	US-08-906-613-102	Sequence 102, App
986	151.5	3.8	5613	4	US-09-561-709B-10	Sequence 10, Appl	1059	145.5	3.7	850	5	PCT-US95-14442A-102	Sequence 102, App
987	151	3.8	2330	1	US-08-461-803-1	Sequence 1, Appli	1060	145	3.7	36755	4	US-09-949-016-16994	Sequence 16994, A
988	151	3.8	2330	1	US-08-215-366A-1	Sequence 1, Appli	1061	145	3.7	38059	4	US-09-328-925-4	Sequence 4, Appli
989	151	3.8	2330	1	US-08-340-539A-1	Sequence 1, Appli	1062	144.5	3.7	769	3	US-09-331-709-1	Sequence 1, Appli
990	151	3.8	2330	2	US-08-461-592B-1	Sequence 1, Appli	1063	144.5	3.7	774	3	US-09-004-731-18	Sequence 18, Appl
991	150.5	3.8	1414	1	US-08-024-868-1	Sequence 1, Appli	1064	144.5	3.7	774	3	US-09-004-731-20	Sequence 20, Appl
992	150.5	3.8	1414	2	US-08-242-097-1	Sequence 1, Appli	1065	144.5	3.7	774	3	US-08-749-699-18	Sequence 18, Appl
993	150.5	3.8	1414	3	US-09-206-695-1	Sequence 1, Appli	1066	144.5	3.7	774	3	US-08-749-699-20	Sequence 20, Appl
994	150.5	3.8	1414	4	US-09-799-118-1	Sequence 1, Appli	1067	144.5	3.7	774	3	US-09-004-729-18	Sequence 18, Appl
995	150.5	3.8	2214	6	US-08-513-278-3	Sequence 3, Appli	1068	144.5	3.7	774	3	US-09-004-729-20	Sequence 20, Appl
996	150.5	3.8	2214	6	5514582-3	Patent No. 5514582	1069	144.5	3.7	1089	3	US-09-004-731-15	Sequence 15, Appl
997	150.5	3.8	2214	6	5514582-3	Patent No. 5514582	1070	144.5	3.7	1089	3	US-09-004-731-17	Sequence 17, Appl
998	150	3.8	789	4	US-09-653-813-1	Sequence 1, Appli	1071	144.5	3.7	1089	3	US-08-749-699-15	Sequence 15, Appl
999	150	3.8	2021	1	US-07-882-325A-3	Sequence 3, Appli	1072	144.5	3.7	1089	3	US-08-749-699-17	Sequence 17, Appl
1000	150	3.8	2021	1	US-08-184-012C-3	Sequence 3, Appli	1073	144.5	3.7	1089	3	US-09-004-729-15	Sequence 15, Appl
1001	149.5	3.8	726	3	US-09-032-215-49	Sequence 49, Appl	1074	144.5	3.7	1089	3	US-09-004-729-17	Sequence 17, Appl
1002	149.5	3.8	726	3	US-09-032-215-50	Sequence 50, Appl	1075	144.5	3.7	1109	3	US-09-004-729-19	Sequence 19, Appl
1003	149.5	3.8	841	3	US-09-032-215-46	Sequence 46, Appl	1076	144.5	3.7	17098	4	US-09-949-016-13119	Sequence 13119, A
1004	149.5	3.8	841	3	US-09-032-215-48	Sequence 48, Appl	1077	144	3.7	490	4	US-09-270-767-29595	Sequence 29595, A
1005	149.5	3.8	881	4	US-09-669-751-112	Sequence 112, App	1078	143.5	3.6	601	4	US-09-949-016-121483	Sequence 121483, A
1006	149.5	3.8	19253	4	US-09-949-016-15131	Sequence 15131, A	1079	143.5	3.6	6101	4	US-09-949-016-1376	Sequence 1376, Ap
1007	149	3.8	840	1	US-07-906-983-1	Sequence 1, Appli	1080	143.5	3.6	7017	4	US-09-949-016-67	Sequence 67, Appl
1008	149	3.8	917	4	US-09-799-451-516	Sequence 516, App	1081	143	3.6	711	3	US-09-004-731-21	Sequence 21, Appl
1009	149	3.8	2385	4	US-09-495-050A-292	Sequence 292, App	1082	143	3.6	711	3	US-08-749-699-21	Sequence 21, Appl
1010	149	3.8	2621	4	US-09-949-016-1377	Sequence 1377, Ap	1083	143	3.6	711	3	US-09-004-729-21	Sequence 21, Appl
1011	148.5	3.8	717	3	US-09-004-731-43	Sequence 43, Appl	1084	143	3.6	2354	4	US-09-023-655-1154	Sequence 1154, Ap
1012	148.5	3.8	717	3	US-09-004-731-45	Sequence 45, Appl	1085	143	3.6	3737	4	US-09-747-371-1	Sequence 1, Appli
1013	148.5	3.8	717	3	US-08-749-699-43	Sequence 43, Appl	1086	142.5	3.6	681	1	US-07-529-198-5	Sequence 5, Appli
1014	148.5	3.8	717	3	US-08-749-699-45	Sequence 45, Appl	1087	142.5	3.6	942	4	US-09-636-382A-3	Sequence 3, Appli
1015	148.5	3.8	717	3	US-09-004-729-43	Sequence 43, Appl	1088	142.5	3.6	1980	1	US-08-278-630A-12	Sequence 12, Appl
1016	148.5	3.8	717	3	US-09-004-729-45	Sequence 45, Appl	1089	142	3.6	649	3	US-08-824-692-21	Sequence 21, Appl
1017	148.5	3.8	841	3	US-09-004-731-40	Sequence 40, Appl	1090	142	3.6	1848	3	US-09-475-460A-31	Sequence 31, Appl
1018	148.5	3.8	841	3	US-09-004-731-42	Sequence 42, Appl	1091	142	3.6	1848	3	US-08-748-061A-31	Sequence 31, Appl
1019	148.5	3.8	841	3	US-08-749-699-40	Sequence 40, Appl	1092	142	3.6	2397	2	US-08-978-404B-2	Sequence 2, Appli
1020	148.5	3.8	841	3	US-08-749-699-42	Sequence 42, Appl	1093	142	3.6	3173	4	US-09-799-451-428	Sequence 428, App
1021	148.5	3.8	841	3	US-09-004-729-40	Sequence 40, Appl	1094	141.5	3.6	1464	3	US-09-188-930-255	Sequence 255, App
1022	148.5	3.8	841	3	US-09-004-729-42	Sequence 42, Appl	1095	141.5	3.6	1464	3	US-09-312-283C-255	Sequence 255, App
1023	148.5	3.8	921	4	US-09-902-540-1978	Sequence 1978, Ap	1096	141.5	3.6	1633	3	US-09-188-930-73	Sequence 73, Appl
1024	148.5	3.8	15572	4	US-09-902-540-1131	Sequence 1131, Ap	1097	141.5	3.6	1635	3	US-09-312-283C-73	Sequence 73, Appl
1025	148	3.8	1878	2	US-08-435-149-17	Sequence 17, Appl	1098	141	3.6	1119	3	US-09-020-956-177	Sequence 177, App
1026	148	3.8	2070	4	US-09-949-016-5494	Sequence 5494, Ap	1099	141	3.6	1119	3	US-09-030-607-177	Sequence 177, App
1027	148	3.8	2070	4	US-09-949-016-5495	Sequence 5495, Ap	1100	141	3.6	1119	3	US-09-439-313-177	Sequence 177, App
1028	148	3.8	2070	4	US-09-949-016-5496	Sequence 5496, Ap	1101	141	3.6	1119	3	US-09-352-616A-177	Sequence 177, App
1029	148	3.8	2070	4	US-09-949-016-5497	Sequence 5497, Ap	1102	141	3.6	1119	3	US-09-232-149A-177	Sequence 177, App
1030	148	3.8	8378	5	PCT-US91-09055-1	Sequence 1, Appli	1103	141	3.6	1119	4	US-09-159-812-177	Sequence 177, App
1031	147.5	3.7	758	3	US-08-906-769-126	Sequence 126, App	1104	141	3.6	1119	4	US-09-636-215-177	Sequence 177, App
1032	147.5	3.7	758	3	US-08-906-616-126	Sequence 126, App	1105	141	3.6	1119	4	US-09-685-166A-177	Sequence 177, App
1033	147.5	3.7	758	3	US-08-639-075A-126	Sequence 126, App	1106	141	3.6	1119	4	US-09-115-453-177	Sequence 177, App
1034	147.5	3.7	758	3	US-09-012-431-126	Sequence 126, App	1107	141	3.6	1119	4	US-09-688-489-177	Sequence 177, App

1108	141	3.6	1119	4	US-09-679-426-177	Sequence 177, App	1181	135.5	3.4	80161	3	US-09-370-700-1	Sequence 1, Appli
1109	141	3.6	1119	4	US-09-759-143-177	Sequence 177, App	1182	135.5	3.4	80161	4	US-09-603-207-1	Sequence 1, Appli
1110	141	3.6	1119	4	US-09-651-236-177	Sequence 177, App	1183	135	3.4	716	4	US-09-423-753-11	Sequence 11, Appl
1111	141	3.6	1129	4	US-09-799-451-171	Sequence 471, App	1184	134.5	3.4	4758	3	US-09-191-647-1	Sequence 1, Appli
1112	141	3.6	1187	4	US-10-000-489-105	Sequence 105, App	1185	134.5	3.4	4758	3	US-09-540-245A-1	Sequence 1, Appli
1113	140	3.5	857	4	US-09-023-655-1046	Sequence 1046, Ap	1186	134.5	3.4	4758	4	US-09-540-153-1	Sequence 1, Appli
1114	140	3.5	857	4	US-09-949-016-4791	Sequence 4791, Ap	1187	134.5	3.4	5933	4	US-09-919-172-23	Sequence 23, Appl
1115	139.5	3.5	768	3	US-09-042-215-34	Sequence 34, Appl	1188	134.5	3.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
1116	139.5	3.5	792	3	US-09-244-111-3	Sequence 3, Appli	1189	134.5	3.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
1117	139.5	3.5	932	3	US-09-032-215-31	Sequence 31, Appl	1190	134	3.4	1638	1	US-08-253-155A-1	Sequence 1, Appli
1118	139.5	3.5	3448	4	US-09-799-451-34	Sequence 34, Appl	1191	134	3.4	1785	4	US-09-148-545-112	Sequence 112, App
1119	139	3.5	923	3	US-08-906-769-144	Sequence 144, App	1192	134	3.4	2430	2	US-08-820-170A-35	Sequence 35, Appl
1120	139	3.5	923	3	US-08-906-616-144	Sequence 144, App	1193	134	3.4	2430	3	US-09-055-699-35	Sequence 35, Appl
1121	139	3.5	923	3	US-08-639-075A-144	Sequence 144, App	1194	134	3.4	2430	3	US-09-273-565-35	Sequence 35, Appl
1122	139	3.5	923	3	US-09-004-731-66	Sequence 66, Appl	1195	134	3.4	2430	3	US-09-565-538-35	Sequence 35, Appl
1123	139	3.5	923	3	US-09-012-431-144	Sequence 144, App	1196	134	3.4	2430	3	US-09-661-468-35	Sequence 35, Appl
1124	139	3.5	923	3	US-08-749-699-66	Sequence 66, Appl	1197	134	3.4	2430	3	US-09-976-165-35	Sequence 35, Appl
1125	139	3.5	923	3	US-09-012-692-144	Sequence 144, App	1198	134	3.4	2977	2	US-08-820-170A-36	Sequence 36, Appl
1126	139	3.5	923	3	US-08-906-613-144	Sequence 144, App	1199	134	3.4	2977	3	US-09-055-699-36	Sequence 36, Appl
1127	139	3.5	923	3	US-09-004-729-66	Sequence 66, Appl	1200	134	3.4	2977	3	US-09-273-565-36	Sequence 36, Appl
1128	139	3.5	1205	4	US-09-976-594-457	Sequence 457, App	1201	134	3.4	2977	3	US-09-565-538-36	Sequence 36, Appl
1129	139	3.5	1333	1	US-08-684-862-9	Sequence 9, Appli	1202	134	3.4	2977	3	US-09-661-468-36	Sequence 36, Appl
1130	138.5	3.5	681	1	US-07-929-198-1	Sequence 1, Appli	1203	134	3.4	2977	4	US-09-976-165-36	Sequence 36, Appl
1131	138.5	3.5	769	4	US-09-023-655-1039	Sequence 1039, Ap	1204	133.5	3.4	654	4	US-09-280-116-57	Sequence 57, Appl
1132	138.5	3.5	4080	4	US-09-016-434-1326	Sequence 1326, Ap	1205	133.5	3.4	767	3	US-08-824-692-25	Sequence 25, Appl
1133	138.5	3.5	5645	4	US-09-023-655-1319	Sequence 1319, Ap	1206	133.5	3.4	5499	3	US-09-592-685-1	Sequence 1, Appli
1134	138.5	3.5	5681	4	US-09-919-172-58	Sequence 58, Appl	1207	133.5	3.4	5499	4	US-09-592-685-1	Sequence 1, Appli
1135	138	3.5	855	3	US-08-906-769-130	Sequence 130, App	1208	133.5	3.4	5502	5	PCT-US95-02251-17	Sequence 17, Appl
1136	138	3.5	855	3	US-08-906-616-130	Sequence 130, App	1209	133.5	3.4	6811	3	US-08-651-472-67	Sequence 67, Appl
1137	138	3.5	855	3	US-08-639-075A-130	Sequence 130, App	1210	133.5	3.4	6811	3	US-08-358-928-67	Sequence 67, Appl
1138	138	3.5	855	3	US-09-012-431-130	Sequence 130, App	1211	133.5	3.4	7263	4	US-09-562-702A-31	Sequence 31, Appl
1139	138	3.5	855	3	US-09-012-692-130	Sequence 130, App	1212	133.5	3.4	7263	4	US-09-561-818A-27	Sequence 27, Appl
1140	138	3.5	855	3	US-08-906-613-130	Sequence 130, App	1213	133.5	3.4	7554	4	US-09-562-702A-29	Sequence 29, Appl
1141	137	3.5	699	1	US-08-738-413B-8	Sequence 8, Appli	1214	133.5	3.4	7554	4	US-09-561-818A-25	Sequence 25, Appl
1142	137	3.5	785	4	US-09-270-767-1349	Sequence 1349, Ap	1215	133	3.4	6049	4	US-08-793-273C-3	Sequence 3, Appli
1143	137	3.5	785	4	US-09-270-767-16631	Sequence 16631, A	1216	133	3.4	6049	5	PCT-US95-1168A-3	Sequence 3, Appli
1144	137	3.5	1213	4	US-09-270-767-12797	Sequence 12797, A	1217	132.5	3.4	865	4	US-09-270-767-1549	Sequence 1549, Ap
1145	137	3.5	2259	2	US-08-513-278-1	Sequence 1, Appli	1218	132.5	3.4	865	4	US-09-270-767-16831	Sequence 16831, A
1146	137	3.5	6153	2	US-08-347-594A-1	Sequence 1, Appli	1219	132.5	3.4	1545	4	US-09-270-767-1178	Sequence 1178, Ap
1147	137	3.5	6942	2	US-08-460-309-3	Sequence 3, Appli	1220	132.5	3.4	1545	4	US-09-270-767-16460	Sequence 16460, A
1148	137	3.5	6942	2	US-08-125-077-3	Sequence 3, Appli	1221	132	3.3	504	4	US-09-636-215-839	Sequence 839, App
1149	137	3.5	9419	4	US-09-562-702A-7	Sequence 7, Appli	1222	132	3.3	504	4	US-09-585-166A-839	Sequence 839, App
1150	137	3.5	9420	4	US-09-562-702A-3	Sequence 3, Appli	1223	132	3.3	504	4	US-09-679-426-839	Sequence 839, App
1151	137	3.5	9534	4	US-09-562-702A-5	Sequence 5, Appli	1224	132	3.3	504	4	US-09-759-143-839	Sequence 839, App
1152	137	3.5	9534	4	US-09-561-709B-8	Sequence 8, Appli	1225	132	3.3	504	4	US-09-651-236-839	Sequence 839, App
1153	137	3.5	9534	4	US-09-917-254-35	Sequence 35, Appl	1226	132	3.3	1448	3	US-09-130-491-9	Sequence 9, Appli
1154	137	3.5	9534	4	US-09-949-016-66	Sequence 66, Appli	1227	132	3.3	2481	3	US-09-188-930-64	Sequence 64, Appl
1155	137	3.5	9535	4	US-09-562-702A-1	Sequence 1, Appli	1228	132	3.3	2481	3	US-09-312-283C-64	Sequence 64, Appl
1156	137	3.5	9537	4	US-09-949-016-1646	Sequence 1646, Ap	1229	131.5	3.3	1109	3	US-09-088-651-6	Sequence 6, Appli
1157	136.5	3.5	493	3	US-09-280-116-166	Sequence 166, App	1230	131.5	3.3	1787	1	US-08-278-630A-13	Sequence 13, Appl
1158	136.5	3.5	681	1	US-07-929-198-3	Sequence 3, Appli	1231	131.5	3.3	6642	1	US-08-727-034-5	Sequence 5, Appli
1159	136.5	3.5	9391	4	US-09-562-702A-11	Sequence 11, Appl	1232	131.5	3.3	6843	1	US-08-727-034-6	Sequence 6, Appli
1160	136.5	3.5	9511	4	US-09-562-702A-9	Sequence 9, Appli	1233	131.5	3.3	6868	4	US-09-919-039-39	Sequence 39, Appl
1161	136.5	3.5	85368	4	US-09-949-016-12211	Sequence 12211, A	1234	131	3.3	3450	2	US-08-751-305-1	Sequence 1, Appli
1162	136	3.4	933	3	US-09-280-116-191	Sequence 191, App	1235	131	3.3	6639	1	US-08-727-034-1	Sequence 1, Appli
1163	136	3.4	4948	4	US-09-562-702A-23	Sequence 23, Appl	1236	131	3.3	6961	1	US-08-727-034-2	Sequence 2, Appli
1164	136	3.4	4948	4	US-09-561-818A-23	Sequence 23, Appl	1237	131	3.3	40261	4	US-09-949-016-11773	Sequence 11773, A
1165	136	3.4	4972	4	US-09-562-702A-27	Sequence 27, Appl	1238	131	3.3	40265	4	US-09-949-016-16168	Sequence 16168, A
1166	136	3.4	5306	4	US-09-562-702A-21	Sequence 21, Appl	1239	130.5	3.3	860	1	US-08-310-416A-19	Sequence 19, Appl
1167	136	3.4	5306	4	US-09-561-818A-21	Sequence 21, Appl	1240	130.5	3.3	860	2	US-08-888-171-19	Sequence 19, Appl
1168	136	3.4	5330	4	US-09-562-702A-25	Sequence 25, Appl	1241	130.5	3.3	969	2	US-08-310-416A-12	Sequence 12, Appl
1169	136	3.4	6153	3	US-08-463-682-2	Sequence 2, Appli	1242	130.5	3.3	969	2	US-08-888-171-12	Sequence 12, Appl
1170	135.5	3.4	768	3	US-09-032-215-35	Sequence 35, Appl	1243	130.5	3.3	1117	4	US-09-148-545-54	Sequence 54, Appl
1171	135.5	3.4	932	3	US-08-906-769-88	Sequence 88, Appl	1244	130.5	3.3	2017	4	US-09-844-311-1	Sequence 1, Appli
1172	135.5	3.4	932	3	US-08-906-616-88	Sequence 88, Appl	1245	130.5	3.3	2056	1	US-08-458-084-1	Sequence 1, Appli
1173	135.5	3.4	932	3	US-08-817-795-88	Sequence 88, Appl	1246	130.5	3.3	2096	1	US-08-205-508-1	Sequence 1, Appli
1174	135.5	3.4	932	3	US-08-639-075A-88	Sequence 88, Appl	1247	130.5	3.3	2096	1	US-08-278-630A-10	Sequence 10, Appl
1175	135.5	3.4	932	3	US-09-012-431-88	Sequence 88, Appl	1248	130.5	3.3	2096	5	PCT-US95-02945-1	Sequence 1, Appli
1176	135.5	3.4	932	3	US-09-032-215-33	Sequence 33, Appl	1249	130.5	3.3	2847	3	US-08-087-007-2	Sequence 2, Appli
1177	135.5	3.4	932	3	US-09-012-692-88	Sequence 88, Appl	1250	130.5	3.3	2847	3	US-08-483-433-2	Sequence 2, Appli
1178	135.5	3.4	932	3	US-08-906-613-88	Sequence 88, Appl	1251	130.5	3.3	2847	5	PCT-US92-05920-2	Sequence 2, Appli
1179	135.5	3.4	932	5	PCT-US95-1444A-88	Sequence 88, Appl	1252	130.5	3.3	5191	1	US-08-340-428B-1	Sequence 1, Appli
1180	135.5	3.4	80161	3	US-09-036-987A-1	Sequence 1, Appli	1253	130.5	3.3	5191	5	PCT-US93-07306-1	Sequence 1, Appli

1254	130	3.3	433	3	US-08-906-769-152	Sequence 152, App	1327	127	3.2	1760	4	US-09-495-050A-139	Sequence 139, App
1255	130	3.3	433	3	US-08-906-616-152	Sequence 152, App	1328	127	3.2	5683	4	US-09-845-583A-7	Sequence 7, Appli
1256	130	3.3	433	3	US-08-639-075A-152	Sequence 152, App	1329	127	3.2	5683	4	US-09-917-254-36	Sequence 36, Appli
1257	130	3.3	433	3	US-09-004-731-80	Sequence 80, Appl	1330	127	3.2	5683	4	US-09-814-915A-78	Sequence 78, Appl
1258	130	3.3	433	3	US-09-012-431-152	Sequence 152, App	1331	126.5	3.2	5184	4	US-09-845-583A-9	Sequence 9, Appli
1259	130	3.3	433	3	US-08-749-699-80	Sequence 80, Appl	1332	126.5	3.2	5184	4	US-09-561-709B-4	Sequence 4, Appli
1260	130	3.3	433	3	US-09-012-692-152	Sequence 152, App	1333	126	3.2	396	4	US-09-621-976-1662	Sequence 1662, Ap
1261	130	3.3	433	3	US-08-906-613-152	Sequence 152, App	1334	126	3.2	735	4	US-09-270-767-12769	Sequence 12769, A
1262	130	3.3	433	3	US-09-004-729-80	Sequence 80, Appl	1335	126	3.2	2413	4	US-09-620-312D-189	Sequence 189, App
1263	130	3.3	433	3	US-09-702-705-109	Sequence 109, App	1336	126	3.2	2413	4	US-09-620-312D-31	Sequence 31, Appl
1264	130	3.3	662	4	US-09-736-457-109	Sequence 109, App	1337	126	3.2	2413	4	US-09-981-649A-31	Sequence 31, Appl
1265	130	3.3	662	4	US-09-671-325-109	Sequence 109, App	1338	126	3.2	3284	6	5258288-3	Patent No. 5258288
1266	130	3.3	662	4	US-09-671-325-109	Sequence 109, App	1339	126	3.2	3284	6	5258288-3	Patent No. 5258288
1267	130	3.3	662	4	US-09-589-184-109	Sequence 109, App	1340	126	3.2	3290	1	US-07-985-691-1	Sequence 1, Appli
1268	130	3.3	662	4	US-09-658-824-109	Sequence 109, App	1341	126	3.2	3290	1	US-08-436-804-1	Sequence 1, Appli
1269	130	3.3	1843	4	US-09-907-794A-131	Sequence 131, App	1342	126	3.2	3290	1	US-08-267-387-1	Sequence 1, Appli
1270	130	3.3	1843	4	US-09-905-125A-131	Sequence 131, App	1343	126	3.2	5583	4	US-09-312-283C-372	Sequence 372, App
1271	130	3.3	1843	4	US-09-902-775A-131	Sequence 131, App	1344	125.5	3.2	797	6	5180819-1	Patent No. 5180819
1272	130	3.3	1843	4	US-09-906-700-131	Sequence 131, App	1345	125.5	3.2	797	6	5180819-1	Patent No. 5180819
1273	130	3.3	1843	4	US-09-903-603A-131	Sequence 131, App	1346	125.5	3.2	866	4	US-09-620-312D-482	Sequence 482, App
1274	130	3.3	1843	4	US-09-904-920A-131	Sequence 131, App	1347	125	3.2	536	3	US-08-705-875A-7	Sequence 7, Appli
1275	130	3.3	1843	4	US-09-909-064-131	Sequence 131, App	1348	125	3.2	536	3	US-09-242-999-7	Sequence 28, Appl
1276	130	3.3	1843	4	US-09-905-381A-131	Sequence 131, App	1349	125	3.2	834	4	US-09-879-792-28	Sequence 67, Appl
1277	130	3.3	1843	4	US-09-906-618-131	Sequence 131, App	1350	125	3.2	1254	4	US-09-312-283C-67	Sequence 1127, Ap
1278	130	3.3	4125	4	US-09-949-016-3697	Sequence 3697, Ap	1351	125	3.2	14861	4	US-09-902-540-1127	Sequence 1480, Ap
1279	130	3.3	4138	1	US-08-323-474-1	Sequence 1, Appli	1352	124.5	3.2	434	4	US-09-702-705-1480	Sequence 1480, Ap
1280	130	3.3	4138	4	US-09-949-016-75	Sequence 75, Appl	1353	124.5	3.2	434	4	US-09-736-457-1480	Sequence 1480, Ap
1281	130	3.3	4138	5	PCT-US93-06093-1	Sequence 1, Appli	1354	124.5	3.2	434	4	US-09-614-124B-1480	Sequence 1480, Ap
1282	129.5	3.3	2115	4	US-09-014-240-1	Sequence 1, Appli	1355	124.5	3.2	434	4	US-09-671-325-1480	Sequence 1480, Ap
1283	129.5	3.3	2116	1	US-07-811-048-9	Sequence 9, Appli	1356	124.5	3.2	434	4	US-09-658-824-1480	Sequence 1480, Ap
1284	129.5	3.3	2220	4	US-09-023-655-1064	Sequence 1064, Ap	1357	124.5	3.2	2820	4	US-09-799-451-370	Sequence 370, App
1285	129.5	3.3	2220	4	US-09-844-311-3	Sequence 3, Appli	1358	124	3.1	700	3	US-09-280-116-68	Sequence 68, Appl
1286	129.5	3.3	2233	4	US-09-014-240-3	Sequence 3, Appli	1359	124	3.1	2397	6	5258288-2	Patent No. 5258288
1287	129.5	3.3	2234	1	US-07-811-048-10	Sequence 10, Appl	1360	124	3.1	2397	6	5258288-2	Patent No. 5258288
1288	129.5	3.3	3759	4	US-09-560-385A-15	Sequence 15, Appl	1361	124	3.1	2899	4	US-08-981-392-24	Sequence 24, Appl
1289	129.5	3.3	3930	4	US-09-560-385A-13	Sequence 13, Appl	1362	124	3.1	2899	4	US-09-270-767-12783	Sequence 12783, A
1290	129.5	3.3	3931	1	US-08-144-121-1	Sequence 1, Appli	1363	123.5	3.1	1376	4	US-09-308-322-24	Sequence 2, Appli
1291	129.5	3.3	3931	2	US-08-735-893-1	Sequence 1, Appli	1364	123.5	3.1	1611	3	US-09-249-697A-2	Sequence 2, Appli
1292	129.5	3.3	5176	3	US-09-182-024-1	Sequence 1, Appli	1365	123.5	3.1	1611	3	US-09-363-316B-2	Sequence 2, Appli
1293	129.5	3.3	5666	4	US-09-949-016-3565	Sequence 3565, Ap	1366	123.5	3.1	1611	3	US-10-136-227A-2	Sequence 2, Appli
1294	128.5	3.3	2179	4	US-09-949-016-3200	Sequence 3200, Ap	1367	123.5	3.1	1611	4	US-09-981-649A-2	Sequence 7, Appli
1295	128.5	3.3	2345	4	US-10-136-227A-29	Sequence 29, Appl	1368	123.5	3.1	2913	1	US-08-243-542-7	Sequence 7, Appli
1296	128.5	3.3	2345	4	US-09-981-649A-27	Sequence 27, Appl	1369	123.5	3.1	2913	1	US-08-477-407-7	Sequence 7, Appli
1297	128.5	3.3	2360	4	US-10-136-227A-27	Sequence 27, Appl	1370	123.5	3.1	2913	1	US-08-484-355-7	Sequence 7, Appli
1298	128.5	3.3	2360	4	US-09-981-649A-27	Sequence 27, Appl	1371	123	3.1	581	3	US-08-824-692-22	Sequence 22, Appl
1299	128.5	3.3	2365	3	US-09-249-697A-5	Sequence 5, Appli	1372	123	3.1	581	3	US-09-183-861-54	Sequence 54, Appl
1300	128.5	3.3	2365	3	US-09-249-697A-18	Sequence 18, Appl	1373	123	3.1	1585	3	US-09-022-765-54	Sequence 54, Appl
1301	128.5	3.3	2365	3	US-09-363-316B-23	Sequence 23, Appl	1374	123	3.1	1585	4	US-09-551-974A-54	Sequence 54, Appl
1302	128.5	3.3	2365	4	US-10-136-227A-5	Sequence 5, Appli	1375	123	3.1	1585	4	US-09-565-501A-54	Sequence 54, Appl
1303	128.5	3.3	2365	4	US-10-136-227A-23	Sequence 23, Appl	1376	123	3.1	1585	4	US-09-639-206A-54	Sequence 54, Appl
1304	128.5	3.3	2365	4	US-10-136-227A-23	Sequence 23, Appl	1377	123	3.1	1585	4	US-09-874-923-54	Sequence 54, Appl
1305	128.5	3.3	2365	4	US-09-981-649A-5	Sequence 5, Appli	1378	123	3.1	3003	4	US-09-807-794A-314	Sequence 314, App
1306	128.5	3.3	2365	4	US-09-981-649A-5	Sequence 5, Appli	1379	123	3.1	3003	4	US-09-905-125A-314	Sequence 314, App
1307	128.5	3.3	2386	4	US-09-949-016-2304	Sequence 2304, Ap	1380	123	3.1	3003	4	US-09-902-775A-314	Sequence 314, App
1308	128	3.2	671	4	US-09-270-767-31113	Sequence 1113, A	1381	123	3.1	3003	4	US-09-906-700-314	Sequence 314, App
1309	128	3.2	957	1	US-08-684-862-11	Sequence 11, Appl	1382	123	3.1	3003	4	US-09-903-603A-314	Sequence 314, App
1310	128	3.2	1758	4	US-09-641-612-8	Sequence 8, Appli	1383	123	3.1	3003	4	US-09-904-920A-314	Sequence 314, App
1311	128	3.2	3971	4	US-09-876-176-1	Sequence 1, Appli	1384	123	3.1	3003	4	US-09-905-381A-314	Sequence 314, App
1312	128	3.2	7286	4	US-08-793-273C-1	Sequence 1, Appli	1385	123	3.1	3003	4	US-09-906-618-314	Sequence 23, Appl
1313	128	3.2	7286	5	PCT-US95-11684-1	Sequence 1, Appli	1386	123	3.1	3003	4	US-09-560-385A-23	Sequence 19, Appl
1314	127.5	3.2	865	3	US-09-796-110-1	Sequence 1, Appli	1387	123	3.1	3469	4	US-09-560-385A-19	Sequence 21, Appl
1315	127.5	3.2	95255	4	US-09-949-016-17067	Sequence 17067, A	1388	123	3.1	3511	4	US-09-560-385A-21	Sequence 17, Appl
1316	127	3.2	315	4	US-09-270-767-1025	Sequence 1025, Ap	1389	123	3.1	3585	4	US-09-560-385A-17	Sequence 15, Appl
1317	127	3.2	315	4	US-09-270-767-16307	Sequence 16307, A	1390	123	3.1	3621	4	US-09-560-385A-17	Sequence 15, Appl
1318	127	3.2	591	4	US-09-380-682-10	Sequence 2, Appli	1391	123	3.1	4108	4	US-09-919-172-15	Sequence 17372, A
1319	127	3.2	591	4	US-09-380-682-10	Sequence 10, Appl	1392	123	3.1	36307	4	US-09-949-016-17372	Sequence 5461, Ap
1320	127	3.2	591	4	US-09-380-682-16	Sequence 16, Appl	1393	122.5	3.1	3124	2	US-09-949-016-5461	Sequence 2, Appli
1321	127	3.2	864	3	US-08-906-769-138	Sequence 138, App	1394	122.5	3.1	3373	2	US-08-897-443-2	Sequence 5754, Ap
1322	127	3.2	864	3	US-08-906-769-138	Sequence 138, App	1395	122.5	3.1	5679	4	US-09-949-016-5754	Sequence 12, Appl
1323	127	3.2	864	3	US-08-639-075A-138	Sequence 138, App	1396	122	3.1	591	4	US-09-380-682-12	Sequence 18, Appl
1324	127	3.2	864	3	US-09-012-431-138	Sequence 138, App	1397	122	3.1	591	4	US-09-380-682-18	Sequence 18, Appl
1325	127	3.2	864	3	US-09-012-692-138	Sequence 138, App	1398	122	3.1	771	2	US-08-394-600B-3	Sequence 3, Appli
1326	127	3.2	864	3	US-08-906-613-138	Sequence 138, App	1399	122	3.1	771	2	US-08-394-600B-22	Sequence 22, Appl

1400 122 3.1 771 4 US-08-395-456C-22 Sequence 22, Appl
1401 122 3.1 771 4 US-08-487-453A-22 Sequence 22, Appl
1402 122 3.1 771 5 PCT-US95-02513-22 Sequence 22, Appl
1403 122 3.1 1197 4 US-09-270-767-1041 Sequence 1031, Ap
1404 122 3.1 1197 4 US-09-270-767-16323 Sequence 16323, A
1405 121 3.1 771 2 US-08-230-428B-3 Sequence 3, Appli
1406 121 3.1 771 4 US-08-395-456C-3 Sequence 3, Appli
1407 121 3.1 771 4 US-08-487-453A-3 Sequence 3, Appli
1408 121 3.1 771 5 PCT-US95-02513-3 Sequence 3, Appli
1409 121 3.1 1523 3 US-09-183-861-21 Sequence 21, Appl
1410 121 3.1 1523 3 US-09-022-765-21 Sequence 21, Appl
1411 121 3.1 1523 3 US-09-551-974A-21 Sequence 21, Appl
1412 121 3.1 1523 4 US-09-555-501A-21 Sequence 21, Appl
1413 121 3.1 1523 4 US-09-639-206A-21 Sequence 21, Appl
1414 121 3.1 1523 4 US-09-874-923-21 Sequence 21, Appl
1415 121 3.1 1531 2 US-08-833-963C-1 Sequence 1, Appli
1416 121 3.1 1741 4 US-09-949-016-1921 Sequence 1921, Ap
1417 121 3.1 2018 3 US-08-980-514-2 Sequence 2, Appli
1418 121 3.1 8224 6 5180808-1 Patent No. 5180808
1419 121 3.1 8224 6 5180808-1 Patent No. 5180808
1420 121 3.1 14638 6 US-09-902-540-1106 Patent No. 5200340
1421 121 3.1 453 6 5200340-3 Patent No. 5200340
1422 120.5 3.1 453 6 5200340-3 Patent No. 5200340
1423 120.5 3.1 639 3 US-09-280-116-139 Sequence 139, App
1424 120.5 3.1 2988 4 US-09-949-016-2383 Sequence 139, App
1425 120.5 3.1 3259 5 PCT-US95-03747-1 Sequence 1, Appli
1426 120.5 3.1 4898 4 US-09-919-497-35 Sequence 35, Appl
1427 120.5 3.1 5075 4 US-09-949-016-100 Sequence 100, App
1428 120.5 3.1 36470 4 US-08-311-731A-123 Sequence 123, App
1429 120.5 3.1 484 4 US-09-621-576-277 Sequence 277, App
1430 120 3.0 3167 4 US-09-949-016-3734 Sequence 3734, App
1431 120 3.0 3167 4 US-09-949-016-3735 Sequence 3735, App
1432 120 3.0 690 4 US-08-395-456C-26 Sequence 26, Appl
1433 119.5 3.0 696 4 US-08-395-456C-24 Sequence 24, Appl
1434 119.5 3.0 1829 6 5514582-1 Patent No. 5514582
1435 119.5 3.0 1829 6 5514582-1 Patent No. 5514582
1436 119.5 3.0 9798 4 US-09-949-016-14022 Sequence 14022, A
1437 119.5 3.0 9801 4 US-09-949-016-12819 Sequence 12819, A
1438 119.5 3.0 591 4 US-09-380-682-14 Sequence 14, Appl
1439 119 3.0 601 4 US-09-949-016-178897 Sequence 178897, A
1440 119 3.0 601 4 US-09-949-016-178901 Sequence 178901, A
1441 119 3.0 16382 3 US-08-718-388-8 Sequence 8, Appli
1442 119 3.0 618 3 US-09-280-116-3 Sequence 3, Appli
1443 118.5 3.0 639 4 US-09-669-751-6 Sequence 6, Appli
1444 118.5 3.0 1381 4 US-09-270-767-28534 Sequence 28534, A
1445 118.5 3.0 1463 5 PCT-US93-05640-10 Sequence 10, Appl
1446 118.5 3.0 2181 4 US-09-252-991A-14909 Sequence 14909, A
1447 118.5 3.0 2184 1 US-07-815-333A-1 Sequence 1, Appli
1448 118.5 3.0 2214 4 US-08-605-221-1 Sequence 1, Appli
1449 118.5 3.0 3387 4 US-09-252-991A-14461 Sequence 14461, A
1450 118.5 3.0 6027 4 US-09-620-312D-517 Sequence 517, App
1451 118.5 3.0 481 4 US-09-270-767-1913 Sequence 1913, Ap
1452 118 3.0 481 4 US-09-270-767-17195 Sequence 17195, A
1453 118 3.0 481 4 US-09-270-767-15871 Sequence 15871, A
1454 118 3.0 1794 2 US-08-427-497B-5 Sequence 5, Appli
1455 118 3.0 4198 4 US-09-949-016-934 Sequence 934, App
1456 118 3.0 4954 4 US-09-949-016-4527 Sequence 4527, Ap
1457 117.5 3.0 670 4 US-09-270-767-589 Sequence 589, App
1458 117.5 3.0 670 4 US-09-270-767-15871 Sequence 15871, A
1459 117.5 3.0 688 3 US-08-824-692-27 Sequence 27, Appl
1460 117.5 3.0 815 3 US-08-906-769-128 Sequence 128, App
1461 117.5 3.0 815 3 US-08-906-616-128 Sequence 128, App
1462 117.5 3.0 815 3 US-08-639-075A-128 Sequence 128, App
1463 117.5 3.0 815 3 US-09-012-431-128 Sequence 128, App
1464 117.5 3.0 815 3 US-09-012-692-128 Sequence 128, App
1465 117.5 3.0 815 3 US-08-906-613-128 Sequence 128, App
1466 117.5 3.0 4314 1 US-08-199-780-2 Sequence 2, Appli
1467 117.5 3.0 4314 2 US-08-316-650-2 Sequence 2, Appli
1468 117.5 3.0 5587 4 US-09-949-016-5651 Sequence 5651, Ap
1469 117.5 3.0 5601 4 US-09-949-016-1039 Sequence 1039, Ap
1470 117.5 3.0 5702 4 US-09-566-921-118 Sequence 118, App
1471 117 3.0 418 4 US-09-270-767-2019 Sequence 2019, Ap
1472 117 3.0 418 4 US-09-270-767-17301 Sequence 17301, A

Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 1031, Ap
Sequence 16323, A
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 1, Appli
Sequence 1921, Ap
Sequence 2, Appli
Patent No. 5180808
Patent No. 5180808
Patent No. 5200340
Patent No. 5200340
Sequence 139, App
Sequence 1, Appli
Sequence 35, Appl
Sequence 100, App
Sequence 123, App
Sequence 277, App
Sequence 3734, App
Sequence 3735, App
Sequence 26, Appl
Sequence 24, Appl
Patent No. 5514582
Patent No. 5514582
Sequence 14022, A
Sequence 12819, A
Sequence 14, Appl
Sequence 178897, A
Sequence 178901, A
Sequence 8, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 28534, A
Sequence 10, Appl
Sequence 14909, A
Sequence 1, Appli
Sequence 1, Appli
Sequence 14461, A
Sequence 517, App
Sequence 1913, Ap
Sequence 17195, A
Sequence 5, Appli
Sequence 934, App
Sequence 4527, Ap
Sequence 589, App
Sequence 15871, A
Sequence 27, Appl
Sequence 128, App
Sequence 128, App
Sequence 128, App
Sequence 128, App
Sequence 128, App
Sequence 128, App
Sequence 128, App
Sequence 2, Appli
Sequence 2, Appli
Sequence 5651, Ap
Sequence 1039, Ap
Sequence 118, App
Sequence 2019, Ap
Sequence 17301, A

Sequence 33, Appl
Sequence 400, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 1, Appli
Sequence 3, Appli
Sequence 41, Appl
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 8, Appli
Sequence 8, Appli
Patent No. 5514787
Patent No. 5514787
Sequence 1, Appli
Sequence 43, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli

US-09-280-116-104
; Sequence 104, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: ROBISON, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
; LENGTH: 2886
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
; NAME/KEY: misc feature
; LOCATION: (1)-(2886)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-104

Alignment Scores:
Pred. No.: 0
Score: 3450.50
Percent Similarity: 94.45%
Best Local Similarity: 94.19%
Query Match: 87.47%
DB: 3
Length: 2886
Matches: 713
Conservative: 2
Mismatch: 5
Indels: 37
Gaps: 1

US-10-063-692-38 (1-720) x US-09-280-116-104 (1-2886)

QY 1 MetGluLeuGlyCysTrpThrGln-LeuGlyLeuThrPheLeuGluLeuLeuLeuSe 20
Db 135 ATGGAGCTGGTGTCTGGACGCTGGGGCTCACTTTCTTCAGCTCCTCTCATCTC 194
QY 20 rSerLeuProArgGluTyrThrValIleGluAlaCysProGlyAlaGluTrpIle 40
Db 195 GTCTTTGCCAAGAGAGTACACAGTCTATTATTAAGCTGCTCCCTGGAGAGTGAATAT 254

QY 40 eMetCysArgGluCysCysGluTyrAspGlnIleGluCys-ValCysProGlyLysArgG 60
Db 255 CATGTGTCGGAGTGTGTGAATATGATCAGATTGAGTGCCTGTCGCCCGGAAAGAGGG 314
QY 60 luValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysL 80
Db 315 AAGTCGTGGGTATACCATCCCTTGTGTCAGGAATGAGGAGATGAGTGTGACTCTCTGCC 374
QY 80 eutleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpG 100
Db 375 TGATCCACCAGGTGTGATACCATCTTTGAAATGCAAGAGCTGCCGAAATGGCTCATGGG 434
QY 100 lyGly--ThrLeuAspAsp-PheTyrVal-LysGlyPheTyr-CysAlaGluCysArgAl 118
Db 435 GGGGGTTACCTTGATGACTTCTATGTGAAGGGGTTCTACTTGTGCAGAGTGGCGAGC 494
QY 118 aGlyTyrTrpGly--GlyAspCysMet-ArgCys-GlyGlnValLeu-ArgAlaProLys 136
Db 495 AGGCTGTACGGAAGGAGACTGCATGCCATGTGGCCAGGTTCTGCCGAACCCCAAG 554
QY 137 GlyGlnIleLeu-LeuGluSerTyr-ProLeuAsnAlaHis-CysGluTrpThrIleHis 155
Db 555 GGTTCAGATTGTGTGAAAGCTATCCCTTAAATGCTCACTTGTGAATGGACCAATTCAT 614
QY 156 AlaIysProGlyPheValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyr 175
Db 615 GCTAAACCTGGGTTGTGATCCCACTAAGATTGTGTCATGTGAGCCTGGAGTTGACTAC 674
QY 176 MetCysGlnTyrAspTyrValGluValArgAspGlyAspAsn-ArgAspGlyGlnIleI 195
Db 675 ATGTGCCAGTATGACTATGTGTGAGTTCGTGATGGAGACAAACCCGCGATGCCAGATCAT 734
QY 195 eLysArgValCysGlyAsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHi 215
Db 735 CAAGCGGTCTGTGGCAACGAGCGCCAGCTCTTATCCAGAGCATAGGATCTCCCATCC 794
QY 215 sval---LeuPheHisSer-AspGlySerLysAsnPheAspGlyPheHisAlaIleTyrG 234
Db 795 CAGCTCCCTCTTCACCTCCGAGTGGCTCCAAAGAAATTTTGACGGTTTCCATGCCATTTATG 854
QY 234 luGluIleThrAlaCysSerSerProCysPheHisAspGlyTyrCysValLeuAspL 254
Db 855 AGNGATCAGACATGTCTCTATCCCTTGTTCATGACGCGACGTGGTCTCTTGACA 914
QY 254 ysaLaGlySerTyrLysCysAlaCysLeuAlaGly-TyrThrGlyGlnArgCysGluAsn 273
Db 915 AGGCTGGATCTTACAAGTGTGCTGTGTCAGGCTTATATCTGGGCAGCGCTGTGAAAT 974
QY 274 LeuLeuGluGluArgAsnCysSerAspProGlyGlyProValAsnGlyTyrGlnLysIle 293
Db 975 CTCCTTGAAGAAAGAACTGCTCAGACCCCTGGGGGCCCTGATGATGGGTACCAAGAAATA 1034
QY 294 ThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaLysIleGlyThrValValSerPhe 313
Db 1035 ACAGGGGGCCCTGGCTTATCAAGGAGCGCATGCTAAATTTGCACCGTGTGTCTTTC 1094
QY 314 PheCysAsnAsnSerTyrValLeuSerGlyAsnGluLysArgThrCysGlnAsnGly 333
Db 1095 TTTTGTAAACAATCCTATGTCTTAGTGGCAATGAGAAAGAACTTGCACGAGCAATGGA 1154
QY 334 GluTrpSerGlyLysGlnProIleCysAlaIleLysAlaCysArgGluProLysIleSerAsp 353
Db 1155 GAGTGGTCAGGGAACAGCCCATCTGCATAAAGCCCTGCCGAGAACCAAGATTTCAGAC 1214
QY 354 LeuValArgArgValLeuProMetGlnValGlnSerArgGluThr-ProLeuHisG1 373
Db 1215 CTGGTGAGAGGAGGTCTTCCGATGAGGTTCCAGTCAAGGGAGACACCAATTCACCA 1274
QY 373 nLeuTyrSerAlaAlaPheSerLysGlnLysLeu--GlnSerAlaProThrLysLysPro 392
Db 1275 GCTATATCTCAGCGCCCTTCAAGACAGAACTTGCAGAGAGTGCCTCAACAGAGCCCA 1334

RESULT 2

US-10-067-422-2
; Sequence 2, Application US/10067422
; Patent No. 6743613
; GENERAL INFORMATION:

Db 1621 TGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCACTGCCTTCAACCAAGGTGCTGCCT 1680

Qv 711 PheLysAspTrpIleGluuArgAsnMetLys 720

1681 TTTAAGACTGGATTGAAAGAAATATGAAA 1710

RESULT 3

```

US-09-620-312D-1006
; Sequence 1006, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_Fl_genes Version 1.0
; SEQ ID NO 1006
; LENGTH: 2142
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (528)..(1604)
US-09-620-312D-1006

```

Alignment Scores:	8.73e-261	Length:	2142
Pred. No.:	2678.50	Matches:	501
Score:	96.73%	Conservative:	0
Percent Similarity:	96.73%	Mismatches:	0
Best Local Similarity:	96.72%	Indels:	17
Query Match:	67.90%	Gaps:	1
DB:	4		

US-10-063-692-38 (1-720) x US-09-620-312D-1006 (1-2142)

QY 220 SerAspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluIleThrAlaCys 239

Db

Qy 240 SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLys 259

db 111 TCCTCATCCCCCTGTTTCATGACGGCAGTGGCTCCTTGACAAAGCTGGATCTTACAAG 170

QY 260 CysAlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeu----- 274

Db
171 TGTGGCTGCTTGGCAGGCTATACCTGGCAGCGCTGTGAATACTTTCTGGAGGCTGGGAG 230

QY 275 -----LeuGluGluArgAsnCysSerAsp 282

231 TCCAGATCAAGCGCTCAGAGATTCAATTGTCTGTCTTGAAGAAAGAAACTTGCTCAGAC 290

QY 643 ValThrAspAsnMetPheCysAlaSerTyrGluProThrAlaProSerAspIleCysThr 662
Db 1371 GTCACTGATACATGTTCTGTGCAGCTGGGAACCCACTGCCCTTCTGATATCTGCAC 1430
QY 663 AlaGluThrGlyGlyIleAlaValSerPheProGlyArgAlaSerProGluProArg 682
Db 1431 GCAGAGACAGGAGCATCGCGCTGTCTCTCCCGGAGCAGCATCTCTGAGCCACGC 1490
QY 683 TrpHisLeuMetGlyLeuValSerTyrSerTyrAspLysThrCysSerHisArgLeuSer 702
Db 1491 TGGCATCTGATGGAGCTGGTCAGCTGCAGCTATGATATAAATGACAGCCACAGCTCTCC 1550
QY 703 ThrAlaPheThrLysValLeuProPheLysAspTyrIleGluArgAsnMetLys 720
Db 1551 ACTGCCCTTCCCAAGGTGCTGCTTTTAAAGACTGGATTGAAAGAAATATGAAA 1604

RESULT 4

US-09-620-312D-969
; Sequence 969, Application US/09620312D
; Patent No. 659662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 659662el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: Pct_Fl_genes Version 1.0
; SEQ ID NO 969
; LENGTH: 2144
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (528)..(1607)
US-09-620-312D-969

Alignment Scores:
Pred. No.: 8,74e-261 Length: 2144
Score: 2678.50 Matches: 501
Percent Similarity: 96.72% Conservative: 0
Best Local Similarity: 96.72% Mismatches: 0
Query Match: 67.90% Indels: 17
DB: 4 Gaps: 1

US-10-063-692-38 (1-720) x US-09-620-312D-969 (1-2144)

QY 220 SerAspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluIleThrAlaCys 239
Db 51 TCCGATGGCTCCAGGAATTTTGACGGTTTCATGCCATTTATGAGGAGATCAGCATGTC 110
QY 240 SerSerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLys 259

Db 111 TCCTCATCCCTTGTGTTTCCATGACGCACGTGCGTCTTGCACAGGCTGATCTTACAAG 170
QY 260 CysAlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeu 274
Db 171 TGTGCTCTGCTTGGCAGGTATCTTGGCAGCGCTGTGAAATCTTCTGGAGGCTGGGAAG 230
QY 275 -----LeuGluGluArgAsnCysSerAsp 282
Db 231 TCCAAGATCAAGCGCTCAGAAAGATTCAATTGCTGTCTCTTGAAGAAAGAACTGTCTCAG 290
QY 283 ProGlyGlyProValAsnGlyTyrGlnLysIleThrGlyGlyProGlyLeuIleAsnGly 302
Db 291 CTTGGGGGGCCCATCAATGGGTACCAAGAAATTAACAGGGGGGCCCTGGGCTTATCAACGGA 350
QY 303 ArgHisAlaLysIleGlyThrValValSerPheCysAsnAsnSerTyrValLeuSer 322
Db 351 CGCCATGCTAAATTTGGCACCGTGGTCTTCTTTTGTAAACAACCTCTATGTTCTTAGT 410
QY 323 GlyAsnGluLysArgThrCysGlnGlnAsnGlyGluTyrSerGlyLysGlnProIleCys 342
Db 411 GGCAATGAGAAAGAACTTGGCAGCAGAAATGGAGAGTGGTCAGGAAACAGCCCATCTGC 470
QY 343 IleLysAlaCysArgGluProLysIleSerAspLeuValArgArgValLeuProMet 362
Db 471 ATAAAGCCTGCCGAGAACCAAGATTTCAGACTCGTGTGAGAGAGAGTCTTCCGATG 530
QY 363 GlnValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSerLysGln 382
Db 531 CAGGTTCACTCAAGGGAGACACCATTTACACAGCTATCTCAGGGGCTTCAGCAGCAG 590
QY 383 LysLeuGlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuProMetGly 402
Db 591 AAATGCAGAGTGCCTTACCAAGAACCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGA 650
QY 403 TyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArgArgLeu 422
Db 651 TACCAACATCTGCATACCAGCTCCAGTATGAGTGCATCTCACCCCTTCTACCCCGCGCT 710
QY 423 GlySerSerArgArgThrCysLeuArgThrGlyLysTyrSerGlyArgAlaProSerCys 442
Db 711 GGCAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTGGAGTGGGGGGGACCATCTCTC 770
QY 443 IleProIleCysGlyLysIleGluAsnIleThrAlaProLysThrGlnGlyLeuArgTyr 462
Db 771 ATCCCTATCTCGGGGAAATTTGAGAACATCACTGCTCCAAAGACCCCAAGGTTGCGCTG 830
QY 463 ProTyrGlnAlaAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeuHisLys 482
Db 831 CCGTGGCAGGCAGCCATCTACAGGAGGACCGCGGGTGCATGACGCGACCTTACACAAG 890
QY 483 GlyAlaTyrPheLeuValCysSerGlyAlaLeuValAsnGluArgThrValValAla 502
Db 891 GGAGCGTGGTTCCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCATCTGTGTGGTGGCT 950
QY 503 AlaHisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeuLysVal 522
Db 951 GCCCACTGTGTACTGACCTGGGGAAGGTCAACCATGATCAAGACAGCAGACCTGAAAGTT 1010
QY 523 ValLeuGlyLysPheTyrArgAspAspArgAspGluLysThrIleGlnSerLeuGln 542
Db 1011 GTTTTGGGGAATTTCTACCGGATGATGACCGGGATGAGAAGACCATTCAGAGACCTTACAG 1070
QY 543 IleSerAlaIleIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAspIleAla 562
Db 1071 ATTTCTGCTATCTATCTGATCCCACTATGACCCCATCTCTGCTGATGCTGATCAGCC 1130
QY 563 IleLeuLysLeuLeuAspLysAlaArgIleSerThrArgValGlnProIleCysLeuAla 582
Db 1131 ATCTGAAGCTCTAGACAAGGCCGCTATCAGCACCCGAGTCCAGCCCATCTCGCTCGCT 1190
QY 583 AlaSerArgAspLeuSerThrSerPheGlnGlnSerHisIleThrValAlaGlyTyrAsn 602

```
Db 1191 GCCAGTCGGGATCTCAGCACTCTCTCCAGGAGTCCACATCACTCTGGCTGGCTGGAAT 1250
QY 603 ValLeuAlaaspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValVal 622
Db 1251 GTCTCGCAGACGTAGGAGCCCTGGCTTCAAGAACGACACACTGGGCTCTGGGGTGGTC 1310
QY 623 SerValValAspSerLeuLeuCysGluGluHISAspHisGlyLleProValSer 642
Db 1311 AGTGTGGTGACTCGCTCTGTGTGAGGACACATGAGGACCATGGCATCCAGTGAGT 1370
QY 643 ValThrAspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspLleCysThr 662
Db 1371 GTCACTGATAAATGTTCTGTGCGAGCTGGGAACCCACATGCCCTTCTGATATCTGCACT 1430
QY 663 AlaGluThrGlyGlyLleAlaAlaValSerPheProGlyArgAlaSerProGluProArg 682
Db 1431 GCAGAGACAGGAGGCATCGCGGTGTCTCTCCCGGAGCAGCATCTCTGTAGCCACGC 1490
QY 683 TrpHisLeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHisArgLeuSer 702
Db 1491 TGGCATCTGATGGAGCTGTGTCAGCTGAGCTATGATAAACAATGACCCACAGGCTCTCC 1550
QY 703 ThrAlaPheThrLysValLeuProPheLysAspTrpIleGluArgAsnMetLys 720
Db 1551 ACTGCCTTCCACCAAGGTGCTGCCTTTTAAAGACTGGATTGAAAGAAATATGAAA 1604

RESULT 5
US-09-280-116-179
; Sequence 179, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: astacin/m 12a metalloproteases
US-09-280-116-179

Alignment Scores:
Pred. No.: 5,5e-81 Length: 505
Score: 893.00 Matches: 166
Percent Similarity: 98.81% Conservative: 0
Best Local Similarity: 98.81% Mismatches: 1
Query Match: 22.64% Indels: 2
DB: 3 Gaps: 0

US-10-063-692-38 (1-720) x US-09-280-116-179 (1-505)

QY 103 LeuAspAspPheTyrValLysGlyPheTyrCysAlaGluCysArgAlaGlyTyrTyrGly 122
Db 3 TTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTCCGAGCAGC-TGGTAGCGA 61
QY 123 GlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnLeuLeuGlu 142
Db 62 GGAGACTGCGATGCGATGTGGCCAGGTTCTCGAGCCCCCAAGGTCAGATTTTGTGGAA 121
QY 143 SerTyrProLeuAsnAlaHisCysGluTrpThrIleHisAlaLysProGlyPheValIle 162
Db 122 AGCTATCCCTAAATGCTCACTGTGAATGACCATTCATGCTAAACCTGGGTTTGTATC 181
QY 163 GlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAspTyrVal 182
Db 182 CAACCTAAGATTTGTGCATGTTGAGCGCTGGAGTTTGACTACATGTGCCAGTATGACTATGTT 241
QY 183 GluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGlyAsnGlu 202
```

```
Db 242 GAGGTTCTGATGGAGACAACCGCGATGCCAGATCATCAAGCGTGTCTGTGGCAACGAG 301
QY 203 ArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSerAspGly 222
Db 302 CGGCCAGCTCTCTATCCAGAGCATAGGATCCTCACTCCAGCTCCTCTTCCACTCCGATGGC 361
QY 223 SerLysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSerSerSer 242
Db 362 TCCAGAAATTTTACAGGTTTTCATGCAATTAATGAGGAGATCACAGCATGCTCTCATCC 421
QY 243 ProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyr-LysCysAlaCy 262
Db 422 CCTGTGTTTCCATGAGCGCACGTCGTCCTTTCAGAGGCTGGATCTTTACAAAGTGTGCTG 481
QY 262 sleuAlaGlyTyrThrGlyGln 269
Db 482 CTTGGCAGGCTATACTGGGCAG 503

RESULT 6
US-08-296-014A-3
; Sequence 3, Application US/08296014A
; Patent No. 5716834
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: Ho, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,014A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3448 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Carinoscorpius rotundicauda
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 18..3074
US-08-296-014A-3

Alignment Scores:
Pred. No.: 1.58e-56 Length: 3448
Score: 665.00 Matches: 222
```

Percent Similarity:	38.90%	Conservative:	118
Best Local Similarity:	25.40%	Mismatches:	304
Query Match:	16.86%	Indels:	230
DB:	1	Gaps:	37
US-10-063-692-38 (1-720) x US-08-296-014A-3 (1-3448)			
Qy	34	ProGlyAlaGluTrpAsnIleMetCysArgGluCysCysGluTyrAspGlnIleGluCys	53
Db	567	CCAAATGGACAGTGGAGTAACCTTCCACCCCAATGATTCGA	614
Qy	54	ValCysProGlyLysArgGlu	62
Db	615	GCCATGTTTCATCTCCAGAACATGGGAAGTGAATGCTCTTAGTGGTGATATGATAGAA	674
Qy	63	GlyTyrThrIleProCysCysArgAsnGluAsnGluCysAspSerCysLeuIleHis	82
Db	675	GGGGCTACTTAA	704
Qy	83	ProGlyCysThrIlePheGluAsnCysLysSerCysArg	101
Db	705	CCCTACTACTTGGTTCAGGAACATTAACCTGTTCAGGGTAATGTCAGTGGGAATGGA	764
Qy	102	ThrLeu	103
Db	765	CAGATACCACAATGTAAGAACTTGGTCTCTGCTGACCTGGATCCTGTAAACCATGCT	824
Qy	103		103
Db	825	GAACACAGGTTAAATGGTGTGGAAACAAAATATGGTCAGTTTCTCAGGCACCTGAA	884
Qy	104	AspAspPheTyrValLysGlyPheTyrCysAlaGluCysArg	117
Db	885	GTGACCTATACGTGTTGCGGTAACTACTTCTGATGGTTTTGACACCTTAAATGTAAC	944
Qy	118	AlaGlyTrpTyrGlyGly	127
Db	945	CCTGATGGGCTTGGTCAGGATCACGCCATCCTGTGTTAAAGTGGCAGACAGAGGTC	1004
Qy	128		133
Db	1005	GACTGTGACAGTAAGCTGTAGACTTCTGGATGATGTTGGTGAACCTGTACAGATCCAC	1064
Qy	134	AlaProLysGlyGlnIleLeuLeuGluSer	145
Db	1065	TGTCCTGCTGGCTGTTTGTGACAGCTGGTGTGTTGGGTACGCCATATACCATGAA	1124
Qy	146	LeuAsnAlaHisCysGluTrpThrIleHisAla	161
Db	1125	CTTTCCTCAGTGTGCTGCAGCCATCCATGCTGCGCAAGCTTCCAAACTCTGGAGGAGCG	1184
Qy	162	Ile	162
Db	1185	GTGCATGTTGTGAACAAATGGCCCTCTAGCTGGACTTCTGGGTAGTGACCTGAATGGGATA	1244
Qy	163	GlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMet	176
Db	1245	AAATCGGAAGAGTTGAAGTCTCTTGGCCGGAGTTTCCGATTTCGATTATGTCGCTTCTCC	1304
Qy	177	CysGlnTyrAspTyrValGluValArgAsp	186
Db	1305	ACAGCAGGTAATACGAGATGCTCGATGGATGGTTTGAGGTAGCAGCAGAACTGTGTGTAC	1364
Qy	187	GlyAspAsnArgAspGlyGlnIleLysArgValCysGlyAsn	202
Db	1365	GTTCATCAAAAACAGAGAGCCTGGGAAGAGCTCAAGGTGTGTGTACCAATATATGGCTGCT	1424
Qy	203	ArgProAlaProIleGlnSer	220
Db	1425	CGTCTTGCTGTGTCGACAAAGATGTAATTCAAATTCGTTGACTGAGACTCTACGAGGG	1484
Qy	221	AspGly	230

```
QY 551 AsnTyrAspProIleLeuLeuAspAlaAlaIleLeuLeuLeuLeuAspLysAla 570
DB 2583 AACTAGACCCCGGCAATCTCAACTTGGACATAGCCCTAATTCACATGAAACCTCTGTT 2642
QY 571 ArgIleSerThrArgValGlnProIleCysLeuAlaAlaSerArgAspLeuSerThrSer 590
DB 2643 ACTTGCACACAGAGTCCACCAATCTGTCTGCCTACT-----GACATCAACA--- 2693
QY 591 PheGlnGluSerHisIle-----ThrValAlaGlyTrpAsnValLeu 604
DB 2694 -----AGAGAACACTTGAAGGAGGGAACATTAGCAGTGTGTGACAGTGGGT----- 2741
QY 605 AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal 624
DB 2742 -----TTGAATGAAACACACACTATTTCAGAGACGATTCAACAAAGCTGTGTACTCTGTT 2795
QY 625 ValAspSerLeuLeuCysGluGluGlnHisGluAspHisGlyIleProValSerValThr 644
DB 2796 GTTGCAGCCAGCACCTGTGNAGAGGGGTACAGAGAGCAGACTTACCCTGCAGTAACA 2855
QY 645 AspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAlaGlu 664
DB 2856 GAGAACATGTTCTGTGAGGTTCACAG---AAGGGACGTTATGATGCTGCAGTGGGGAC 2912
QY 665 ThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTrpHis 684
DB 2913 AGTGGAGGA-----CCTTTAGTGTGTGTGATGATTCGGTACCAGAAAGCGGTGGTGC 2966
QY 685 LeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHis---ArgLeuSerThr 703
DB 2967 TTGGAAGGATTTGCTAGCTGGGCGAGTCCAGTGGGATGTGGCAGGCGACAGTACGGG 3026
QY 704 AlaPheThrLysValLeuProPheLysAspTrpIleGluArg 717
DB 3027 GGCTTCACTAAAGTTAAAGTTTTCCTGTCATGATGAGGAG 3068

RESULT 7
US-08-596-405-3
; Sequence 3, Application US/08596405
; Patent No. 5858706
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: Ho, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscopus
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolaach & Birch
; STREET: 810 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/596,405
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 3:
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3448 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Carcinoscopus rotundicauda
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 18..3074
; US-08-596-405-3

Alignment Scores:
Pred. No.: 1,58e-56 Length: 3448
Score: 665.00 Matches: 222
Percent Similarity: 38.90% Conservative: 118
Best Local Similarity: 25.40% Mismatches: 304
Query Match: 16.86% Indels: 230
DB: 2 Gaps: 37

US-10-063-692-38 (1-720) x US-08-596-405-3 (1-3448)

QY 34 ProGlyAlaGluTrpAsnIleMetCysArgGluCysCysGluTyrAspGlnIleGluCys 53
DB 567 CCMAATGGACAGTGGAGTAACCTTCCACCACAATGTTATCGA-----GAATGT 614
QY 54 ValCysProGlyLysArgGlu-----ValVal 62
DB 615 GCCATGGTTTCATCTCCAGAACATGGGAAAGTAATGCTCTTAGTGGTGATATGATAGAA 674
QY 63 GlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeuIleHis 82
DB 675 GGGGCTACTTTA-----CGGTTCTCATGTGATAGT----- 704
QY 83 ProGlyCysThrIlePheGluAsnCysLysSerCysArg---AsnGlySerTrpGlyGly 101
DB 705 CCTACTACTTGTGTTGGTCAAGAAACATTAACTGTGAGGGTAATGTCAGTGGTAATGGA 764
QY 102 ThrLeu----- 103
DB 765 CAGATACCACAAATGTAAGAACTTGGTCTTCTGTGCTGACCTGGATCCTGTAAACCATGCT 824
QY 103 ----- 103
DB 825 GAACACAAGGTTAAATTTGGTGTGGAAACAAATAATATGGTCAGTTTCTCAAGGCACAGAA 884
QY 104 -----AspAspPheTyrValLysGlyPheTyrCysAlaGluCysArg 117
DB 885 GTGACCTATACGTGTTCGGGTAACACTACTTCTGTATGGGTTTTCACACCTTAAATAATGTAAC 944
QY 118 -----AlaGlyTrpTyrGlyGly-----AspCysMetArg----- 127
DB 945 CCTGATGGGTCTTGGTCAGGATCAGACCATCCTGTGTGTTAAAGTGGCAGACAGAGGTC 1004
QY 128 -----CysGlyGlnValLeuArg----- 133
DB 1005 GACTGTGCACAGTAAAGCTGTAGACTTCTTGGATGATGTTGGTGAACCTGTGAGATCCAC 1064
QY 134 AlaProLysGlyGlnIleLeuLeuGluSer-----TyrPro 145
DB 1065 TGTCTGTCTGGCTGTTCTTTGACAGCTGGTGTGTGGGTACAGCATATACCATGAA 1124
QY 146 LeuAsnAlaHisCysGluTrpThrIleHisAla-----LysProGlyPheVal 161
DB 1125 CTTTCTCAGTGTGTGTGTCAGGCATCATCTGCTGCAAGCTTCCAAACTCTGGAGGAGCG 1184
QY 162 Ile----- 162
DB 1185 GTGCATGTTGTGAACAAATGGCCCCCTACTCGGACTTTCCTGGGTAGTACCTGAATGGGATA 1244
```

QY 163 -----GlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMet----- 176
Db 1245 AAATCGGAAGATTGAAGTCTCTCCCGGAGTTTCGCGATTATGTCCTGCTCC 1304
QY 177 -----CysGlnTyrAspTyrValGluValArgAsp----- 186
Db 1305 ACAGCAGGTAAATCAGGATGCTCGATGATGGTTTGGGTAGCAGAGACTGTGTGTAC 1364
QY 187 -----GlyAspAsnArgAspGlyGlnIleIleLysArgValCysGlyAsn-----Glu 202
Db 1365 GTTACATCAAAACAGAGAGCCTGGGAAAGAGCTCAAGGTGTGTGTACCAATATGGCTGCT 1424
QY 203 ArgProAlaProIleGlnSer-----IleGlySerSerLeuHisValLeuPheHisSer 220
Db 1425 CGTCTGTGCTGGGCAAAAGATGTAATCCAAATTCGTTGACTGAGACTCTACGAGGG 1484
QY 221 AspGly-----SerLysAsnPheAspGlyPheHis----- 230
Db 1485 AAAGGGTTAAACACCAACCGTGGATAGGATTGCACAGACTAGATGCTGAGAAGCCCTTTATT 1544
QY 231 -----AlaIleTyrGluGluIleThrAlaCysSerSer 241
Db 1545 TGGGAGTTAATGGATCGTAGTAATGTGTTCTGAATGATAACCTAACATTCTGGGCTCT 1604
QY 242 SerProCysPheHisAspGlyThrCysValLeu-----AspLysAlaGlySer 257
Db 1605 GCGGAACCTGGAAATGAACCTAATCTGTGTATATGACATCCCAAGATCATGCTGCTGCT 1664
QY 258 ---TyrLysCysAlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuGlu 276
Db 1665 GTGTGGAAACCAAGTCAATGTTTTCAGCCCTCAAGTTTGTGTCATGATGGATCTGTCA 1724
QY 277 GluArgAsn-----CysSerAspProGlyGlyProValAsnGlyTyrGlnLysIle 293
Db 1725 GACAGAAATAAGGCAAAATGCGATGATCTCGATCACTGGAAATGACACGCCACACTT 1784
QY 294 ThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaLysIleGlyThrValSerPhe 313
Db 1785 CATGGCAAAAGT-----ATTGATGGGTCTCTGCT-----GGTCTCTTAAAGGTAC 1832
QY 314 PheCysAsnAsnSerTyrValLeuSerGlyAsnGluLysArgThrCysGlnAsnGly 333
Db 1833 AGCTGTGAGTTCTCCACTACCTCAGTGGAACTGAAACCGTAACCTGTGACAAACAAATGGC 1892
QY 334 GluTrpSerGlyLysGlnProIleCysIleLys-----AlaCysArgGluProLysIle 351
Db 1893 ACATGGAGTGTCTCTAAACCTCGATGATCAAAAGTCATCACTGCCAAACCCCTGTA 1952
QY 352 SerAspLeuValArgArgValLeuProMetGlnValGlnSerArgGluThrProLeu 371
Db 1953 CCATCATATGTTCTGTGGAAATCAAAACCC-----CCAAAGTCGACAAACTCGATA 2003
QY 372 HisGlnLeuTyrSerAlaAlaPheSerLysGlnLysLeuGln-----SerAlaPro 388
Db 2004 AGTCGTGTGGTCACTCTTCTGAGGTGCGCAGGTTCACCCCTCCCAATAGCTAGACGA 2063
QY 389 ThrLysLysProAlaLeuProPheGlyAsp----- 398
Db 2064 GCCAAACCTCTCCAAACCTAGATCTCACACCCCTCTACTGTGGACTGGCTCTTAA 2123
QY 399 -----LeuProMetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSer 416
Db 2124 GTTAAACTACTGAAGTCAATACCGGTAGGTCTCGAGCCATCTACACGTGCGAGTCG 2183
QY 417 ProPheTyrArgArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTrpSer 436
Db 2184 AGATACACCAACTACTGTGATCTCAAGGCGAGAGATGTCACCTTAATGAAACTGGAGT 2243
QY 437 GlyArgAlaProSerCysIleProIleCysGlyLysIleGlyAsnIleThrAlaPro--- 455
Db 2244 GGTCCGCCAGGAGTGTATCCAGTTTGTGGAGGTGACACTCTCTCTCTCTCTCTT 2303
QY 456 -----LysThrGlnGlyLeuArgTrpProTrpGlnAlaAlaIleTyrArg 470

Db 2304 ATCTGGAAATGGGAATTTACAGAAATAGGTGAGTGGCGGTGGCAGGAGGAATCTCTAGA 2363
QY 471 ArgThrSerGlyValHisAspGlySerLeuHisLysGlyAlaTrpPheLeuValCysSer 490
Db 2364 TGGCTTGCA-----GACCACAAATATGTGTGTCTTCACGTGTGGA 2402
QY 491 GlyAlaLeuValAsnGluArgThrValValAlaAlaHisCysValThrAspLeuGly 510
Db 2403 GGATCTCTATTAATGAGAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2462
QY 511 LysValThrMetIleLysThrAlaAspLeuLysValValLeuGlyLysPheTyrArgAsp 530
Db 2463 ACTGCTGAGATATTGACCCCAATCAGTTTAAATATGTTCTGGCAAGTACTACCGTAT 2522
QY 531 AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleLeuHisPro 550
Db 2523 GACAGTAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2582
QY 551 AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLeuLysLeuAspLysAla 570
Db 2583 AACTACGACCCCGCAATCTCACTTTGACATAGCCCTTAATCACTGAAAACTCCTGTT 2642
QY 571 ArgIleSerThrArgValGlnProIleCysLeuAlaAlaSerArgAspLeuSerThrSer 590
Db 2643 ACTTTGACAAACACGAGTCCAAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2693
QY 591 PheGlnLysSerHisIle-----ThrValAlaGlyTyrAsnValLeu 604
Db 2694 -----AGAAACACTTGAAGAGGAGGACATTAGCAGTGTGACAGTTGGGT----- 2741
QY 605 AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal 624
Db 2742 -----TTGAATGAAACAAACACCTATTTCAGAGACGATTCAACAAAGCTGTGCTACCTGTT 2795
QY 625 ValAspSerLeuLysCysGluGlnHisGluAspHisGlyIleProValSerValThr 644
Db 2796 GTTGCAGCCAGCACCTGTGTAAGAGGGGTACAAAGAGCAGACTTACCACTGACAGTAACA 2855
QY 645 AspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAlaGlu 664
Db 2856 GAGAACATGTTCTGTGAGGTATACAG-----AAGGAGCTTATGATGCTGCGAGTGGGAC 2912
QY 665 ThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTrpHis 684
Db 2913 AGTGGAGGA-----CCTTTAGTGTGTTGCTGATGATTCCTGATCCGAAAGCGGTGGTC 2966
QY 685 LeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHis---ArgLeuSerThr 703
Db 2967 TTGGAAGGGATGTCAGTGGGCGAGTCCAGTGGATGTGGCAAGCGCAACCACTACGGG 3026
QY 704 AlaPheThrLysValLeuProPheLysAspTrpIleGluArg 717
Db 3027 GGCTTCACTAAAGTTAACTGTTTCTGTCATGATGATGAGCAG 3069

RESULT 8

US-08-877-620-3

: Sequence 3, Application US/08877620

: Patent No. 5985590

: GENERAL INFORMATION:

: APPLICANT: Ding, Jeak Ling

: APPLICANT: Ho, Bow

: TITLE OF INVENTION: The Cloned Factor C cDNA of the

: TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscopus

: TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme

: NUMBER OF SEQUENCES: 4

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Birch, Stewart, Kolasch & Birch

: STREET: 8110 Gatehouse Road, Suite 500 East

: CITY: Falls Church

: STATE: Virginia

: COUNTRY: USA

: ZIP: 22042

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/877,620
 FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/596,405

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Murphy, Jr., Gerald M.

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1781-105P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

TELEX: 248345

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 3448 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: both

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Carinoscorpius rotundicauda

FEATURE:

NAME/KEY: CDS

LOCATION: 18..3074

US-08-877-620-3

Alignment Scores:

Pred. No.: 1.58e-56 Length: 3448

Score: 665.00 Matches: 222

Percent Similarity: 38.90% Conservative: 118

Best Local Similarity: 25.40% Mismatches: 304

Query Match: 16.86% Indels: 230

DB: 2 Gaps: 37

US-10-063-692-38 (1-720) x US-08-877-620-3 (1-3448)

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,620
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/596,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3448 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Carinoscorpius rotundicauda
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 18..3074
; US-08-877-620-3

Alignment Scores:
Pred. No.: 1.58e-56 Length: 3448
Score: 665.00 Matches: 222
Percent Similarity: 38.90% Conservative: 118
Best Local Similarity: 25.40% Mismatches: 304
Query Match: 16.86% Indels: 230
DB: 2 Gaps: 37

US-10-063-692-38 (1-720) x US-08-877-620-3 (1-3448)

QY 34 ProGlyAlaGluTrpAsnIleMetCysArgGluCysCysGluTrpAspGlnIleGluCys 53
Db 34 ProGlyAlaGluTrpAsnIleMetCysArgGluCysCysGluTrpAspGlnIleGluCys 53
QY 567 CCAATGGACAGTGGAGTAACTTCCACCCCAATGATTTCGA-----GAATGT 614
Db 567 CCAATGGACAGTGGAGTAACTTCCACCCCAATGATTTCGA-----GAATGT 614
QY 54 ValCysProGlyLysArgGlu-----ValVal 62
Db 54 ValCysProGlyLysArgGlu-----ValVal 62
QY 615 GCCATGGTTTCATCCAGAACATGGGAAAGTGAATGCTCTTAGTGGTGATATGATAGAA 674
Db 615 GCCATGGTTTCATCCAGAACATGGGAAAGTGAATGCTCTTAGTGGTGATATGATAGAA 674
QY 63 GlyTrpThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeuIleHis 82
Db 63 GlyTrpThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeuIleHis 82
QY 675 GGGGCTACTTTA-----CGGTTCCTCATGTGATAGT----- 704
Db 675 GGGGCTACTTTA-----CGGTTCCTCATGTGATAGT----- 704
QY 83 ProGlyCysThrIlePheGluAsnCysLysSerCysArg---AsnGlySerTrpGlyGly 101
Db 83 ProGlyCysThrIlePheGluAsnCysLysSerCysArg---AsnGlySerTrpGlyGly 101
QY 705 CCCTACTACTTGAATGGTCAAGAACATTAACTGTCAAGGTAATGTCAGTGAATGGA 764
Db 705 CCCTACTACTTGAATGGTCAAGAACATTAACTGTCAAGGTAATGTCAGTGAATGGA 764
QY 102 ThrLeu----- 103
Db 102 ThrLeu----- 103
QY 765 CAGATACCACAAATGTAAGAACTTGGTCTTCTGCTCGCTGATCGATCCTGTAACCACTGCT 824
Db 765 CAGATACCACAAATGTAAGAACTTGGTCTTCTGCTCGCTGATCGATCCTGTAACCACTGCT 824
QY 103 ----- 103
Db 103 ----- 103
QY 825 GAACACAAAGGTTAAATTTGGTGTGGAAACAAAATATATGGTCAGTTTCTCAAGGCACGTGAA 884
Db 825 GAACACAAAGGTTAAATTTGGTGTGGAAACAAAATATATGGTCAGTTTCTCAAGGCACGTGAA 884
QY 104 -----AspAspPheTrpValLysGlyPheTrpCysAlaGluCysArg 117
Db 104 -----AspAspPheTrpValLysGlyPheTrpCysAlaGluCysArg 117
QY 885 GTGACCTATACGTGTTCCGGTAACTACTTCTTGATGGGTTTGTGACACCTTAAATATGTAAC 944
Db 885 GTGACCTATACGTGTTCCGGTAACTACTTCTTGATGGGTTTGTGACACCTTAAATATGTAAC 944

118 -----AlaGlyTrpTrpGlyGly-----AspCysMetArg----- 127
945 CCTGATGGGTCTTGGTCAAGGATCACAGCCATCCTGTGTTAAAGTGCAGACAGAGGTC 1004
128 -----CysGlyGlnValLeuArg----- 133
1005 GACTGTGACAGTAAAGCTGTAGACTTCTTGGATGATGTTGGTGAACCTGTCCAGATCCAC 1064
134 AlaProLysGlyGlnIleLeuLeuGluSer-----TyrPro 145
1065 TGTCTCTGCTGGCTGTTCTTTTACAGCTGCTGCTGCTGGGTACAGCCATATACCATGAA 1124
146 LeuAsnAlaHisCysGluTrpThrIleHisAla-----LysProGlyPheVal 161
1125 CTTTCTCAGTGTGCTGCAGCCATCCATGCTGGCAAGCTTCCAAACTCTGGAGGAGCG 1184
162 Ile----- 162
1185 GTGCATGTTGTGNAACAATGGCCCTACTCGGACTTCTGGGTAGTACCTGAATGGGATA 1244
163 -----GlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMet----- 176
1245 AAATCGGAAGAGTTGAAGTCTCTTGCCTGGAGTTTCCGATTCCGATTATGCTGCTCTCC 1304
177 -----CysGlnTrpAspTyrValGluValArgAsp----- 186
1305 ACAGCAGGTAATTCAGAGATGCTCTGATGATGGTGTGGGTAGACAGGAACTGTGTGTAC 1364
187 -----GlyAspAsnArgAspGlyGlnIleLeuValArgValCysGlyAsn-----Glu 202
1365 GTTACATCAAAACAGAGAGCCTGGGAAGAGCTCAAGGTGTGTGTTACCAATATGGTGCT 1424
203 ArgProAlaProIleGlnSer-----IleGlySerSerLeuHisValLeuPheHisSer 220
1425 CGTCTTGTGCTGCTGCACAAAGATGTAATTCAAATTCGTTGACTGAGACTTACGAGGG 1484
221 AspGly---SerLysAsnPheAspGlyPheHis----- 230
1485 AAAGGTTTAAACACCAACGCTGGATAGGATTGCACAGACTAGATCTGAGAGAGCCCTTTATT 1544
231 -----AlaIleTrpGluGluIleThrAlaCysSerSer 241
1545 TGGGAGTTAATGATCGTAGTAACTGTTCTGAATGATAACCTTAACATTTCTGGGCTCT 1604
242 SerProCysPheHisAspGlyThrCysValLeu-----AspLysAlaGlySer 257
1605 GGCGAACCTGGAATGAAACTAACTGTATATATGACATCCAAAGATCAGTTGCACTCT 1664
258 ---TyrLysCysAlaCysLeuAlaGlyThrGlyGlnArgCysGluAsnLeuGlu 276
1665 GTGTGAAAACCAAGTCACTGTTTTCAGCCCTCAAGTTTCTGATGATGGATCTGCTCA 1724
277 GluArgAsn-----CysSerAspProGlyGlyProValAsnGlyTrpGlnLysIle 293
1725 GACAGAAATAAACCCAAATGCGATGATCTCTGGATCACTGGAAATGACAGCCACACTT 1784
294 ThrGlyGlyProGlyLeuLeuAsnGlyArgHisAlaLysIleGlyThrValValSerPhe 313
1785 CATGGCAAAAGT-----ATTGATGGGTTCTATGCT-----GGTCTTCTATAAGGTAC 1832
314 PheCysAsnAsnSerTrpValLeuSerGlyAsnGluLysArgThrCysGlnAsnGly 333
1833 AGCTGTGAGGTTCTTCACCTACCTCAGTGGAACTGAAACCCCTTAACCTGTCACAAATGGC 1892
334 GluTrpSerGlyLysGlnProIleCysIleLys-----AlaCysArgGluProLysIle 351
1893 ACATGGAGTCTCTTAAACCTCGATGATCAAAAGTCATCACTGCCAAACCCCTCGTA 1952
352 SerAspLeuValArgArgValLeuProMetGlnValGlnSerGluThrProLeu 371
1953 CCATCATATGTTCTGTGGAAATCAAAACC-----CCAAAGTCGGAACAACTCGATA 2003

```

```
QY 372 HisGlnLeuTyrSerAlaAlaPheSerLysGlnLysLeuGln-----SerAlaPro 388
DB 2004 AGTCGGTGTGGGTGCACCTTTCTTTCAGGTTGCCACGGTTACCCCTCCCAATAGCTAGACGA 2063
QY 389 ThrLysLysProAlaLeuProPheGlyAsp----- 398
DB 2064 GCCAAACCTCTCCAAACCTAGATCTCAACACCTCTACTGTGGACTTGGCTTCTTAAA 2123
QY 399 -----LeuProMetGlyTyrGlnHisLeuHisLeuGlnLeuGlnTyrGluCysIleSer 416
DB 2124 GTTAAACTACTGAAGTCATTATCCGGGTAGGGTCTCGAGCCACTTACACGTCGGAGTCG 2183
QY 417 ProPheTyrArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTrpSer 436
DB 2184 AGATACACAACTACTTGGATCTCAAGGCAGAGATGTGACTCTAATGGAAATCGAGT 2243
QY 437 GlyArgAlaProSerCysIleProIleCysGlyLysIleGluAsnIleThrAlaPro--- 455
DB 2244 GGTGGCCAGCGAGCTGTATTCAGTTTGGACGGTCAGACTCTCTCTCTCTCTCTCTTT 2303
QY 456 -----LysThrGlnGlyLeuArgTrpProTrpGlnAlaIleLysArg 470
DB 2304 ATCTGGAATGGGAATCTACAGAAATAGGTCACTGGCCGTGGCAGGAGGAATCTCTAGA 2363
QY 471 ArgThrSerGlyValHisAspGlySerLeuHisLysGlyAlaTrpPheLeuValCysSer 490
DB 2364 TGGCTTGGCA-----GACCACAAATATGTGGTTCTCCAGTGGGA 2402
QY 491 GlyAlaLeuValAsnGluArgThrValValAlaAlaHisCysValThrAspLeuGly 510
DB 2403 GGATCTCTATTGAATGAGAAATAGATCGTCACTGCTGCCACTGTGTCACTACTCTGCT 2462
QY 511 LysValThrMetIleLysThrAlaAspLeuLysValValLeuGlyLysPheTyrArgAsp 530
DB 2463 ACTGCTGAGATTATTCACCCCAATCAGTTTAAATGTATCTGGSCAAGTACTACCGTGT 2522
QY 531 AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleLeuHisPro 550
DB 2523 GACAGTAGAGACGACTATGTACAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2582
QY 551 AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLeuLysLeuLeuAspAla 570
DB 2583 AACTACGACCCCGGCAATCTCACTTTGATAGCCCTTAATCTCACTGAAATCTCTGTT 2642
QY 571 ArgIleSerThrArgValGlnProIleCysLeuAlaAlaSerArgAspLeuSerThrSer 590
DB 2643 ACTTTGACAAACAGAGTCCAAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2693
QY 591 PheGlnGluSerHisIle-----ThrValAlaGlyTrpAsnValLeu 604
DB 2694 -----AGAGAACACTTGAAGGAGGGAACATTAGCAGTGTGTGACAGGTTGGGT----- 2741
QY 605 AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal 624
DB 2742 -----TTGAATGAAACACACCTTATTCAGACGCAATTCACACGCTGTGCTACTCTGT 2795
QY 625 ValAspSerLeuLeuCysGluGlnHisGluAspHisGlyIleProValSerValThr 644
DB 2796 GTTGACCCAGCAGCCTGTGAAGAGGGGTACAGAGAGCAGACTTACCCTGACAGTAACA 2855
QY 645 AspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAlaGlu 664
DB 2856 GAGAACATGTTCTGTGTCAGGTTTACAAAG---AAGGGAGCTTATGATCGCTGCACTGGGGAC 2912
QY 665 ThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTrpHis 684
DB 2913 AGTGGAGGA-----CCTTAGTGTGTGTGATGATTCGGTACCGAAGGCGGTGGGTC 2966
QY 685 LeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHis---ArgLeuSerThr 703
DB 2967 TTGAAGGAGATGTACAGTGGGCGAGTCCAGTGGGATGGCGAGCGGACACCACTGACGG 3026
QY 704 AlaPheThrLysValLeuProPheLysAspTrpIleGluArg 717
```

```
DB 3027 GGCTTCACTAAAGTTAAACGTTTTTCTCTGTCTCATGGATTAGGCAG 3068
RESULT 9
US-09-287-368-3
; Sequence 3, Application US/09287368A
; Patent No. 6645724
; GENERAL INFORMATION:
; APPLICANT: DING, Jeak Ling
; APPLICANT: HO, Bow
; TITLE OF INVENTION: Assays for Endotoxin and Methods for Removal of Endotoxin
; from a Sample Using Recombinant Factor C
; FILE REFERENCE: 1781-0185P
; CURRENT APPLICATION NUMBER: US/09/287,368A
; EARLIER FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: 09/201,786
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/081,767
; EARLIER FILING DATE: 1998-05-21
; EARLIER APPLICATION NUMBER: 60/058,816
; EARLIER FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3448
; TYPE: DNA
; ORGANISM: Carinoscorpius rotundicauda
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(3074)
; FEATURE:
; OTHER INFORMATION: any n or Xaa = Unknown
US-09-287-368-3
Alignment Scores:
Pred. No.: 1,58e-56 Length: 3448
Score: 665.00 Matches: 222
Percent Similarity: 38.90% Conservative: 118
Best Local Similarity: 25.40% Mismatches: 304
Query Match: 16.86% Indels: 230
DB: 4 Gaps: 37
US-10-063-692-38 (1-720) x US-09-287-368-3 (1-3448)
QY 34 ProGlyValAlaGluTrpAsnIleMetCysArgGluCysCysGluTyrAspGlnIleGluCys 53
DB 567 CCAAAATGGACAGTGGAGTAACTTTCCACCCCAATGTATTGCA-----GAATGT 614
QY 54 ValCysProGlyLysArgGlu-----ValVal 62
DB 615 GCCATGGTTTCATCTCCAGAACATGGGAAAGTGAATGCTCTTAGTGGTGATATGATAGAA 674
QY 63 GlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeuIleHis 82
DB 675 GGGGCTACTTTTA-----CGTTCTCATGTGATAGT----- 704
QY 83 ProGlyCysThrIlePheGluAsnCysLysSerCysArg---AsnGlySerTrpGlyGly 101
DB 705 CCTTACTACTTGTATTGGTCAAGAACATTAACTGTGAGGGTAATGGTCAGTGGATGGA 764
QY 102 ThrLeu----- 103
DB 765 CAGATACCACAAATGTAAGAACTTGGTCTTCTGTGCTGACCTGGATCCTGTAAACCATGCT 824
QY 103 ----- 103
DB 825 GAACACAGGTTAAATTTGGTGTGGAAACAAAATATGGTCAGTTTCTCAAGGCACCTGAA 884
QY 104 -----AspAspPheTyrValLysGlyPheTyrCysAlaGluCysArg 117
DB 885 GTGACCTATACGTGTTCGGGTAACTACTTCTTGTATGGGTTTTCACACCTTAAATGTAAC 944
QY 118 -----AlaGlyTrpTyrGlyGly-----AspCysMetArg----- 127
```

```
Db      945  CCTGATGGGTCTTGGTCAGGATCACAGCCATCCTGTTGTTAAAGTCGACACAGAGGTC 1004
QY      128  -----CysGlyGlnValLeuArg----- 133
Db      1005  GACTGTGACAGTAAGAGCTGTAGACTTCTTGATGATGTTGGTGAACTGTGCAGGATCCAC 1064
QY      134  AlaProGlyGlnIleLeuLeuGluSer-----TyrPro 145
Db      1065  TGTCTCTGCTGGCTGTTCTTTTGACAGCTGTGTCTGTGGGTACAGCCATATACCATGAA 1124
QY      146  LeuAsnAlaHisCysGluTrpThrIleHisAla-----LysProGlyPheVal 161
Db      1125  CTTTCTCAGTGTGTGTGTCAGCCATCCATGCTGGCAAGCTTCCAAACTCTGGAGGCG 1184
QY      162  Ile----- 162
Db      1185  GTGCATGTTGTGAACAATGGCCCTACTCGGACTTTCTGGGTAGTGACCTGAATGGGATA 1244
QY      163  -----GlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMet----- 176
Db      1245  AATCGGAAGAGTGTGAAGTCTCTTGGCCGGAGTTTCCGATTCGATTATGTCTCCCTCC 1304
QY      177  -----CysGlnTyrAspTyrValGluValArgAsp----- 186
Db      1305  ACAGCAGGTAAATCAGAGATGCTCTGATGGATGTTGAGGTAGACGAGAACTGTGTGTAC 1364
QY      187  -----GlyAspAsnArgAspGlyGlnIleIleLysArgValCysGlyAsn-----Glu 202
Db      1365  GTTACATCAAAACAGAGAGCTCGGAAAGAGCTCAAGGTGTGTGTACCAATATGGCTGCT 1424
QY      203  ArgProAlaProIleGlnSer-----IleGlySerSerLeuHisValLeuPheHisSer 220
Db      1425  CGTCTTGCTGTGTCGCAAAAGATGTAATTCCTCAATTCGTGTGACTGAGACTTACGAGGG 1484
QY      221  AspGly---SerLysAsnPheAspGlyPheHis----- 230
Db      1485  AAAGGGTTAAACACCACGTGGATGAGTATGCACAGACTAGATCGTGAGAGCCCTTTATT 1544
QY      231  -----AlaIleTyrGluIleThrAlaCysSerSer 241
Db      1545  TGGGAGTTAATGATCGTAGTAATGTGGTTCTGAATGATAACCTTAACATTCTGGGCTCT 1604
QY      242  SerProCysPheHisAspGlyThrCysValLeu-----AspLysAlaGlySer 257
Db      1605  GCGCAACCTCGAAATGAACATAACTGTGTATATATGACATCCAAAGATCAGTTGCACTCT 1664
QY      258  ---TyrLysCysAlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuGlu 276
Db      1665  GTGTGGAACCAAGTCATGTTTTCAGCCCTCAAGTTTCTGATGATGGATCTGTCA 1724
QY      277  GluArgAsn-----CysSerAspProGlyGlyProValAsnGlyTyrGlnLysIle 293
Db      1725  GACAGAAATAAGCCAAATCGGATGATCTCTGGATCACTGGAAAATGGACACCCACACTT 1784
QY      294  ThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaLysIleGlyThrValValSerPhe 313
Db      1785  CATGGCAAAAGT-----ATTGATGGGTCTCTATGCT-----GGTTCTCTATAAGGTAC 1832
QY      314  PheCysAsnAsnSerTyrValLeuSerGlyAsnGlnLysArgThrCysGlnGlnAsnGly 333
Db      1833  AGCTGTGAGGTTCTCCACTACCTCAGTGGAACTGMAACCGTAACCTTGTATACAAATGGC 1892
QY      334  GluTrpSerGlyLysGlnProIleCysIleLys-----AlaCysArgGluProLysIle 351
Db      1893  ACATGGAGTCTCTAAACCTCGATGATCAAAAGTCATCACTACCTGCCCCAACCCCTGTGA 1952
QY      352  SerAspLeuValArgArgValLeuProMetGlnValGlnSerArgGluThrProLeu 371
Db      1953  CCATCATATATGTTCTGTGGAAATCAAAACC-----CCAAAGTCGGAACAAACTCGATA 2003
QY      372  HisGlnLeuTyrSerAlaAlaPheSerLysGlnLysLeuGln-----SerAlaPro 388
Db      2004  AGTCGTGTTGGTCCACCTTTCTTGTAGGTTGCCACGGTTTACCCTCCCTCCATTAGCTAGACGA 2063
QY      389  ThrLysLysProAlaLeuProPheGlyAsp----- 398
Db      2064  GCCAAACCTCTCCAAACCTAGATCTCCACAAACCTCTACTGTGTGACTTGGCTTTCTTAA 2123
QY      399  -----LeuProMetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSer 416
Db      2124  GTTAAACTACCTTGAGGTCTTACCGGGTAGGTCTCGAGCCATCTACACGTCGAGTCG 2183
QY      417  PropheTyrArgArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTrpSer 436
Db      2184  AGATACTACGAACCTACTTCGATCTCAAGCAGGAGATGTGACTCTAATGGAACCTGGAGT 2243
QY      437  GlyArgAlaProSerCysIleProIleCysGlyLysIleGluAsnIleThrAlaPro--- 455
Db      2244  GGTGCGCCACGAGCTGTATTCCAGTTTGTGACGGTCACTCTCCTCGTCTCTCTCTTT 2303
QY      456  -----LysThrGlnGlyLeuArgTyrProIleProIleAlaIleTyrArg 470
Db      2304  ATCTGGAATGGGAATTTCTACAGAAATAGGTCTAGTGGCCGTGGCAGCAGGAATCTCTAGA 2363
QY      471  ArgThrSerGlyValHisAspGlySerLeuHisLysGlyAlaTrpPheLeuValCysSer 490
Db      2364  TGGCTTGCA-----GACCACAATATGTGTTTCTCCAGTGTGGA 2402
QY      491  GlyAlaLeuValAsnGluArgThrValValValAlaAlaHisCysValThrAspLeuGly 510
Db      2403  GGATCTCTATTGAATGAGAAATGGATCGTCACTGTGCCACCTGTGTCACTACTCTGCT 2462
QY      511  LysValThrMetIleLysThrAlaAspLeuValLeuGlyValLeuGlyLysPheTyrArgAsp 530
Db      2463  ACTGTGAGATATTGACCCCAATCACTTTAAATGTATCTGGSCAAGTACTACCTGAT 2522
QY      531  AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleLeuHisPro 550
Db      2523  GACAGTAGAGACGACTATGTACAAAGTAAGAGGCTCTTGTGAGATCCACGTGAATCCT 2582
QY      551  AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLeuLysLeuAspLysAla 570
Db      2583  AACTAGACCCCGCAATCTCACTTTGACATAGCCCTTAATCACTGAAACCTCTGTT 2642
QY      571  ArgIleSerThrArgValGlnProIleCysLeuAlaAlaSerArgAspLeuSerThrSer 590
Db      2643  ACTTGTACACACAGATCCACCAATCTGTCTGCCTACT-----GACATCAACA--- 2693
QY      591  PheGlnGluSerHisIle-----ThrValAlaGlyTrpAsnValLeu 604
Db      2694  -----AGAGAACACTTGAAGGAGGGAACATTAGCAGTGTGTGACAGTTGGGT----- 2741
QY      605  AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal 624
Db      2742  -----TTGAATGAAACCAACACCTTATTGACAGACGATTCACAAAGCTGTGCTACCTGTT 2795
QY      625  ValAspSerLeuLeuCysGluGlnGlnHisGluAspHisGlyIleProValSerValThr 644
Db      2796  GTTGCAGCCAGCACCTGTGAGAGGGGTACAGGAAGCAGACTTACCACCTGACAGTAACA 2855
QY      645  AspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAlaGlu 664
Db      2856  GAGAACATGTTCTGTGCGAGGTTTACAAG---AAGGGACGTTATGATGCTCGAGTGGGAC 2912
QY      665  ThrGlyGlyIleAlaValSerPheProGlyArgAlaSerProGluProArgTrpHis 684
Db      2913  AGTGGAGGA-----CCTTTAGTGTGTGATGATTCCTCGTACCGGAAGCGGTGGGTC 2966
QY      685  LeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHis---ArgLeuSerThr 703
Db      2967  TTGGAAGGATGTGCTAGTGGGCGAGTCCCGAGTGGATGTGCCAAGGCGAGTACGGG 3026
QY      704  AlaPheThrLysValLeuProPheLysAspTrpIleGluArg 717
Db      3027  GGCTTCACTAAAGTTAAACGTTTCTCTGTCTATGGATTAGGCAG 3068
QY      Db
```


Db	2184	AGATACTACGAACCTACTTGGATCTCAAGGCAGAGATGTGACTCTAATGAAACTGGAGT	2243
Qy	437	GlyArgAlaProSerCysIleProIleCysGlyLysIleGluAsnIleThrAlaPro---	455
Db	2244	GGTCGGCCACGAGCTGTATTCAGTTTGTGGACGGTCAGACTCTCTCGTCTCTCTTTT	2303
Qy	456	-----LysThrGlnGlyLeuArgTTPProTTPGlnAlaIleIleTyrArg	470
Db	2304	ATCTGGNAATGGGAATCTACAGAAATAGTTCAGTGGCCGTCGCGGAGGAGGAATCTCTAGA	2363
Qy	471	ArgThrSerGlyValHisAspGlySerLeuHisGlyLysGlyAlaTTPheLeuValCysSer	490
Db	2364	TGGCTTGCA-----GACCACAATATGTGGTTCTCCAGTGTGGA	2402
Qy	491	GlyAlaLeuValAsnGluArgThrValValValAlaAlaHisCysValThrAspLeuGly	510
Db	2403	GGATCTCTAATTGAATGAGAAATGGTCGTCACTGCTGCCCACTGTGTCACTACTCTGCT	2462
Qy	511	LysValThrMetIleLysThrAlaAspLeuLysValValLeuGlyLysPheTyrArgAsp	530
Db	2463	ACTGCTCGAGATTATTGACCCCAATCAGTTTAAATGTATCTGGCAGTAGTACTACCGTGAT	2522
Qy	531	AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleIleLeuHisPro	550
Db	2523	GACGTAGACAGATGATGTATGATACAGTAAAGAGAGGCTCTTGAGATCCACGTGAATCCT	2582
Qy	551	AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLeuLysLeuLeuAspLysAla	570
Db	2583	AACTACGACCCCGCAATCTCACTTTTGACATAGCCCTAATTCAACTGAAAACTCCTGTT	2642
Qy	571	ArgIleSerThrArgValGlnProIleCysLeuAlaIleSerArgAspLeuSerThrSer	590
Db	2643	ACTTTGACAAACAGAGTCCCAACCAATCTGTCTGCTACT-----GACATCAACAACA	2693
Qy	591	PheGlnGlutSerHisIle-----ThrValAlaGlyTTPAsnValLeu	604
Db	2694	-----AGAGAACACTTGAGAGGGGAACATTAGCAGTGTGACAGTGTGGGGT-----	2741
Qy	605	AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal	624
Db	2742	-----TTGAATGAAACAACACACTTATTCAGACAGGATTCAACAGCTGTGCTACCTGTT	2795
Qy	625	ValAspSerLeuLeuCysGluGluGlnHisGluAspHisGlyIleProValSerValThr	644
Db	2796	GTTTCAGCCGACACCTGTGAAGAGGGGTACAGGAAGCAGACTTACCACATGCAGATAACA	2855
Qy	645	AspAsnMetPheCysAlaSerTTPGluProThrAlaProSerAspIleCysThrAlaGlu	664
Db	2856	GAGAACATGTTCTGTGAGGTTCACAG-----AAGGGAGCTTATGATGCTCGATGGGGAC	2912
Qy	665	ThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTTPHis	684
Db	2913	AGTCGAGA-----CCTTTAGTGTGCTGATGATTCCTCCGTACCGAAGGCGGTGGGTC	2966
Qy	685	LeuMetGlyLeuValSerTTPSerTyrAspLysThrCysSerHis---ArgLeuSerThr	703
Db	2967	TTGAAGGATGTTCAGTGGGCGAGTCCCACTGGATGTGGCAGGCGAACCGATACGGG	3026
Qy	704	AlaPheThrLysValLeuProPheLysAspTTPIleGluArg	717
Db	3027	GGCTTCACTAAAGTTAAGTTTTCTGTCACTGGATTAGGAC	3068

```

; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,014A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4182 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Carinoscorpis rotundicauda
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 569..3817
; US-08-296-014A-1
;
; Alignment Scores:
; Pred. No.: 2,17e-56
; Score: 665.00
; Percent Similarity: 38.90%
; Best Local Similarity: 25.40%
; Query Match: 16.86%
; DR: 1
; Gaps: 37
; Indels: 230
; Mismatches: 304
; Conservative: 118
; Matches: 222
; Length: 4182

```

RESULT 11
US-08-296-014A-1
: Sequence 1, Application US/08296014A
: Patent No. 5716834
: GENERAL INFORMATION:
: APPLICANT: Ding, Jeak Ling
: APPLICANT: Ho, Bow
: TITLE OF INVENTION: The Cloned Factor C cDNA of the
: TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius
: TITLE OF INVENTION: rotundicauda and Purification of Factor C
: TITLE OF INVENTION: Proenzyme

Db 1568 GAACACAAAGGTAAATTTGGTGGAAACAAAATATATGGTCAGTTTCTCAAGGCACCTGAA 1627
Qy 104 -----AspAspPheTyrValLysGlyPheTyrCysAlaGluCysArg 117
Db 1628 GTGACCTATAGCTGTCGGGTAACTACTTCTTGATGGTTTGGACACCTTAAATATGTAAC 1687
Qy 118 -----AlaGlyTyrTyrGlyGly-----AspCysMetArg 127
Db 1688 CCTGATGGGCTTGGTCAGGATCACGCCATCCTCTGTGTTAAAGTGGCAGACAGAGGTC 1747
Qy 128 -----CysGlyGlnValLeuArg----- 133
Db 1748 GACTGTGACAGTAAAGCTGTAGACTTCTTGGATGATGTTGGTGAACCTGTGAGATCCAC 1807
Qy 134 AlaProLysGlyGlnLeuLeuGluSer-----TyrPro 145
Db 1808 TGTCTGCTGGCTGTTCTTTTGACACAGCTGGTACTGTGTGGGGTACAGCCATATACCATGAA 1867
Qy 146 LeuAsnAlaHisCysGluTyrThrIleHisAla-----LysProGlyPheVal 161
Db 1868 CTTTCTCTCAGTGTGTGTCGAGCCATCATGCTGGCAAGCTTCCAAACTCTGGAGGAGCG 1927
Qy 162 Ile----- 162
Db 1928 GTGCATGTTGTGAACAAATGGCCCTACTCGGACTTTCTGGGTAGTACCTGAATGGGATA 1987
Qy 163 -----GlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMet----- 176
Db 1988 AAATCCGAAGAGTTGAAGTCTCTTGGCCGAGTTTCCGATTCGATTATGTGTCAGTTCTCTCC 2047
Qy 177 -----CysGlnTyrAspTyrValGluValArgAsp----- 186
Db 2048 ACAGCAGGTAAATCAGGATGCTCTGATGGATGTTTGAGGTAGACAGCACTGTGTGTAC 2107
Qy 187 -----GlyAspAsnArgAspGlyGlnIleIleIysArgValCysGlyAsn-----Glu 202
Db 2108 GTTACATCAAAACAGAGAGCTGGGAAAGAGCTCAAGGTGTGTGTACCAATATGTGGTCT 2167
Qy 203 ArgProAlaProIleGlnSer-----IleGlySerSerLeuHisValLeuPheHisSer 220
Db 2168 CGTCTTGCTGTGGCAAAAGATGTAAATTCCAAATTCATTTGACTGAGACTCTACAGGG 2227
Qy 221 AspGly-----SerLysAsnPheAspGlyPheHis----- 230
Db 2228 AAAGGGTTAAACCAACAGCTGGATAGGATTCACAGACTAGATGCTGAGAGCCCTTTATT 2287
Qy 231 -----AlaIleTyrGluGluIleThrAlaCysSerSer 241
Db 2288 TGGGAGTTAATGATCGTAGTAATGTGGTTCTGAATGATAACCTACATTTCTGGGCTCT 2347
Qy 242 SerProCysPheHisAspGlyThrCysValLeu-----AspLysAlaGlySer 257
Db 2348 GCGCAACCTGGAATGAACCTAATCTGTATATATGACATCCCAAGATCAGTTGTCAGTCT 2407
Qy 258 -----TyrLysCysAlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuLeuGlu 276
Db 2408 GTGTGGAAAACCAAGTCACTTTTCAGCCCTCAAGTTTCTTCCATGATGATGATCTGCTCA 2467
Qy 277 GluArgAsn-----CysSerAspProGlyGlyProValAsnGlyTyrGlnLysIle 293
Db 2468 GACAGAAATAAACCCAAATCCGATGATCCTGGATCACTGGAAATGACACGCCACACT 2527
Qy 294 ThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaLysIleGlyThrValValSerPhe 313
Db 2528 CATGGACAAAGT-----ATTGATGGTTCATGCT-----GGTCTTCATTAAGGTAC 2575
Qy 314 PheCysAsnAsnSerTyrValLeuSerGlyAsnGluLysArgThrCysGlnGlnAsnGly 333
Db 2576 AGCTGTGAGGTTCTCCACTACCTCAGTGGAACTGAAACCGCTTAACCTGTGACAAATGGC 2635
Qy 334 GluTyrSerGlyLysGlnProIleCysIleLys-----AlaCysArgGluProLysIle 351
Db 2636 ACATGAGGTGCTCTCTAAACCTCGATGTATCAAAAGTCATCACCTGCCAAAACCCCTCTGTA 2695

Qy 352 SerAspLeuValArgArgValLeuProMetGlnValGlnSerArgGluThrProLeu 371
Db 2696 CCATCATATGTTCTGTGGAAATCAAAACCC-----CAAAGTCGACAAACCTCGATA 2746
Qy 372 HisGlnLeuTyrSerAlaAlaPheSerLysGlnLysLeuGln-----SerAlaPro 388
Db 2747 AGTCGTGTTGGGTGTCACCTTTCTTTGAGGTTGCCACGGTTACCTCCCATTTAGCCAGACGA 2806
Qy 389 ThrLysLysProAlaLeuProPheGlyAsp----- 398
Db 2807 GCCAAACCTCTCCAAACCTAGATCCTCAACCCCTCTACTGTGGACTTGGCTTCTTAAA 2866
Qy 399 -----LeuProMetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSer 416
Db 2867 GTTAAACTACTCAAGGTGTCATTACCGGTAGGTGTCGAGCCATTTACACGTGGAGTCG 2926
Qy 417 ProPheTyrArgArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTyrSer 436
Db 2927 AGATCTACGAACCTACTTGGATCTCAAGGCAGAGATGTGACTCTAATATGAAACTGGAGT 2986
Qy 437 GlyArgAlaProSerCysIleProIleCysGlyLysIleGluAsnIleThrAlaPro--- 455
Db 2987 GGTCCGCCAGCAGCTGTATTCAGTTTGTGGACGTCAGACTCTCTCTCTCTCTCTTT 3046
Qy 456 -----LysThrGlnGlyLeuArgTyrProTyrGlnAlaIleTyrArg 470
Db 3047 ATCTGGAATGGGAATTTCTACAGAAATAGGTGTCAGTCGCGGTGGCAGGCAGGAATCTCTAGA 3106
Qy 471 ArgThrSerGlyValHisAspGlySerLeuHisGlyAlaTyrPheLeuValCysSer 490
Db 3107 TGGCTTTGCA-----GACCACAATATGTGGTTCTTCCAGTGGGA 3145
Qy 491 GlyValLeuValAsnGluArgThrValValAlaAlaHisCysValThrAspLeuGly 510
Db 3146 GGATCTCTATTGTAATGAGAAATGGATCGTCACCTGCTGCCACCTGTCTCACTACTCTGCT 3205
Qy 511 LysValThrMetIleLysThrAlaAspLeuLysValValLeuGlyLysPheTyrArgAsp 530
Db 3206 ACTGCTGAGATTATTGACCCCAATCAGTTTAAATGTATCTGGGCAAGTACTACCGGTAT 3265
Qy 531 AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleLeuHisPro 550
Db 3266 GACAGTAGAGACACTATGTACAAAGTAAGAGAGGCTCTTGAGATCCACGCTGAATCCT 3325
Qy 551 AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLysLeuLeuAspLysAla 570
Db 3326 AACTACGACCCCGGCAATCTCAACTTTGACATAGCCCTTAATTCACCTGAAAACCTCCTGTT 3385
Qy 571 ArgIleSerThrArgValGlnProIleCysLeuAlaAlaSerArgAspLeuSerThrSer 590
Db 3386 ACTTTGACAAACAGAGTCCAAACCAATCTGTCTGCCTACT-----GACATCAACAACA 3436
Qy 591 PheGlnGluSerHisIle-----ThrValAlaGlyTyrAsnValLeu 604
Db 3437 -----AGAGAACACTTGAAGGAGGGAACATTAGCAGTGTGTGACAGTTGGGT----- 3484
Qy 605 AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal 624
Db 3485 -----TTGAATGAAAACCAACCTTATTCAGACAGCAITTCACACAGCTGTGCTACCTGTT 3538
Qy 625 ValAspSerLeuLeuCysGluGlnHisGluAspHisIleGlyIleProValSerValThr 644
Db 3539 GTTGACCCAGCAGCCTGTGAGAGGGGTCAAGAGAGAGAGAGACTTACCCTGACAGTAACA 3598
Qy 645 AspAsnMetPheCysAlaSerTyrGluProThrAlaProSerAspIleCysThrAlaGlu 664
Db 3599 GAGAACATGTTCTGTGTCAGGTTACAG---AAGGGACGTTATGATGCTCGTCGAGGAC 3655
Qy 665 ThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTyrHis 684
Db 3656 AGTGGAGGA-----CCTTTAGTGTGTGATGATTCCTCGTACCGAAGGCGGTGGTCT 3709

Db 2408 GTGGGAACCAAGTCATGTTTTCAGCCCTCAAGTTTCTGCTGATGATGGATCTGTCA 2467
QY 277 GluArgAsn-----CysSerAspProGlyProValAsnGlyTyrGlnLysIle 293
Db 2468 GACAGAAATAAGCCAAATCGGATGATCTCTGGATCACTGGAAATGGACACGCCACACTT 2527
QY 294 ThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaLysIleGlyThrValValSerPhe 313
Db 2528 CATGGCAAAAGT-----ATTGATGGGTCTCTATGCT-----GGTCTCTATAAGGTAC 2575
QY 314 PheCysAsnAsnSerTyrValLeuSerGlyAsnGluLysArgThrCysGlnGlnAsnGly 333
Db 2576 AGCTGTGAGGTTCTCACTACCTCAGTGGAACTGAACCGTAATCTGTACAAATGGC 2635
QY 334 GluTrpSerGlyLysGlnProIleCysIleLys-----AlaCysArgGluProLysIle 351
Db 2636 ACATGAGTGCTCTTAACCTCGATGTATCAAAAGTCATCACTGCCAAACCCCTGTGA 2695
QY 352 SerAspLeuValArgArgValLeuProMetGlnValGlnSerArgGluThrProLeu 371
Db 2696 CCATCATATATGTTCTGTGGAATCAAAACC-----CCAAAGTCGCAAACTCGATA 2746
QY 372 HisGlnLeuTyrSerAlaAlaPheSerLysGlnLysLeuGln-----SerAlaPro 388
Db 2747 AGTCGTGTTGGTCACTCTTCTTGAGGTGCCACGGTTACCCCTCCCATTTAGCCAGACA 2806
QY 389 ThrLysLysProAlaLeuProPheGlyAsp-----GAGGAGGAGGAGGAGGAGG 398
Db 2807 GCCAAACCTCTCCAAACCTAGATCTCAACACCTCTACTGTGGACTTGGCTTCTAAA 2866
QY 399 -----LeuProMetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSer 416
Db 2867 GTTAACTACTGTAAGGTCAATACCGGTGAGGTCTCGAGCCATTTACACGTGCGAGTGC 2926
QY 417 ProPheTyrArgArgLeuGlySerSerArgThrCysLeuArgThrGlyLysTrpSer 436
Db 2927 AGTACTACAACTACTTGATCTCAAGCAGAGATGTGACTCTTAATGGAACTGGAGT 2986
QY 437 GlyArgAlaProSerCysIleProIleCysGlyLysIleGluAsnIleThrAlaPro--- 455
Db 2987 GGTGCGCCAGCGAGCTGATTCAGTTTGTGGAGGTGAGCTCTCTCTCTCTCTCTTT 3046
QY 456 -----LysThrGlnGlyLeuArgTrpProTrpGlnAlaLysIleTyrArg 470
Db 3047 ATCTGGAATGGAAATCTACAGAAATAGTCTAGTGGCGGTGAGCAGCAATCTCTAGA 3106
QY 471 ArgThrSerGlyValHisAspGlySerLeuHisLysGlyAlaTrpPheLeuValCysSer 490
Db 3107 TGGCTTGCA-----GACCACAATATGTGGTTCTCCAGTGTGGA 3145
QY 491 GlyAlaLeuValAsnGluArgThrValValAlaAlaHisCysValThrAspLeuGly 510
Db 3146 GGATCTCTATTGAATGAGAAATGATCGTCACTGCTGCCCATGTGTCACTACTCTGT 3205
QY 511 LysValThrMetIleLysThrAlaAspLeuLysValValLeuGlyLysPheTyrArgAsp 530
Db 3206 ACTGCTGAGATTTATGACCCCAATCAGTTTAAATATGATCTGGCAAGTACTACCGTGT 3265
QY 531 AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleIleLeuHisPro 550
Db 3266 GACAGTAGAGAGATGACTATGTACAAATGTAAGAGAGGCTCTTGAGATCCACGTGAATCT 3325
QY 551 AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLeuLysLeuAspLysAla 570
Db 3326 AACTAGACCCCGCAATCTCACTTTGATAGAGCCCTTAATCACTGAAACTCTCTGT 3385
QY 571 ArgIleSerThrArgValGlnProIleCysLeuAlaAlaSerArgAspLeuSerThrSer 590
Db 3386 ACTTTGACAAACAGAGTCCAAACCAATCTGTCTGCTACT-----GACATCAACA--- 3436
QY 591 PheGlnGluSerHisIle-----ThrValAlaGlyTrpAsnValLeu 604

Db 3437 -----AGAAACACCTTGAAGAGGGGAAACATTAGCAGTGTGTGACAGTTGGGGT----- 3484
QY 605 AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal 624
Db 3485 -----TTGAATGAAACAAACACCTATTTCAGAGACGATTCAACAGCTGTGCTACCTGTT 3538
QY 625 ValAspSerLeuLeuCysGluGluGlnHisGluAspHisGlyIleProValSerValThr 644
Db 3539 GTTGACGCCAGCACCTGTGAAGAGGGGTACAGGAAGACAGACTTACCACATGACAGTAACA 3598
QY 645 AspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAlaGlu 664
Db 3599 GAGAACATGTTCTGTCAGGTACAAG-----AAGGAGCTTATGATGCTCGCTGCGGGGAC 3655
QY 665 ThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTrpHis 684
Db 3656 AGTGGAGGA-----CCTTAGTGTGCTGTGATGATCCCGTACCGAAAGCGGTGGGTC 3709
QY 685 LeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHis---ArgLeuSerThr 703
Db 3710 TTGGAAGGGATTGTGCTGAGCTGGGCGCAGTCCCGTGGATGTGGCAAGGCGCAACAGTACGGG 3769
QY 704 AlaPheThrLysValLeuProPheLysAspTrpIleGluArg 717
Db 3770 GGCTTCACCTAAAGTTAAACGTTTCTCTGTCATGATTAGGCAG 3811

RESULT 13
US-08-877-620-1
; Sequence 1, Application US/08877620
; Patent No. 5985590
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: Ho, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpis
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,620
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/596,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4182 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLSCULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

ORIGINAL SOURCE:									
ORGANISM: Carcinoscopus rotundicauda									
FEATURE:									
NAME/KEY: CDS									
LOCATION: 569..3817									
S-08-877-620-1									
Alignment Scores:									
red. No.: 2.17e-56 Length: 4182									
core: 665.00 Matches: 222									
Conservative: 118									
Similarity: 38.90%									
Local Similarity: 25.40%									
Mismatches: 304									
Indels: 230									
Query Match: 16.86%									
Gaps: 37									
US-10-063-692-38 (1-720) x US-08-877-620-1 (1-4182)									
QY	34	ProGlyAlaGluTrpAsnIleMetCysArgGluCysGluTyrAspGlnIleGluCys	53						
Db	1310	CCAAATGGACAGTGGAGTAACCTTTCCACCCTAAATGATTTCGA	1357						
QY	54	ValCysProGlyLysArgGlu	62						
Db	1358	GCCATGGTTTCATCTCCAGAACATGGGAAGTGAATGCTCTTAGTGGTATATAGTAA	1417						
QY	63	GlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeuIleHis	82						
Db	1418	GGGGCTACTTTA	1447						
QY	83	ProGlyCysThrIlePheGluAsnCysLysSerCysArg	101						
Db	1448	CCCTACTACTTGATTGGTCAAGAAACATTAACTGTCAGGGTAATGGTCAGTGGAAATGGA	1507						
QY	102	ThrLeu	103						
Db	1508	CAGATACCAATGTAAGAACTTAGTCTTCTGCTGACCTGGATCCTGTAAACCATGCT	1567						
QY	103		103						
Db	1568	GAACACAGGTTAAATTTGGTGTGGAAACAAAATATATGTCAGTTTCTCTCAAGCACTGAA	1627						
QY	104	AspAspPheTyrValLysGlyPheTyrCysAlaGluCysArg	117						
Db	1628	GTGACCTATACGTGTTCCGGTAACCTACTTCTGATGGGTTTTCACACCTTAAATATGTAAC	1687						
QY	118	AlaGlyTrpTyrGlyGly	127						
Db	1688	CCTGATGGGTCTTGGTCAGGATCACAGCCATCTGTGTAAAGTGGCAGACAGAGAGTCT	1747						
QY	128		133						
Db	1748	GACTGTGACAGTAAAGCTGTAGACTTCTTGGATGATGTTGGTGAACCTGTCAAGATCCAC	1807						
QY	134	AlaProLysGlyGlnIleLeuLeuGluSer	145						
Db	1808	TGTCCTGCTGGCTGTTCTTTGACAGCTGGTACTGTGTGGGGTACAGCCATATACCATGAA	1867						
QY	146	LeuAsnAlaHisCysGluTrpThrIleHisAla	161						
Db	1868	CTTTCCTCAGTGTGCTGCAGCCATCATGCTGGCAAGCTTCCAACTCTGGAGGAGCG	1927						
QY	162	Ile	162						
Db	1928	GTGCATGTTGTGAACAATGGCCCTTCTCGGACTTCTTGGGTAGTGACCTGAAATGGGATA	1987						
QY	163	GlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMet	176						
Db	1988	AAATCCGAAGATTGAAGTCTCTTGGCCGGAGTTTCCGATTTCGATTATGTCAGTTCTCTCC	2047						
QY	177		186						
Db	2048	ACAGCAGGTAATCAGGATGTCCTGATGGATGGTTTGGGTAGCAGACGAGAACTGTGTGTAC	2107						

QY	187	GlyAspAsnArgAspGlyGlnIleLeuLysArgValCysGlyAsn	202		
Db	2108	GTTACATCAAAACACAGAGCCCTGGGAAAGAGCTCAAGGTGTGTGTACCAATATGGCTGCT	2167		
QY	203	ArgProAlaProIleGlnSer	220		
Db	2168	CGTCTTGCTGCTGCGCAAAAGATGTAATTCCAAATTCATTGACTGAGACTCTACGAGGG	2227		
QY	221	AspGly	230		
Db	2228	AAAGGGTTAAACAACACCGTAGGATTGCAAGACTAGACTAGCTGAGAAAGCCCTTTATT	2287		
QY	231		241		
Db	2288	TGGGAGTTAATGGATCGTAGTAATGTGGTCTGAATGATAACCTAACATCTCTGGGCTCT	2347		
QY	242	SerProCysPheHisAspGlyThrCysValLeu	257		
Db	2348	GGCGAACCTGGAAATGAAACTAATCTGTATATATATGGACATCCAAGATCAGTTGCAGTCT	2407		
QY	258	TyrLysCysAlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuLeuGlu	276		
Db	2408	GTGTGAAACCAACGATCATGTTTTCAGCCCTCAAGTTTTCGTCATGATGGAATCTGTCA	2467		
QY	277	GluArgAsn	293		
Db	2468	GAACAGAAATAAGCCAAATGCGATGATCTCTGATCACTCGMAAATGACACGCCACACAT	2527		
QY	294	ThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaIleGlyThrValValSerPhe	313		
Db	2528	CATGGACAAAGT	2575		
QY	314	PheCysAsnAsnSerTyrValLeuSerGlyAsnGluLysArgThrCysGlnGlnAsnGly	333		
Db	2576	AGCTGTGAGGTTCTCCACTACCTCAGTGAACCGTAAACCGTAACTGTGACAAACAAATGGC	2635		
QY	334	GluTrpSerGlyLysGlnProIleCysIleLys	351		
Db	2636	ACATGAGTGTCTCTAAACCTCGATGTATCAAGTCACTCACCTGCCAAACCCCTCTGTA	2695		
QY	352	SerAspLeuValArgArgValLeuProMetGlnValGlnSerArgGluThrProLeu	371		
Db	2696	CCATCATATGTTCTCTGGAAATCAAAACC	2746		
QY	372	HisGlnLeuTyrSerAlaAlaPheSerLysGlnLysLeuGln	388		
Db	2747	AGTCGTGTTGGGTCACTTCTTTGAGGTTGCCACGGTTACCCCTCCCATTTAGCCAGACA	2806		
QY	389	ThrLysLysProAlaLeuProPheGlyAsp	398		
Db	2807	GCCAAACCTCTCCAAACCTAGATCCTCAACCCCTCTACTGTGGACTTGGCTTCTTAA	2866		
QY	399	LeuProMetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSer	416		
Db	2867	GTTAAACTACTCAAGGTCTATTCAGGGTAGGGTCTCGAGCCATTTACAGCTGGAGTCG	2926		
QY	417	ProPheTyrArgArgLeuGlySerSerArgThrCysLeuArgThrGlyLysTyrSer	436		
Db	2927	AGATACCAACTACTTGGATCTCAAGGAGAGATGTACTCTAATGAAATCGAGT	2986		
QY	437	GlyArgAlaProSerCysIleProIleCysGlyLysIleGluAsnIleThrAlaPro	455		
Db	2987	GGTGGCCAGGAGCTGATTTCCAGTTTGTGGAGGGTCAGACTCTCTCTCTCTCTTTT	3046		
QY	456		470		
Db	3047	ATCTGGAATGGGAATCTACAGAAATAGGTCACTGGCCGTGGCAGGAGGAATCTCTAGA	3106		
QY	471	ArgThrSerGlyValHisAspGlySerLeuHisLysGlyAlaTrpPheLeuValCysSer	490		
Db	3107	TGGCTTGC	3145		
QY	491	GlyAlaLeuValAsnGluArgThrValValAlaAlaHisCysValThrAspLeuGly	510		

```
Db 3146 GGAATCTTATGATGAAATGATGCTCACTGCTGCCACTGTGFCACCTACTCTGCT 3205
Qy 511 LysValThrMetIleLysThrAlaAspLeuLysValValLeuGlyLysPheTyrArgAsp 530
Db 3206 ACTGCTGAGATTATGACCCCAATCATGTTTAAATGATCTTGGCAAGTACTACCGTGAT 3265
Qy 531 AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleLeuHisPro 550
Db 3266 GACAGTAGACGACGATGATGATACCAAGTAAAGAGGCTCTTGAGATCCACGCTGAATCCT 3325
Qy 551 AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLeuLysLeuLeuAspAla 570
Db 3326 AACTACGACCCCGCAATCTCAACTTTGACATAGCCCTTAATCAACTGAAATCTCTGTT 3385
Qy 571 ArgIleSerThrArgValGlnProIleCysLeuAlaAlaSerArgAspLeuSerThrSer 590
Db 3386 ACTTGGACACACGAGTCCACCACTGCTGCTGCTACT-----GACATCACACA--- 3436
Qy 591 PheGlnGluSerHisIle-----ThrValAlaGlyTyrAsnValLeu 604
Db 3437 -----AGAGAACACTTGAAGAGGGAACATTAGCAGTGGTGACAGGTTGGGGT----- 3484
Qy 605 AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal 624
Db 3485 -----TTGAATGAAACAAACACCTATTTCAGACGATTCACCAAGCTGTGCTACCTGTT 3538
Qy 625 ValAspSerLeuLeuCysGluGluGlnHisGluAspHisGlyIleProValSerValThr 644
Db 3539 GTTGACGCCAGCACCTGTGAAGAGGGGTACAGGAAGCAGACTTACCACTGACGATGAACA 3598
Qy 645 AspAsnMetPheCysAlaSerTyrGluProThrAlaProSerAspIleCysThrAlaGlu 664
Db 3599 GAGAACATGTTCTGTGCGAGGTTACAAG---AAGGACGTTTATGATGCTGCTGACGTGGGAC 3655
Qy 665 ThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProAlaGlyTyrHis 684
Db 3656 AGTGGAGGA-----CCTTTAGTGTGTTGCTGATGATTCCTGATCCGAAAGCGGTGGTGC 3709
Qy 685 LeuMetGlyLeuValSerTyrSerTyrAspLysThrCysSerHis---ArgLeuSerThr 703
Db 3710 TTGAAGAGGATGTCAGTGGGCGAGTCCAGCTGGATGGTGGCAAGCGGAACAGTAGGGG 3769
Qy 704 AlaPheThrLysValLeuProPheLysAspTyrIleGluArg 717
Db 3770 GGCTTCACTAAAGTTAAAGTTTTCCTGTCATGATTAGGCAG 3811
```

RESULT 14

```
US-09-287-368-1
; Sequence 1, Application US/09287368A
; Patent No. 6645724
; GENERAL INFORMATION:
; APPLICANT: DING, Jeak Ling
; APPLICANT: HO, Bow
; TITLE OF INVENTION: Assays for Endotoxin and Methods for Removal of Endotoxin
; FILE REFERENCE: 1781-0165P
; CURRENT APPLICATION NUMBER: US/09/287,368A
; CURRENT FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: 09/201,786
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/081,767
; EARLIER FILING DATE: 1998-05-21
; EARLIER APPLICATION NUMBER: 60/058,816
; EARLIER FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4182
; TYPE: DNA
; ORGANISM: Carinoscorpius rotundicauda
; FEATURE:
; NAME/KEY: CDS
```

```
; LOCATION: (569)..(3817)
; FEATURE:
; OTHER INFORMATION: any n or xaa = Unknown
US-09-287-368-1

Alignment Scores:
Pred. No.: 2,17e-56 Length: 4182
Score: 665.00 Matches: 222
Percent Similarity: 38.90% Conservative: 118
Best Local Similarity: 25.40% Mismatches: 304
Query Match: 16.86% Indels: 230
DB: 4 Gaps: 37
```

US-10-063-692-38 (1-720) x US-09-287-368-1 (1-4182)

```
Qy 34 ProGlyAlaGluTyrAsnIleMetCysArgGluCysCysGluTyrAspGlnIleGluCys 53
Db 1310 CCMAATGGACAGTGGAGTAACTTTCCACCMAATGATTCGA-----GAATGT 1357
Qy 54 ValCysProGlyLysArgGlu-----ValVal 62
Db 1358 GCCATGTTTCATCTCCAGAACATGGGAAAGTGAATGCTCTTAGTGGTGATATGATGAA 1417
Qy 63 GlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeuHis 82
Db 1418 GGGGCTACTTTA-----CGGTTCTCATGTGATAGT----- 1447
Qy 83 ProGlyCysThrIlePheGluAsnCysLysSerCysArg---AsnGlySerTyrGlyGly 101
Db 1448 CCTACTACTTGTATGTCAGGAAACATTAACCTGTGAGGGTAAATGGTCAGTGGAAATGGA 1507
Qy 102 ThrLeu----- 103
Db 1508 CAGATACCACAAATGTAAGAACTTAGTCTTCTGTCTGCTGACCTGGATCCTGTAAACCATGCT 1567
Qy 103 ----- 103
Db 1568 GAACACAGGTTAAATTTGGTGTGGAAACAAAATATGGTCAGTTTCTCAAGGCACCTGAA 1627
Qy 104 -----AspAspPheTyrValLysGlyPheTyrCysAlaGluCysArg 117
Db 1628 GTGACCTATACGTGTGGGTAACTACTTCTTGATGGGTTTTCACACCTTAAATATGAAC 1687
Qy 118 -----AlaGlyTyrTyrGlyGly-----AspCysMetArg----- 127
Db 1688 CCTGATGGGTCTTGGTCAGGATCACAGCCATCCTGTGTTAAAGTGGCAGACAGAGGTC 1747
Qy 128 -----CysGlyGlnValLeuArg----- 133
Db 1748 GACTGTGACAGTAAAGCTGTAGACTTCTTGGATGATGTTGGTGAACCTGTGACGATCCAC 1807
Qy 134 AlaProLysGlyGlnIleLeuLeuGluSer-----TyrPro 145
Db 1808 TGTCTCTGCTGGCTGTTCTTTTGACAGCTGGTACTGTGTGGGGTACAGCCATATACCATGAA 1867
Qy 146 LeuAsnAlaHisCysGluTyrThrIleHisAla-----LysProGlyPheVal 161
Db 1868 CTTTCTCAGTGTGTGTCAGCCATCCATGTGGCAAGCTTCCAAACTCTGGAGGCG 1927
Qy 162 Ile----- 162
Db 1928 GTGCAATGTTGTGAACAATGGCCCTACTCGGACTTCTTGGGTAGTAGCCTGAATGGATA 1987
Qy 163 -----GlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMet----- 176
Db 1988 AAATCCGAAGATTGAAGTCTCTTGGCCGAGTTTCCGATTTCGATTATGTCAGTCTCTCC 2047
Qy 177 -----CysGlnTyrAspTyrValGluValArgAsp----- 186
Db 2048 ACAGCAGGTAATCAGGATGCTCTGATGGATGGTTGGTGGTAGCAGCAGAACTGTGTGTAC 2107
Qy 187 -----GlyAspAsnArgAspGlyGlnIleLeuLysArgValCysGlyAsn-----Glu 202
```

Db 2108 GTTACATCAAAACAGAGAGCGCTGGGAAAGAGCTCAAGGTGTGTGTACCAATATGGCTGCT 2167
QY 203 ArgProAlaProIleGlnSer-----IleGlySerSerIleHisValLeuLeuPheHisSer 220
Db 2168 CGTCTTGCTGTGCTGACAAAGATGTAATTCAAATTCATTCAGTGAGAGCG 2227
QY 221 AspGly---SerLysAsnPheAspGlyPheHis----- 230
Db 2228 AAAGGGTTAAACCAACACGCTGATAGATTGCACAGACTAGATGCTGAGAGCGCTTTATT 2287
QY 231 -----AlaIleTyrGluGluIleThrAlaCysSerSer 241
Db 2288 TGGGAGTTAATCGTAGTAGTAATGTGTTCTGAATGATAACCTAATTCCTGGGCTCT 2347
QY 242 SerProCysPheHisAspGlyThrCysValLeu-----AspLysAlaGlySer 257
Db 2348 GCGCAACCTGGAAATGAATACTGTGTATATATGGACATCCAAAGATCAGTTGCGAGTCT 2407
QY 258 ---TyrLysCysAlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuLeuGlu 276
Db 2408 GTGTGGAAACCAAGTCATGTTTTCAGCCCTCAGTTTGTGTCATGATGATCGTCA 2467
QY 277 GluArgAsn-----CysSerAspProGlyGlyProValAsnGlyTyrGlnLysIle 293
Db 2468 GACAGAAATAAGCCAAATGCGATGATCTCGATCACTGGAAATGGACAGCCACACTT 2527
QY 294 ThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaLysIleGlyThrValValSerPhe 313
Db 2528 CATGGACAAAGT-----ATTGATGGGTTCTATGCT-----GGTTCTTCTATAAGGTAC 2575
QY 314 PheCysAsnAsnSerTyrValLeuSerGlyAsnGluLysArgThrCysGlnGlnAsnGly 333
Db 2576 AGCTGTGAGGTTCTCCACACTACCTCAGTGGAACTGAACCGTAATCTGTACAAATATGCG 2635
QY 334 GluTrpSerGlyLysGlnProIleCysIleLys-----AlaCysArgGluProLysIle 351
Db 2636 ACATGGAGTGCTCTTAACCTCGATGATCAAAAGTCATCACCTGCCAAACCCCTGTA 2695
QY 352 SerAspLeuValArgArgValLeuProMetGlnValGlnSerArgGluThrProLeu 371
Db 2696 CCATCATATATGTTCTGTGAAATCAAAACCC-----CCAAAGTCGGACAACTCGATA 2746
QY 372 HisGlnLeuTyrSerAlaAlaPheSerLysGlnLysLeuGln-----SerAlaPro 388
Db 2747 AGTCGTGTGGGTCACTTCTTGAGGTGGCCAGGTTACCCCTCCATTCAGTACGACAGCA 2806
QY 389 ThrLysLeuProAlaLeuProPheGlyAsp----- 398
Db 2807 GCCAAACCTCTCCAAACCTAGATCCTCAACACCTCTACTGTGGACTTGGCTTCTAAA 2866
QY 399 -----LeuProMetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSer 416
Db 2867 GTTAAACTACTGAAGGTCAATTACCGGTAGGTCTCGAGCCATTTACACGTGCGAGTCG 2926
QY 417 ProPheTyrArgArgLeuGlySerSerArgTyrCysLeuArgThrGlyLysTrpSer 436
Db 2927 AGATCTACGAATCTACTTGTGATTCAGGCGAGAGATGTGACTCTAATGGAACACTGAGT 2986
QY 437 GlyArgAlaProSerCysIleProIleCysGlyLysIleGluAsnIleThrAlaPro--- 455
Db 2987 GGTGCGCCAGAGCTGATTCAGTTTGTGGACGGTCAGACTCTCTCTGTTCTCTCTTTT 3046
QY 456 -----LysThrGlnGlyLeuArgTrpProThrGlnAlaAlaIleTyrArg 470
Db 3047 ATCTGGAATGGGAATTTCTACAGAAATAGGTCACTGGCCGTGGCAGCGAGGAATCTCTAGA 3106
QY 471 ArgThrSerGlyValHisAspGlySerLeuHisLysGlyAlaTrpPheLeuValCysSer 490
Db 3107 TGGCTTGTGA-----GACCACAAATATGGTTTCTCCAGTGTGGA 3145
QY 491 GlyAlaLeuValAsnGluArgThrValValAlaAlaHisCysValThrAspLeuGly 510
Db 3146 GGATCTCTATTGAATGAGAAATGGATCGTCACTGCTGCCCACTGTGTCACTACTCTGCT 3205

QY 511 LysValThrMetIleLysThrAlaAspLeuLysValValLeuGlyLysPheTyrArgAsp 530
Db 3206 ACTGCTGAGATTATTGACCCCAATCAGTTTAAATGTATCTGGCAAGTACTACCTGAT 3265
QY 531 AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleLeuHisPro 550
Db 3266 GACAGTAGACGACGATCATGTACAAGTAAGAGAGGCTCTTGAGATCCACGTGAATCCT 3325
QY 551 AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLeuLysLeuLeuAspLysAla 570
Db 3326 AACTAGACCCCGCAATCTCAACTTTCATAGAGCCCTAATTCACACTGAAAACTCTGTT 3385
QY 571 ArgIleSerThrArgValGlnProIleCysLeuAlaAlaSerArgAspLeuSerThrSer 590
Db 3386 ACTTTGACAAACAGAGTCCAAACCAATCTGTCTGCCTACT-----GACATCAACA--- 3436
QY 591 PheGlnGluSerHisIle-----ThrValAlaGlyTrpAsnValLeu 604
Db 3437 -----AGAGAACACTTGAAGGAGGGAACATTAGCAGTGTGTGACAGTTGGGT----- 3484
QY 605 AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal 624
Db 3485 -----TTGAATGAAACAAACACCTATTTCAGAGACGATTCAACAAAGCTGTCTACTGTT 3538
QY 625 ValAspSerLeuLeuCysGluGlnHisGluAspHisGlyIleProValSerValThr 644
Db 3539 GTTCGACGCGACCTGTGAGAGGGGTACAGGAGAGAGACTTACCATCTGACAGTAACA 3598
QY 645 AspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAlaGlu 664
Db 3599 GAGAACATCTCTGTGCGGTTTACAAG---AAGGGACGTTATGATCGCTGCAGTGGGAC 3655
QY 665 ThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTrpHis 684
Db 3656 AGTGGAGGA-----CCTTAGTGTGTTGCTGATGATTCCTGATCCGATACCGAAAGCGGTGGTC 3709
QY 685 LeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHis---ArgLeuSerThr 703
Db 3710 TTGGAAGGATGTCTAGCTGGGCGAGTCCAGTGGATGTGGCAAGCGCAACAGTACGGG 3769
QY 704 AlaPheThrLysValLeuProPheLysAspTrpIleGluArg 717
Db 3770 GGCTTCACTAAAGTTAAACGTTTCTCTGTCTGATGATTAGGCAG 3811

RESULT 15

US-09-626-795-1
; Sequence 1, Application US/09626795
; Patent No. 6719973
; GENERAL INFORMATION:
; APPLICANT: DING, Jeak Ling
; APPLICANT: HO, Bow
; TITLE OF INVENTION: Use of Recombinant Factor C to Induce Bacteriostasis
; FILE REFERENCE: 4810-61737
; CURRENT APPLICATION NUMBER: US/09/626,795
; CURRENT FILING DATE: 2000-07-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4182
; TYPE: DNA
; ORGANISM: Carinoscorpius rotundicauda
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (569)..(3817)
US-09-626-795-1

Alignment Scores:
Pred. No.: 2,17e-56 Length: 4182
Score: 665.00 Matches: 222
Percent Similarity: 38.90% Conservative: 118
Best Local Similarity: 25.40% Mismatches: 304
Query Match: 16.86% Indels: 230


```

DB: 4 Gaps: 37
US-10-063-692-38 (1-720) x US-09-626-795-1 (1-4182)
QY 34 ProGlyAlaGluTrpAsnIleMetCysArgGluCysCysGluTrpArgGlnIleGluCys 53
DB 1310 CCNAATGGACAGTGGAGTAACCTTCCACCAATGTAATTCGA-----GATGT 1357
QY 54 ValCysProGlyLysArgGlu-----ValVal 62
DB 1358 GCCATGTTTCATCTCCAGAACATGGGAAAGTGAATGCTCTTAGTGGTATATGATAGAA 1417
QY 63 GlyTrpThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeuIleHis 82
DB 1418 GGGGCTCATTTTA-----CGTTCTCATGTGATGT-----1447
QY 83 ProGlyCysThrIlePheGluAsnCysLysSerCysArg---AsnGlySerTrpGlyGly 101
DB 1448 CCTACTACTTGTGTCAGGAACATTAACCTGTCAAGGTAATGTCAGTGGATGGA 1507
QY 102 ThrLeu-----103
DB 1508 CAGATACCACAAATGTAAGAACTTAGTCTTCTGTCTGACCTGGATCCTGTAAACCATGCT 1567
QY 103 -----103
DB 1568 GAACACAAGTTAAATTCGTGTGGAAACAAAATATGTCAGTCTTCTCAAGGCATGAA 1627
QY 104 -----AspAspPheTrpValLysGlyPheTrpCysAlaGluCysArg 117
DB 1628 GTGACCTATACGTGTTCGGTAACTACTCTTGTATGGGTTTGCACACCTTAAATGTAA 1687
QY 118 -----AlaGlyTrpTrpGlyGly-----AspCysMetArg-----127
DB 1688 CCTGATGGCTCTTGGTCAGGATCACAGCCATCCTGTGTTAAAGTGGCAGACAGAGAGTC 1747
QY 128 -----CysGlyGlnValLeuArg-----133
DB 1748 GACTGTGACAGTAAGCTGTAGACTTCTTGGATGATGTTGGTGAACCTGTGAGATCCAC 1807
QY 134 AlaProLysGlyGlnIleLeuLeuGluSer-----TyrPro 145
DB 1808 TGCTCTGCTGGCTGTTCTTTGACAGCTGTGTACTGTGTGGGTACAGCCATATACCATGAA 1867
QY 146 LeuAsnAlaHisCysGluTrpThrIleHisAla-----LysProGlyPheVal 161
DB 1868 CTTTCTCAGTGTGTGTCAGCCATCCATGCTGGCAAGCTTCCAAACTCTGGAGAGCG 1927
QY 162 Ile-----162
DB 1928 GTGCAATGTTGAAACAATGGCCCTACTCGGACTTCTCGGGTAGTGCACCTGAATGGGATA 1987
QY 163 -----GlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMet-----176
DB 1988 AAATCGAAGAGTTGAAGTCTCTTGCCCGAGTTTCCGATTGATGTGATGTGATGCTCCTCC 2047
QY 177 -----CysGlnTrpAspTrpValGluValArgAsp-----186
DB 2048 ACAGCAGGTAATCAGATGTCTCGATGGATGTTGAGGTAGACGAGAATCTGTGTATC 2107
QY 187 -----GlyAspAsnArgAspGlyGlnIleLysArgValCysGlyAsn-----Glu 202
DB 2108 GTTATACAAAACAGAGACCTGGGAAAGAGCTCAAGGTGTGTGTACCAATATGCGTGTCT 2167
QY 203 ArgProAlaProIleGlnSer-----IleGlySerSerLeuHisValLeuPheHisSer 220
DB 2168 CGTCTTGTCTGTGACAAAAGATGTAATTCAAATTCAATTCATTGCTGAGACTCTACAGGG 2227
QY 221 AspGly---SerLysAsnPheAspGlyPheHis-----230
DB 2228 AAAGGGTTAACACACACGCTGGATAGGATTCACAGACTAGATGCTCAGAGAGCCCTTATT 2287
QY 231 -----AlaIleTyrGluGluIleThrAlaCysSerSer 241
2288 TGGGAGTTAATGGATCGTAGTAATGTGTTCTGAATGATAACCTAACATCTTGGGCTCT 2347
242 SerProCysPheHisAspGlyThrCysValLeu-----AspLysAlaGlySer 257
2348 GCGCAACCTCGGAATGAACCTAACTGTGTATATATATATATATATATATATATATATATAT 2407
258 ---TyrLysCysAlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuLeuGlu 276
2408 GTGTGGAACCAACCAAGTCATGTTTTCAGCCCTCAAGTTCCTTGTGATGATGATCTGTCA 2467
277 GluArgAsn-----CysSerAspProGlyGlyProValAsnGlyTyrGlnLysIle 293
2468 GACAGAAATAAGCCAAATGCCATGCTCTGATCATCTGGAATAATGACACGCCACACTT 2527
294 ThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaLysIleGlyThrValValSerPhe 313
2528 CATGCACAAAGT-----ATTGATGGTTCATGCT-----GGTTCCTATATAAGGTAC 2575
314 PheCysAsnAsnSerTyrValLeuSerGlyAsnGluLysArgThrCysGlnGlnAsnGly 333
2576 AGCTGTGAGGTTCTCCACTTACCTCAGTGGAACTGAAACCGTAACCTGTACACAAATGGC 2635
334 GluTrpSerGlyLysGlnProIleCysIleLys-----AlaCysArgGluProLysIle 351
2636 ACATGGAGTCTCTTAAACCTCGATGATCAAGTCATCACCTGCCAAACCCCTCTGTA 2695
352 SerAspLeuValArgArgValLeuProMetGlnValGlnSerArgGluThrProLeu 371
2696 CCATCATATGTTCTGTGGAAATCAACCC-----CCAAGTCGGACAAACTCGATA 2746
372 HisGlnLeuTrpSerAlaAlaPheSerLysGlnLysLeuGln-----SerAlaPro 388
2747 AGCTGTGTTGGTTCACCTTCTTGTAGGTTGCCACGGTTTACCCCTCCCATTTAGCCAGACA 2806
389 ThrLysLysProAlaLeuProPheGlyAsp-----398
2807 GCCAAACCTCTCTCAAAACCTAGATCTCTCAACACCTTACTGTGGACTTGGCTTTCTAAA 2866
399 -----LeuProMetGlyTyrGlnHisLeuHisThrGlnLeuGlnTrpGluCysIleSer 416
2867 GTTAAACTACCTGAAGGTCATTACCGGTAGGTCTCGAGCCATTTACACGTGCGAGTCG 2926
417 PropheTyrArgArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTrpSer 436
2927 AGATACTACGAACCTTGGATCTCAAGCAGACAGATGTGACTCTAATGGAAACTGGAGT 2986
437 GlyArgAlaProSerCysIleProIleCysGlyLysIleGluAsnIleThrAlaPro--- 455
2987 GGTGCGCAGCAGCTGTATTCCAGTTGTGGACGGTCAGACTCTCCTCGTTCCTCTTTT 3046
456 -----LysThrGlnGlyLeuArgTrpTrpTrpGlnAlaAlaIleTyrArg 470
3047 ATCTGGAATGGGAATCTTACAGAAATAGGTCAAGTGGCGGTGCGCAGCAGGAATCTCTAGA 3106
471 ArgThrSerGlyValHisAspGlySerLeuHisLysGlyAlaTrpPheLeuValCysSer 490
3107 TGGCTTGCA-----GACCACAAATATGTGTTCTTCCAGTGTGGA 3145
491 GlyAlaLeuValAsnGluArgThrValValValAlaAlaHisCysValThrAspLeuGly 510
3146 GGATCTCTATTGAATGAGAAATGGATCGTCTGTGCCCACTGTGTCACTTCTCTGTCT 3205
511 LysValThrMetIleLysThrAlaAspLeuLysValValLeuGlyLysPheTyrArgAsp 530
3206 ACTGCTGAGATTATTGACCCCAATCAGTTTAAATGTATCTGGCAAGTACTACCGTGAT 3265
531 AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleLeuHisPro 550
3266 GACAGTAGACAGCTATGTATGTAAGTAGAGAGGCTCTTGGAGATCCACGTGAATCCT 3325
551 AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLeuLysLeuLeuAspLysAla 570

```

```
Db 3326 AACTACGACCCGGCAATCTCAACTTTGACATAGCCCTAATTCAACTGAAAACTCCTGTT 3385
Qy 571 ArgIleSerThrArgValGlnProIleCysLeuAlaAlaSerArgAspLeuSerThrSer 590
Db 3386 ACTTTGACAACACGAGTCCAACCAATCTGTGCTTACT-----GACATCACACA--- 3436
Qy' 591 PheGlnGluSerHisIle-----ThrValAlaGlyTrpAsnValLeu 604
Db 3437 -----AGAGAACACTTGAAGGAGGGAACATTAGCAGTGTGTGACAGTTGGGT----- 3484
Qy 605 AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal 624
Db 3485 -----TTGAATGAAAACAACACCTATTTCAGAGACGATTCAACAAGCTGTGCTTACCTGTT 3538
Qy 625 ValAspSerLeuLeuCysGluGlnHisGluAspHisGlyIleProValSerValThr 644
Db 3539 GTTGCAGCCAGCACCTGTGAAGAGGGGTACAGGAAGACGAGACTTACCCTGACAGTAACA 3598
Qy 645 AspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAlaGlu 664
Db 3599 GAGAACATGTTCTGTGCGAGTTACAAG-----AAGGGACGTTATGATGCTGCAGTGGGGAC 3655
Qy 665 ThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTrpHis 684
Db 3656 AGTGGAGGA-----CCTTTAGTGTGCTGTGATGATTCCCGTACCAGAAAGCGGTGGGTC 3709
Qy 685 LeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHis---ArgLeuSerThr 703
Db 3710 TTGGAAGGGATTGTCAGCTGGGCGAGTCCCGAGTGGATGTGGCAAGCGCAACCAAGTACGGG 3769
Qy 704 AlaPheThrLysValLeuProPheLysAspTrpIleGluArg 717
Db 3770 GGCTTCACAAAGTTAACGTTTTCCTGTCATGGATTAGCGAG 3811
```

Search completed: May 10, 2005, 03:44:55
Job time : 461 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2005, 11:21:33 ; Search time 333 Seconds
(without alignments)
13984.515 Million cell updates/sec

Title: US-10-063-692-37
Perfect score: 2846
Sequence: 1 cgcctgggaccagccg...aaaaaaaaaaaaaaaa 2846

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/ECTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1880	65.1	2144	4	US-09-620-312D-969
2	1827	64.2	2142	4	US-09-620-312D-1006
3	1787	62.8	2259	4	US-10-067-422-2
4	370	13.0	505	3	US-09-280-116-179
5	329	11.6	2886	3	US-09-280-116-104
6	134	4.7	1459	4	US-09-537-654-3
7	134	4.7	3275	3	US-09-370-838-151
8	134	4.7	3275	4	US-09-854-133-151
9	133	4.7	240	1	US-08-628-417-6
10	133	4.7	396	4	US-09-640-173-53
11	133	4.7	396	4	US-09-713-550-53
12	133	4.7	396	4	US-09-825-294-53
13	133	4.7	396	4	US-09-970-966-53
14	133	4.7	1696	4	US-09-835-811-1
15	133	4.7	1798	3	US-09-797-906-1
16	133	4.7	2262	4	US-09-311-021-171
17	133	4.7	2447	2	US-09-014-969-14
18	132	4.6	2394	4	US-09-800-729-33
19	130	4.6	1447	3	US-09-443-041A-27
20	130	4.6	1738	4	US-09-918-909A-27
21	129	4.5	1051	3	US-09-245-041-10
22	129	4.5	1051	4	US-09-358-055B-10
23	129	4.5	1051	4	US-09-893-238-10
24	128	4.5	1985	4	US-09-907-794A-212
25	128	4.5	1985	4	US-09-905-125A-212
26	128	4.5	1985	4	US-09-902-775A-212
27	128	4.5	1985	4	US-09-906-700-212
28	128	4.5	1985	4	US-09-903-603A-212
29	128	4.5	1985	4	US-09-904-920A-212
30	128	4.5	1985	4	US-09-905-381A-212
31	128	4.5	1985	4	US-09-906-618-212
32	128	4.5	2674	3	US-09-817-180-1
33	128	4.5	2674	4	US-10-003-295-1
34	128	4.5	2674	4	US-09-461-325-44
35	127	4.5	569	4	US-10-012-542-44
36	127	4.5	569	4	US-10-115-123-44
37	127	4.5	569	4	US-09-967-908A-1
38	127	4.5	6409	4	US-10-159-151-1
39	127	4.5	6409	4	US-09-620-405B-465
40	126	4.4	674	4	US-09-433-826B-465
41	126	4.4	674	4	US-09-604-287A-465
42	126	4.4	674	4	US-09-834-759-465
43	126	4.4	674	4	US-09-590-751A-465
44	126	4.4	674	4	US-09-551-621-465
45	126	4.4	2082	2	US-08-785-310A-2
46	124	4.4	144	1	US-08-702-344-26
47	122	4.3	144	1	US-09-640-173-33
48	118	4.1	396	4	US-09-713-550-33
49	118	4.1	396	4	US-09-825-294-33
50	118	4.1	396	4	US-09-970-966-33
51	118	4.1	117	1	US-08-702-344-3
52	117	4.1	117	1	US-09-073-569-1
53	116	4.1	1813	3	US-09-071-224-3
54	116	4.1	2269	3	US-09-394-645-1
55	114	4.0	2269	3	US-09-243-560B-1
56	114	4.0	4064	4	US-09-873-737A-3
57	114	4.0	396	4	US-09-640-173-16
58	113	4.0	396	4	US-09-713-550-16
59	113	4.0	396	4	US-09-825-294-16
60	113	4.0	396	4	US-09-970-966-16
61	113	4.0	2246	3	US-09-363-708-3
62	113	4.0	2246	4	US-09-083-587-3
63	113	4.0	111	4	US-09-621-976-14677
64	111	3.9	111	4	US-09-904-615-16
65	111	3.9	2634	3	US-09-463-238-3
66	111	3.9	249	4	US-09-621-976-1322
67	110	3.9	249	4	US-09-601-537-10
68	110	3.9	882	4	US-09-311-021-107
69	110	3.9	1034	4	US-09-311-021-105
70	110	3.9	4121	4	US-09-601-537-9
71	110	3.9	121	3	US-09-297-535-23
72	109	3.8	121	3	US-09-297-535-20
73	109	3.8	1048	4	US-09-489-847-38
74	109	3.8	2186	3	US-09-360-545-66
75	108	3.8	9589	1	US-07-925-695-1
76	108	3.8	9589	1	US-07-925-695-2
77	108	3.8	282	4	US-09-621-976-18648
78	106	3.7	2038	4	US-09-885-723-6
79	106	3.7	2184	3	US-08-955-918C-1
80	106	3.7	2184	3	US-08-697-766A-1
81	106	3.7	130	4	US-09-621-976-12892
82	105	3.7	1771	4	US-09-907-794A-158
83	105	3.7	1771	4	US-09-866-028-36
84	105	3.7	1771	4	US-09-905-125A-158
85	105	3.7	1771	4	US-09-902-775A-158
86	105	3.7	1771	4	US-09-906-700-158
87	105	3.7	1771	4	US-09-944-457-36
88	105	3.7	1771	4	US-09-904-158
89	105	3.7	1771	4	US-09-903-603A-158
90	105	3.7	1771	4	US-09-904-920A-158
91	105	3.7	1771	4	US-09-905-064-158
92	105	3.7	1771	4	US-09-905-381A-158
93	105	3.7	1771	4	US-09-906-618-158
94	105	3.7	1872	3	US-09-801-052-1
95	105	3.7	1872	3	US-10-020-121-1
96	104	3.7	1066	1	US-08-157-101A-4
97	103	3.6	194	4	US-09-621-976-9596
98	103	3.6	1024	4	US-09-328-475C-50
99	102	3.6	1024	4	US-09-621-976-14804
100	102	3.6	177	4	US-09-621-976-1047

c 101	102	3.6	396	4	US-09-640-173-10	Sequence 10, Appl	174	88	3.1	1508	3	US-09-039-046-1	Sequence 1, Appl
c 102	102	3.6	396	4	US-09-713-550-10	Sequence 10, Appl	175	88	3.1	1746	4	US-09-485-529-57	Sequence 57, Appl
c 103	102	3.6	396	4	US-09-825-294-10	Sequence 10, Appl	176	88	3.1	1768	4	US-09-485-529-13	Sequence 13, Appl
c 104	102	3.6	396	4	US-09-970-966-10	Sequence 10, Appl	177	88	3.1	2434	4	US-09-489-847-67	Sequence 67, Appl
c 105	102	3.6	708	4	US-09-270-767-13081	Sequence 13081, A	178	87	3.1	246	4	US-09-621-976-13617	Sequence 13617, A
c 106	102	3.6	1882	3	US-09-370-253-1	Sequence 1, Appl	179	87	3.1	1342	4	US-09-489-847-89	Sequence 89, Appl
c 107	101	3.5	140	1	US-08-628-417-5	Sequence 5, Appl	180	87	3.1	2852	3	US-09-027-137-2	Sequence 2, Appl
c 108	101	3.5	578	3	US-09-602-877A-95	Sequence 95, Appl	181	87	3.1	2852	3	US-09-344-441-2	Sequence 2, Appl
c 109	100	3.5	949	4	US-09-489-847-35	Sequence 35, Appl	182	87	3.1	3334	4	US-09-668-119-2	Sequence 2, Appl
c 110	99	3.5	1273	4	US-09-270-767-14731	Sequence 14731, A	183	86	3.0	147	4	US-09-621-976-8551	Sequence 8551, Ap
c 111	99	3.5	1474	3	US-08-821-994-64	Sequence 64, Appl	184	86	3.0	357	4	US-09-621-976-16058	Sequence 16058, A
c 112	99	3.5	6671	1	US-08-280-443-1	Sequence 1, Appl	185	86	3.0	1037	4	US-09-489-847-112	Sequence 112, App
c 113	99	3.5	6671	1	US-08-457-459-1	Sequence 1, Appl	186	86	3.0	1052	4	US-09-489-847-23	Sequence 23, App
c 114	99	3.5	6671	1	US-08-555-678-1	Sequence 1, Appl	187	86	3.0	1198	1	US-09-248-335-27	Sequence 27, Appl
c 115	99	3.5	6671	5	PCT-US95-02275-1	Sequence 1, Appl	188	86	3.0	1817	1	US-08-473-981A-5	Sequence 5, Appl
c 116	98	3.4	98	1	US-08-088-658-42	Sequence 42, Appl	189	86	3.0	1817	2	US-08-474-087-5	Sequence 5, Appl
c 117	98	3.4	98	2	US-08-471-907A-42	Sequence 42, Appl	190	86	3.0	1878	3	US-09-465-558-39	Sequence 39, Appl
c 118	98	3.4	98	4	US-09-621-976-12160	Sequence 12160, A	191	86	3.0	2527	4	US-09-244-805-29	Sequence 29, Appl
c 119	98	3.4	98	4	US-09-621-976-15091	Sequence 15091, A	192	85	3.0	85	4	US-09-621-976-13395	Sequence 13395, A
c 120	98	3.4	196	4	US-09-442-054A-42	Sequence 42, Appl	193	85	3.0	85	4	US-09-621-976-14949	Sequence 14949, A
c 121	98	3.4	196	4	US-09-442-054A-42	Sequence 42, Appl	194	85	3.0	146	4	US-09-621-976-8550	Sequence 8550, Ap
c 122	98	3.4	1454	3	US-09-372-422A-19	Sequence 19, Appl	195	85	3.0	331	4	US-09-621-976-16100	Sequence 16100, A
c 123	97	3.4	97	4	US-09-621-976-12430	Sequence 12430, A	196	85	3.0	630	1	US-08-185-414E-1	Sequence 1, Appl
c 124	97	3.4	240	4	US-09-621-976-1324	Sequence 1324, Ap	197	85	3.0	812	3	US-09-091-097-7	Sequence 7, Appl
c 125	97	3.4	4419	4	US-09-620-312D-187	Sequence 187, App	198	85	3.0	1020	4	US-09-328-475C-43	Sequence 43, Appl
c 126	96	3.4	147	4	US-09-621-976-10254	Sequence 10254, A	199	84	3.0	147	4	US-09-621-976-10383	Sequence 10383, A
c 127	96	3.4	1117	3	US-09-247-373B-33	Sequence 33, Appl	200	84	3.0	176	4	US-09-621-976-13903	Sequence 13903, A
c 128	95	3.3	1308	4	US-10-151-832-1	Sequence 1, Appl	201	84	3.0	272	4	US-09-270-767-11902	Sequence 11902, A
c 129	95	3.3	2806	3	US-09-653-839-9	Sequence 9, Appl	202	84	3.0	1602	1	US-08-530-950-3	Sequence 3, Appl
c 130	95	3.3	2806	3	US-10-202-619-9	Sequence 9, Appl	203	84	3.0	1602	3	US-08-888-429A-3	Sequence 3, Appl
c 131	95	3.3	4086	4	US-09-702-705-1801	Sequence 1801, Ap	204	84	3.0	1602	3	US-09-149-879-3	Sequence 3, Appl
c 132	95	3.3	4086	4	US-09-736-457-1801	Sequence 1801, Ap	205	84	3.0	1602	4	US-09-057-009-3	Sequence 3, Appl
c 133	95	3.3	4086	4	US-09-671-325-1801	Sequence 1801, Ap	206	84	3.0	1602	4	US-09-593-653-3	Sequence 3, Appl
c 134	94	3.3	123	4	US-09-621-976-12330	Sequence 12330, A	207	84	3.0	1725	4	US-09-668-097A-21	Sequence 21, Appl
c 135	94	3.3	194	4	US-09-621-976-801	Sequence 801, App	208	84	3.0	1781	4	US-09-818-512-1	Sequence 1, Appl
c 136	94	3.3	365	4	US-09-043-861-3	Sequence 3, Appl	209	84	3.0	1895	3	US-09-444-336-7	Sequence 7, Appl
c 137	94	3.3	558	4	US-09-501-115-5	Sequence 5, Appl	210	84	3.0	2239	3	US-09-196-390-1	Sequence 1, Appl
c 138	93	3.3	550	4	US-09-501-115-5	Sequence 5, Appl	211	84	3.0	2239	4	US-09-952-677-1	Sequence 1, Appl
c 139	93	3.3	1414	4	US-09-621-976-14689	Sequence 14689, A	212	83	2.9	83	4	US-09-621-976-14751	Sequence 14751, A
c 140	92	3.2	92	4	US-09-621-976-13820	Sequence 13820, A	213	83	2.9	83	4	US-09-621-976-14959	Sequence 14959, A
c 141	92	3.2	105	4	US-08-545-196B-10	Sequence 10, Appl	214	83	2.9	127	4	US-09-621-976-13933	Sequence 13933, A
c 142	92	3.2	1582	3	US-08-545-196B-12	Sequence 12, Appl	215	83	2.9	163	4	US-09-621-976-9608	Sequence 9608, Ap
c 143	92	3.2	1582	3	US-10-164-595-29	Sequence 29, Appl	216	83	2.9	1069	3	US-09-372-422A-7	Sequence 7, Appl
c 144	92	3.2	3438	4	US-09-621-976-13620	Sequence 13620, A	217	83	2.9	1835	3	US-09-485-549-1	Sequence 1, Appl
c 145	91	3.2	92	4	US-09-621-976-16010	Sequence 16010, A	218	82	2.9	554	4	US-09-696-168A-14	Sequence 14, Appl
c 146	91	3.2	362	4	US-09-800-729-78	Sequence 78, Appl	219	82	2.9	612	4	US-09-902-540-1357	Sequence 1357, Ap
c 147	91	3.2	1141	4	US-09-720-317A-19	Sequence 19, Appl	220	82	2.9	990	4	US-08-486-049-1	Sequence 1, Appl
c 148	91	3.2	2311	4	US-09-149-476-24	Sequence 24, Appl	221	82	2.9	2625	4	US-09-621-976-13152	Sequence 13152, A
c 149	91	3.2	2323	3	Patent No. 5168051-9	Patent No. 5168051	222	81	2.8	7724	4	US-09-621-976-10335	Sequence 10335, A
c 150	91	3.2	2671	6	Sequence 10543, A	Sequence 10543, A	223	81	2.8	81	4	US-09-621-976-16784	Sequence 16784, A
c 151	91	3.2	2671	6	Sequence 35, Appl	Sequence 35, Appl	224	81	2.8	160	4	US-09-621-976-16784	Sequence 16784, A
c 152	90	3.2	193	4	Sequence 1, Appl	Sequence 1, Appl	225	81	2.8	190	4	US-08-455-633A-35	Sequence 35, Appl
c 153	90	3.2	1098	3	Sequence 187, App	Sequence 187, App	226	81	2.8	271	4	PCT-US94-05354-35	Sequence 35, Appl
c 154	90	3.2	1545	4	Sequence 1, Appl	Sequence 1, Appl	227	81	2.8	1114	3	US-09-152-060-41	Sequence 41, Appl
c 155	90	3.2	2665	3	Sequence 23, Appl	Sequence 23, Appl	228	81	2.8	1114	3	US-09-621-976-13152	Sequence 13152, A
c 156	90	3.2	3116	4	Sequence 5, Appl	Sequence 5, Appl	229	81	2.8	1114	3	US-09-621-976-10380	Sequence 10380, A
c 157	90	3.2	3715	4	Sequence 8, Appl	Sequence 8, Appl	230	81	2.8	1114	3	US-09-621-976-16324	Sequence 16324, A
c 158	89	3.1	89	4	Sequence 13, Appl	Sequence 13, Appl	231	81	2.8	1114	3	US-09-780-641-1	Sequence 1, Appl
c 159	89	3.1	89	4	Sequence 15134, A	Sequence 15134, A	232	81	2.8	1114	3	US-09-443-041A-29	Sequence 29, Appl
c 160	89	3.1	1091	4	Sequence 16008, A	Sequence 16008, A	233	81	2.8	1210	3	US-09-453-323-1	Sequence 1, Appl
c 161	89	3.1	1193	3	Sequence 16019, A	Sequence 16019, A	234	80	2.8	1636	3	US-09-578-194-6	Sequence 6, Appl
c 162	89	3.1	1411	3	Sequence 101, App	Sequence 101, App	235	80	2.8	3124	3	US-09-734-030-1	Sequence 1, Appl
c 163	89	3.1	1411	3	Sequence 1, Appl	Sequence 1, Appl	236	80	2.8	3124	4	US-10-153-921-1	Sequence 1, Appl
c 164	89	3.1	1411	4	Sequence 13, Appl	Sequence 13, Appl	237	80	2.8	3124	4	US-10-689-689-1	Sequence 1, Appl
c 165	89	3.1	1445	3	Sequence 16226, A	Sequence 16226, A	238	79	2.8	242	4	US-09-621-976-16320	Sequence 16320, A
c 166	89	3.1	1641	4	Sequence 376, App	Sequence 376, App	239	79	2.8	242	4	US-09-621-976-16226	Sequence 16226, A
c 167	89	3.1	1641	4	Sequence 376, App	Sequence 376, App	240	79	2.8	242	4	US-09-907-794A-376	Sequence 376, App
c 168	89	3.1	1641	4	Sequence 376, App	Sequence 376, App	241	79	2.8	242	4	US-09-905-125A-376	Sequence 376, App
c 169	89	3.1	1662	4	Sequence 376, App	Sequence 376, App	242	79	2.8	242	4		
c 170	88	3.1	351	4			243	79	2.8	242	4		
c 171	88	3.1	359	4			244	79	2.8	242	4		
c 172	88	3.1	359	4			245	79	2.8	242	4		
c 173	88	3.1	1248	4			246	79	2.8	242	4		

247	79	2.8	997	4	US-09-902-775A-376	Sequence 376, App	320	75	2.6	1492	4	US-09-369-247-23	Sequence 23, Appl
248	79	2.8	997	4	US-09-906-700-376	Sequence 376, App	321	75	2.6	1925	4	US-09-148-545-128	Sequence 128, App
249	79	2.8	997	4	US-09-903-603A-376	Sequence 376, App	322	75	2.6	2550	6	5258287-23	Patent No. 5258287
250	79	2.8	997	4	US-09-904-920A-376	Sequence 376, App	323	75	2.6	2550	6	5258287-23	Patent No. 5258287
251	79	2.8	997	4	US-09-909-064-376	Sequence 376, App	324	74	2.6	109	4	US-09-621-976-14592	Sequence 14592, A
252	79	2.8	997	4	US-09-905-381A-376	Sequence 376, App	325	74	2.6	165	4	US-09-621-976-8127	Sequence 8127, Ap
253	79	2.8	997	4	US-09-906-638-376	Sequence 376, App	326	74	2.6	166	4	US-09-621-976-18390	Sequence 18390, A
254	79	2.8	1013	4	US-09-322-409-6	Sequence 6, Appl	327	74	2.6	185	4	US-09-621-976-16779	Sequence 16779, A
c 255	79	2.8	1013	4	US-09-322-409-8	Sequence 8, Appl	328	74	2.6	1147	1	US-08-665-716-1	Sequence 1, Appl
256	79	2.8	1013	4	US-09-451-527-6	Sequence 6, Appl	329	74	2.6	1172	1	US-07-945-288-9	Sequence 9, Appl
c 257	79	2.8	1013	4	US-09-451-527-8	Sequence 8, Appl	330	74	2.6	1172	1	US-08-462-831-9	Sequence 9, Appl
258	79	2.8	1013	4	US-08-340-820-24	Sequence 24, Appl	331	74	2.6	1172	1	US-08-461-809-9	Sequence 9, Appl
259	79	2.8	1493	1	US-08-593-535-24	Sequence 24, Appl	332	74	2.6	1172	1	US-08-461-441-9	Sequence 9, Appl
260	79	2.8	1736	3	US-09-182-816-22	Sequence 22, Appl	333	74	2.6	1172	5	PCT-US93-08518-9	Sequence 9, Appl
c 261	79	2.8	1736	3	US-09-182-816-24	Sequence 24, Appl	334	74	2.6	1927	3	US-09-336-536-66	Sequence 66, Appl
262	79	2.8	1736	3	US-09-471-528-22	Sequence 22, Appl	335	74	2.6	41736	4	US-09-949-016-17091	Sequence 17091, A
c 263	79	2.8	1736	3	US-09-471-528-24	Sequence 24, Appl	336	73	2.6	73	4	US-09-621-976-14963	Sequence 14963, A
c 264	79	2.8	1736	3	US-09-634-530-22	Sequence 22, Appl	337	73	2.6	188	4	US-09-621-976-10364	Sequence 10364, A
c 265	79	2.8	1736	3	US-09-634-530-24	Sequence 24, Appl	338	73	2.6	189	4	US-09-621-976-14761	Sequence 14761, A
266	79	2.8	2202	3	US-09-465-558-59	Sequence 59, Appl	339	73	2.6	552	4	US-09-461-325-111	Sequence 111, App
267	78	2.7	78	4	US-09-621-976-14824	Sequence 14824, A	340	73	2.6	552	4	US-10-012-542-111	Sequence 111, App
268	78	2.7	78	4	US-09-621-976-15092	Sequence 15092, A	341	73	2.6	552	4	US-10-012-542-111	Sequence 111, App
c 269	78	2.7	270	2	US-08-520-678A-30	Sequence 30, Appl	342	73	2.6	1129	3	US-09-227-357-40	Sequence 40, Appl
c 270	78	2.7	270	3	US-08-897-126-30	Sequence 30, Appl	343	73	2.6	1296	4	US-09-461-325-29	Sequence 29, Appl
271	78	2.7	639	4	US-09-482-273-49	Sequence 49, Appl	344	73	2.6	1296	4	US-10-012-542-29	Sequence 29, Appl
272	78	2.7	1332	2	US-09-057-762-1	Sequence 1, Appl	345	73	2.6	1296	4	US-10-115-123-29	Sequence 29, Appl
273	78	2.7	1332	3	US-08-326-119A-1	Sequence 1, Appl	346	73	2.6	1378	3	US-09-149-476-308	Sequence 208, App
274	78	2.7	1361	4	US-09-489-847-64	Sequence 64, Appl	347	73	2.6	1606	4	US-09-820-004-1	Sequence 1, Appl
275	78	2.7	2146	4	US-10-003-392-3	Sequence 3, Appl	348	73	2.6	1872	3	US-09-291-922-27	Sequence 27, Appl
276	78	2.7	5021	4	US-09-949-016-786	Sequence 786, App	349	73	2.6	2045	3	US-09-152-060-22	Sequence 22, Appl
c 277	77	2.7	77	4	US-08-956-171E-2883	Sequence 2883, Ap	350	73	2.6	2628	1	US-08-143-219-1	Sequence 1, Appl
c 278	77	2.7	77	4	US-08-781-986A-2883	Sequence 2883, Ap	351	72	2.5	72	4	US-09-621-976-10145	Sequence 10145, A
279	77	2.7	79	4	US-09-621-976-15090	Sequence 15090, A	352	72	2.5	72	4	US-09-621-976-14815	Sequence 14815, A
c 280	77	2.7	196	4	US-09-644-460-40	Sequence 40, Appl	353	72	2.5	72	4	US-09-621-976-14842	Sequence 14842, A
281	77	2.7	215	4	US-09-621-976-15321	Sequence 15321, A	354	72	2.5	101	3	US-09-404-879A-293	Sequence 293, App
282	77	2.7	215	4	US-09-248-335-57	Sequence 57, Appl	355	72	2.5	101	4	US-09-338-933-293	Sequence 293, App
283	77	2.7	1297	4	US-09-800-729-80	Sequence 80, Appl	356	72	2.5	101	4	US-09-215-681-293	Sequence 293, App
284	77	2.7	1692	4	US-09-821-803A-5	Sequence 5, Appl	357	72	2.5	101	4	US-09-216-003A-293	Sequence 293, App
285	77	2.7	2407	3	US-09-370-807-7	Sequence 7, Appl	358	72	2.5	101	4	US-09-667-857-293	Sequence 293, App
286	77	2.7	2407	3	US-09-921-259-7	Sequence 7, Appl	359	72	2.5	250	4	US-09-621-976-18893	Sequence 18893, A
287	77	2.7	2744	3	US-09-071-101-1	Sequence 1, Appl	360	72	2.5	588	4	US-09-205-258-64	Sequence 64, Appl
288	77	2.7	2744	3	US-09-369-618-1	Sequence 1, Appl	361	72	2.5	1046	1	US-08-361-457B-4	Sequence 4, Appl
289	77	2.7	2744	3	US-09-369-617-1	Sequence 1, Appl	362	72	2.5	1046	1	US-08-484-332C-4	Sequence 4, Appl
290	76	2.7	76	4	US-09-621-976-14831	Sequence 14831, A	363	72	2.5	1074	3	US-09-248-335-67	Sequence 67, Appl
291	76	2.7	76	4	US-09-621-976-14915	Sequence 14915, A	364	72	2.5	1100	3	US-07-861-458C-4	Sequence 4, Appl
292	76	2.7	84	1	US-08-664-596B-3	Sequence 3, Appl	365	72	2.5	2065	3	US-09-370-473-5	Sequence 5, Appl
293	76	2.7	84	1	US-08-738-367-3	Sequence 3, Appl	366	71	2.5	71	4	US-09-621-976-14905	Sequence 14905, A
294	76	2.7	179	4	US-09-621-976-18054	Sequence 18054, A	367	71	2.5	72	4	US-09-621-976-9837	Sequence 9837, Ap
295	76	2.7	347	4	US-09-621-976-16026	Sequence 16026, A	368	71	2.5	80	1	US-07-920-281C-25	Sequence 25, Appl
296	76	2.7	763	4	US-09-743-207-3	Sequence 3, Appl	369	71	2.5	80	3	US-08-466-277-25	Sequence 25, Appl
297	76	2.7	1023	1	US-08-252-966B-16	Sequence 16, Appl	370	71	2.5	80	4	US-09-688-842-25	Sequence 25, Appl
298	76	2.7	2445	4	US-09-949-016-781	Sequence 781, App	371	71	2.5	100	4	US-09-621-976-12774	Sequence 12774, A
299	76	2.7	2539	4	US-10-144-198-21	Sequence 21, Appl	372	71	2.5	1123	3	US-09-152-060-15	Sequence 15, Appl
300	76	2.7	2989	6	5378464-1	Patent No. 5378464	373	71	2.5	1214	4	US-08-780-717-28	Sequence 28, Appl
301	76	2.7	2989	6	5378464-1	Patent No. 5378464	374	71	2.5	1544	4	US-09-187-999-14	Sequence 14, Appl
302	76	2.7	3080	3	US-09-099-041A-25	Sequence 25, Appl	375	71	2.5	4880	3	US-09-031-563-1	Sequence 1, Appl
303	76	2.7	3080	3	US-09-245-281-25	Sequence 25, Appl	376	71	2.5	4880	3	US-09-392-277-1	Sequence 1, Appl
304	76	2.7	3080	3	US-09-207-359B-25	Sequence 25, Appl	377	71	2.5	4880	4	US-09-258-000-1	Sequence 1, Appl
305	76	2.7	3080	4	US-09-340-620A-25	Sequence 25, Appl	378	71	2.5	5125	3	US-09-031-563-4	Sequence 4, Appl
306	76	2.7	3080	4	US-09-865-364-25	Sequence 25, Appl	379	71	2.5	5125	3	US-09-392-277-4	Sequence 4, Appl
307	76	2.7	3366	4	US-09-596-141C-6	Sequence 6, Appl	380	71	2.5	5125	4	US-09-258-000-4	Sequence 4, Appl
308	76	2.7	3366	4	US-09-595-526C-6	Sequence 6, Appl	381	71	2.5	8100	4	US-09-554-337-4	Sequence 4, Appl
309	76	2.7	10442	4	US-09-596-141C-1	Sequence 1, Appl	382	71	2.5	11517	1	US-07-920-281C-1	Sequence 1, Appl
310	76	2.7	10474	4	US-09-595-526C-7	Sequence 7, Appl	383	71	2.5	11517	3	US-08-466-277-1	Sequence 1, Appl
311	76	2.7	10474	4	US-09-596-141C-9	Sequence 9, Appl	384	71	2.5	11517	4	US-09-688-842-1	Sequence 1, Appl
312	76	2.7	10474	4	US-09-596-141C-9	Sequence 9, Appl	385	71	2.5	15538	4	US-09-554-337-1	Sequence 1, Appl
313	76	2.7	10474	4	US-09-595-526C-7	Sequence 7, Appl	386	70	2.5	169	4	US-09-621-976-11249	Sequence 11249, A
314	76	2.7	10474	4	US-09-595-526C-9	Sequence 9, Appl	387	70	2.5	318	4	US-09-621-976-10247	Sequence 10247, A
315	75	2.6	75	4	US-09-621-976-14892	Sequence 14892, A	388	70	2.5	593	4	US-09-904-615-59	Sequence 59, Appl
c 316	75	2.6	844	4	US-09-690-942-3	Sequence 3, Appl	389	70	2.5	1206	3	US-09-465-558-53	Sequence 53, Appl
317	75	2.6	1133	4	US-09-916-204-1	Sequence 1, Appl	390	70	2.5	1461	3	US-08-722-126A-4	Sequence 4, Appl
318	75	2.6	1133	4	US-10-282-048-1	Sequence 1, Appl	391	70	2.5	1461	5	PCT-US95-04258-4	Sequence 4, Appl
319	75	2.6	1279	3	US-09-248-335-25	Sequence 25, Appl	392	70	2.5	2218	4	US-09-016-434-1157	Sequence 1157, Ap

393	70	2.5	2218	4	US-10-329-668-7	Sequence 7, Appli	466	66	2.3	1062	4	US-09-796-766-3	Sequence 3, Appli
394	70	2.5	2527	1	US-08-496-631-1	Sequence 1, Appli	467	66	2.3	1138	4	US-09-800-729-44	Sequence 44, Appl
395	70	2.5	3527	1	US-08-909-965C-7	Sequence 1, Appli	468	66	2.3	1201	4	US-09-461-325-36	Sequence 36, Appl
396	70	2.5	5173	1	US-08-242-677-1	Sequence 1, Appli	469	66	2.3	1201	4	US-10-012-542-36	Sequence 36, Appl
397	69	2.4	69	4	US-09-621-976-14105	Sequence 14105, A	470	66	2.3	1201	4	US-10-115-123-36	Sequence 1, Appli
398	69	2.4	69	4	US-09-621-976-14869	Sequence 14869, A	471	66	2.3	1383	4	US-09-735-846-1	Sequence 1, Appli
399	69	2.4	69	4	US-09-573-080A-447	Sequence 447, App	472	66	2.3	1660	4	US-09-722-971-9	Sequence 9, Appli
400	69	2.4	84	4	US-09-621-976-14571	Sequence 14571, A	473	66	2.3	2442	4	US-09-575-081B-3	Sequence 3, Appli
401	69	2.4	98	4	US-09-621-976-11744	Sequence 11744, A	474	66	2.3	3848	3	US-09-112-096-28	Sequence 28, Appl
402	69	2.4	231	4	US-09-621-976-16317	Sequence 16317, A	475	66	2.3	3668	3	US-09-112-096-14	Sequence 14, Appl
403	69	2.4	253	4	US-09-621-976-12799	Sequence 12799, A	476	66	2.3	5668	4	US-09-636-215-777	Sequence 777, App
404	69	2.4	299	4	US-09-621-976-10211	Sequence 10211, A	477	66	2.3	5668	4	US-09-685-166A-777	Sequence 777, App
405	69	2.4	664	4	US-09-904-615-66	Sequence 66, Appl	478	66	2.3	5668	4	US-09-679-426-777	Sequence 777, App
406	69	2.4	1196	4	US-09-065-040-2	Sequence 2, Appli	479	66	2.3	5668	4	US-09-759-143-777	Sequence 777, App
407	69	2.4	1325	1	US-08-306-691B-51	Sequence 51, Appl	480	66	2.3	5668	4	US-09-651-236-777	Sequence 777, App
408	69	2.4	1325	2	US-08-464-517-1	Sequence 1, Appli	481	66	2.3	7286	3	US-09-331-581-3	Sequence 3, Appli
409	69	2.4	1325	2	US-08-246-361A-1	Sequence 1, Appli	482	66	2.3	7938	3	US-09-331-581-14	Sequence 14, Appl
410	69	2.4	1325	2	US-08-463-772-1	Sequence 1, Appli	483	66	2.3	65	4	US-09-621-976-14743	Sequence 14743, A
411	69	2.4	1325	5	PCT-US93-05000-1	Sequence 1, Appli	484	65	2.3	65	4	US-09-621-976-14853	Sequence 14853, A
412	69	2.4	1509	3	US-09-149-476-179	Sequence 179, App	485	65	2.3	94	3	US-09-404-879A-261	Sequence 261, App
413	69	2.4	1546	4	US-09-901-151-1	Sequence 1, Appli	486	65	2.3	94	4	US-09-338-933-261	Sequence 261, App
414	69	2.4	1844	4	US-10-003-392-7	Sequence 7, Appli	487	65	2.3	94	4	US-09-215-681-261	Sequence 261, App
415	69	2.4	3200	1	US-08-444-405-1	Sequence 1, Appli	488	65	2.3	94	4	US-09-216-003A-261	Sequence 261, App
416	69	2.4	3200	1	US-08-384-850-1	Sequence 1, Appli	489	65	2.3	94	4	US-09-667-857-261	Sequence 261, App
417	69	2.4	4456	3	US-09-095-443-1	Sequence 1, Appli	490	65	2.3	159	4	US-09-621-976-17448	Sequence 17448, A
418	68	2.4	70	4	US-09-621-976-13579	Sequence 13579, A	491	65	2.3	336	4	US-09-621-976-16013	Sequence 16013, A
419	68	2.4	73	4	US-09-621-976-14729	Sequence 14729, A	492	65	2.3	338	4	US-09-621-976-16041	Sequence 16041, A
420	68	2.4	75	4	US-09-621-976-12516	Sequence 12516, A	493	65	2.3	341	4	US-09-621-976-16135	Sequence 16135, A
421	68	2.4	259	4	US-09-621-976-16294	Sequence 16294, A	494	65	2.3	358	4	US-09-621-976-927	Sequence 927, App
422	68	2.4	931	4	US-09-482-273-31	Sequence 31, Appl	495	65	2.3	991	3	US-09-924-747-25	Sequence 25, Appl
423	68	2.4	1359	3	US-09-387-574-11	Sequence 11, Appl	496	65	2.3	991	3	US-09-247-373B-25	Sequence 25, Appl
424	68	2.4	1359	3	US-09-668-096-11	Sequence 11, Appl	497	65	2.3	991	3	US-09-296-715-25	Sequence 25, Appl
425	68	2.4	1512	2	US-08-908-965C-8	Sequence 8, Appli	498	65	2.3	1069	4	US-09-205-258-74	Sequence 74, Appl
426	68	2.4	1738	2	US-08-373-482A-2	Sequence 2, Appli	499	65	2.3	1406	4	US-10-000-489-81	Sequence 81, Appl
427	68	2.4	2276	4	US-09-205-258-183	Sequence 183, App	500	65	2.3	1700	2	US-08-897-340-4	Sequence 4, Appli
428	68	2.4	4239	4	US-09-815-048-1	Sequence 1, Appli	501	65	2.3	1700	3	US-09-252-329-4	Sequence 4, Appli
429	68	2.4	6200	3	US-09-439-923-1	Sequence 1, Appli	502	65	2.3	1740	4	US-09-709-103-45	Sequence 45, Appl
430	68	2.4	6200	4	US-09-711-202A-1	Sequence 1, Appli	503	65	2.3	1740	4	US-09-439-410A-45	Sequence 45, Appl
431	68	2.4	6200	4	US-09-711-205A-1	Sequence 1, Appli	504	65	2.3	1801	4	US-09-709-103-3	Sequence 3, Appli
432	68	2.4	8638	4	US-10-029-907-6	Sequence 6, Appli	505	65	2.3	1801	4	US-09-439-410A-3	Sequence 3, Appli
433	67	2.4	67	4	US-09-621-976-11909	Sequence 11909, A	506	65	2.3	1868	3	US-09-739-455-1	Sequence 1, Appli
434	67	2.4	67	4	US-09-621-976-13917	Sequence 13917, A	507	65	2.3	2096	3	US-09-008-481A-10	Sequence 10, Appl
435	67	2.4	67	4	US-09-621-976-14753	Sequence 14753, A	508	65	2.3	2096	3	US-09-195-666A-16	Sequence 16, Appl
436	67	2.4	69	4	US-09-621-976-12006	Sequence 12006, A	509	65	2.3	2096	3	US-09-309-592-10	Sequence 10, Appl
437	67	2.4	76	4	US-09-621-976-12446	Sequence 12446, A	510	65	2.3	2096	3	US-09-635-705-16	Sequence 16, Appl
438	67	2.4	84	4	US-09-621-976-14577	Sequence 14577, A	511	65	2.3	2096	3	US-08-634-858A-16	Sequence 16, Appl
439	67	2.4	260	2	US-08-520-678A-29	Sequence 29, Appl	512	65	2.3	2096	3	US-08-869-927C-16	Sequence 2, Appli
440	67	2.4	260	3	US-08-897-126-29	Sequence 29, Appl	513	65	2.3	2187	3	US-09-127-219B-2	Sequence 2, Appli
441	67	2.4	283	4	US-09-621-976-16989	Sequence 16989, A	514	65	2.3	2271	4	US-09-205-258-243	Sequence 243, App
442	67	2.4	316	4	US-09-513-999C-838	Sequence 838, App	515	65	2.3	2291	4	US-09-220-132-114	Sequence 114, App
443	67	2.4	536	1	US-08-341-568-1	Sequence 1, Appli	516	65	2.3	2291	4	US-09-814-915A-95	Sequence 95, Appl
444	67	2.4	536	2	US-08-911-020-1	Sequence 1, Appli	517	65	2.3	2329	4	US-08-800-729-11	Sequence 11, Appl
445	67	2.4	688	6	5498694-3	Patent No. 5498694	518	65	2.3	3975	4	US-09-270-767-3	Sequence 3, Appli
446	67	2.4	688	6	5498694-3	Patent No. 5498694	519	64	2.2	64	4	US-09-621-976-14858	Sequence 14858, A
447	67	2.4	746	3	US-09-013-810-1	Sequence 1, Appli	520	64	2.2	69	1	US-08-702-344-7	Sequence 7, Appli
448	67	2.4	1412	4	US-09-614-912-197	Sequence 197, App	521	64	2.2	138	4	US-09-621-976-9595	Sequence 9595, Ap
449	67	2.4	1441	3	US-08-821-994-63	Sequence 63, Appl	522	64	2.2	227	2	US-08-520-678A-28	Sequence 28, Appl
450	67	2.4	1485	3	US-09-372-422A-39	Sequence 39, Appl	523	64	2.2	227	3	US-08-897-126-28	Sequence 28, Appl
451	67	2.4	1559	4	US-09-489-847-42	Sequence 42, Appl	524	64	2.2	231	4	US-09-621-976-16456	Sequence 16456, A
452	67	2.4	1560	4	US-09-500-495A-5	Sequence 5, Appli	525	64	2.2	258	4	US-09-621-976-15353	Sequence 15353, A
453	67	2.4	2158	1	US-07-602-608-1	Sequence 1, Appli	526	64	2.2	335	4	US-09-621-976-16061	Sequence 16061, A
454	67	2.4	2158	1	US-08-261-578-1	Sequence 1, Appli	527	64	2.2	687	4	US-09-774-639-106	Sequence 106, App
455	66	2.3	66	4	US-09-621-976-12404	Sequence 12404, A	528	64	2.2	789	3	US-09-020-956-32	Sequence 32, Appl
456	66	2.3	66	4	US-09-621-976-14819	Sequence 14819, A	529	64	2.2	789	3	US-09-030-607-32	Sequence 32, Appl
457	66	2.3	68	4	US-09-621-976-11613	Sequence 11613, A	530	64	2.2	789	3	US-09-439-313-32	Sequence 32, Appl
458	66	2.3	68	4	US-09-621-976-11912	Sequence 11912, A	531	64	2.2	789	3	US-09-352-616A-32	Sequence 32, Appl
459	66	2.3	68	4	US-09-621-976-12005	Sequence 12005, A	532	64	2.2	789	3	US-09-232-149A-32	Sequence 32, Appl
460	66	2.3	105	3	US-09-284-627-23	Sequence 23, Appl	533	64	2.2	789	4	US-09-159-812-32	Sequence 32, Appl
461	66	2.3	293	4	US-09-621-976-16965	Sequence 16965, A	534	64	2.2	789	4	US-09-636-215-32	Sequence 32, Appl
462	66	2.3	443	4	US-09-936-885A-1	Sequence 1, Appli	535	64	2.2	789	4	US-09-685-166A-32	Sequence 32, Appl
463	66	2.3	572	3	US-09-342-653-5	Sequence 5, Appli	536	64	2.2	789	4	US-09-115-453-32	Sequence 32, Appl
464	66	2.3	759	4	US-09-465-559-5	Sequence 5, Appli	537	64	2.2	789	4	US-09-688-489-32	Sequence 32, Appl
465	66	2.3	796	1	US-08-104-073-2	Sequence 2, Appli	538	64	2.2	789	4	US-09-679-426-32	Sequence 32, Appl

C 539	64	2.2	789	4	US-09-759-143-32	Sequence 32, Appl	612	62	2.2	1864	3	US-09-149-476-130	Sequence 130, App
C 540	64	2.2	789	4	US-09-651-236-32	Sequence 32, Appl	613	62	2.2	2203	4	US-09-801-861-1	Sequence 1, Appl
541	64	2.2	793	5	PCT-US95-06406A-21	Sequence 21, Appl	614	62	2.2	2203	4	US-10-224-562-1	Sequence 1, Appl
542	64	2.2	958	2	US-08-757-046A-5	Sequence 5, Appl	615	62	2.2	2205	3	US-08-888-077A-41	Sequence 41, Appl
543	64	2.2	958	3	US-09-447-208-5	Sequence 5, Appl	616	62	2.2	2438	4	US-09-393-634-4	Sequence 4, Appl
544	64	2.2	958	3	US-09-135-988-5	Sequence 5, Appl	617	62	2.2	2718	4	US-09-667-135-1	Sequence 1, Appl
545	64	2.2	958	3	US-09-277-716-5	Sequence 5, Appl	618	62	2.2	2882	4	US-09-949-016-724	Sequence 17, Appl
546	64	2.2	958	3	US-08-597-274A-5	Sequence 5, Appl	619	62	2.2	3214	1	US-08-484-105-17	Sequence 17, Appl
547	64	2.2	958	3	US-08-908-909-5	Sequence 5, Appl	620	62	2.2	3214	1	US-08-484-106-17	Sequence 17, Appl
548	64	2.2	958	3	US-09-609-161B-5	Sequence 5, Appl	C 621	62	2.2	4055	4	US-09-620-312D-706	Sequence 706, App
549	64	2.2	958	3	US-08-990-103-5	Sequence 5, Appl	622	61	2.1	61	4	US-09-621-976-14680	Sequence 14680, A
550	64	2.2	958	4	US-09-746-485A-5	Sequence 5, Appl	623	61	2.1	61	4	US-09-621-976-14681	Sequence 14681, A
551	64	2.2	958	4	US-10-126-139-5	Sequence 5, Appl	624	61	2.1	61	4	US-09-621-976-14682	Sequence 14682, A
552	64	2.2	958	4	US-10-126-778-5	Sequence 5, Appl	625	61	2.1	61	4	US-09-621-976-14683	Sequence 14683, A
553	64	2.2	958	4	US-10-126-777-5	Sequence 5, Appl	626	61	2.1	61	4	US-09-621-976-14948	Sequence 14948, A
554	64	2.2	1578	3	US-09-416-050A-1	Sequence 1, Appl	627	61	2.1	63	4	US-09-621-976-13480	Sequence 13480, A
555	64	2.2	1578	3	US-09-664-800-1	Sequence 1, Appl	628	61	2.1	137	4	US-09-621-976-18434	Sequence 18434, A
556	64	2.2	1578	3	US-09-665-309-1	Sequence 1, Appl	629	61	2.1	145	4	US-09-621-976-16688	Sequence 16688, A
557	64	2.2	1578	3	US-09-661-569-1	Sequence 1, Appl	630	61	2.1	148	4	US-09-621-976-17447	Sequence 17447, A
558	64	2.2	1637	4	US-09-205-258-178	Sequence 178, App	631	61	2.1	148	4	US-09-621-976-17450	Sequence 17450, A
559	64	2.2	1651	4	US-09-800-729-41	Sequence 41, Appl	632	61	2.1	263	3	US-09-091-097-26	Sequence 26, Appl
560	64	2.2	1981	4	US-09-720-317A-3	Sequence 3, Appl	633	61	2.1	266	4	US-09-621-976-16813	Sequence 16813, A
561	64	2.2	3581	2	US-08-738-349-1	Sequence 1, Appl	634	61	2.1	350	4	US-09-621-976-15342	Sequence 15342, A
562	64	2.2	4860	4	US-09-949-016-296	Sequence 296, App	C 635	61	2.1	470	3	US-09-020-956-102	Sequence 102, App
563	63	2.2	63	4	US-09-621-976-13842	Sequence 13842, A	C 636	61	2.1	470	3	US-09-030-607-102	Sequence 102, App
564	63	2.2	63	4	US-09-621-976-14756	Sequence 14756, A	C 637	61	2.1	470	3	US-09-439-313-102	Sequence 102, App
565	63	2.2	142	4	US-09-621-976-10801	Sequence 10801, A	C 638	61	2.1	470	3	US-09-352-616A-102	Sequence 102, App
566	63	2.2	146	4	US-09-621-976-16695	Sequence 16695, A	C 639	61	2.1	470	3	US-09-232-149A-102	Sequence 102, App
567	63	2.2	153	4	US-09-621-976-17451	Sequence 17451, A	C 640	61	2.1	470	4	US-09-159-812-102	Sequence 102, App
568	63	2.2	323	4	US-09-621-976-10374	Sequence 10374, A	C 641	61	2.1	470	4	US-09-636-215-102	Sequence 102, App
569	63	2.2	334	4	US-09-621-976-16044	Sequence 16044, A	C 642	61	2.1	470	4	US-09-685-165A-102	Sequence 102, App
570	63	2.2	734	4	US-09-949-016-413	Sequence 413, App	C 643	61	2.1	470	4	US-09-115-453-102	Sequence 102, App
571	63	2.2	985	4	US-09-322-409-25	Sequence 25, Appl	C 644	61	2.1	470	4	US-09-688-489-102	Sequence 102, App
572	63	2.2	985	4	US-09-322-409-27	Sequence 27, Appl	C 645	61	2.1	470	4	US-09-679-426-102	Sequence 102, App
573	63	2.2	985	4	US-09-451-527-25	Sequence 25, Appl	C 646	61	2.1	470	4	US-09-759-143-102	Sequence 102, App
574	63	2.2	985	4	US-09-451-527-27	Sequence 27, Appl	C 647	61	2.1	470	4	US-09-651-236-102	Sequence 102, App
575	63	2.2	1075	3	US-08-400-006B-6	Sequence 6, Appl	548	61	2.1	972	1	US-07-915-934-1	Sequence 1, Appl
576	63	2.2	1522	3	US-09-413-574-1	Sequence 1, Appl	549	61	2.1	972	1	US-08-325-947-1	Sequence 1, Appl
577	63	2.2	1523	3	US-09-157-603-4	Sequence 4, Appl	650	61	2.1	1023	4	US-09-229-947-38	Sequence 38, Appl
578	63	2.2	1525	3	US-09-587-436-4	Sequence 4, Appl	651	61	2.1	1486	4	US-09-461-325-73	Sequence 73, Appl
579	63	2.2	1525	3	US-08-927-165A-4	Sequence 4, Appl	652	61	2.1	1486	4	US-10-012-542-73	Sequence 73, Appl
580	63	2.2	2010	1	US-07-864-475A-4	Sequence 4, Appl	653	61	2.1	1486	4	US-10-115-123-73	Sequence 73, Appl
581	63	2.2	2010	2	US-08-468-249A-4	Sequence 4, Appl	654	61	2.1	1780	3	US-09-202-548B-5	Sequence 5, Appl
582	63	2.2	2083	4	US-09-716-129-41	Sequence 41, Appl	655	61	2.1	1780	4	US-09-942-858-5	Sequence 5, Appl
583	63	2.2	2091	3	US-08-813-818-1	Sequence 1, Appl	656	61	2.1	1780	4	US-10-461-180-5	Sequence 5, Appl
584	63	2.2	2091	4	US-10-199-333-1	Sequence 1, Appl	657	61	2.1	2218	4	US-09-205-258-103	Sequence 103, App
585	63	2.2	2389	4	US-09-789-875-7	Sequence 7, Appl	658	61	2.1	2312	4	US-09-103-331-1	Sequence 1, Appl
586	63	2.2	2481	2	US-08-630-118A-1	Sequence 1, Appl	659	61	2.1	2312	4	US-09-631-594-45	Sequence 45, Appl
587	63	2.2	2481	2	US-08-838-399-1	Sequence 1, Appl	660	61	2.1	2378	3	US-08-802-805D-20	Sequence 20, Appl
588	63	2.2	2481	3	US-09-235-839-1	Sequence 1, Appl	661	61	2.1	2378	4	US-08-860-370-1	Sequence 1, Appl
589	63	2.2	2481	3	US-09-327-035-1	Sequence 1, Appl	662	61	2.1	2381	1	US-08-021-608D-9	Sequence 9, Appl
590	63	2.2	2604	2	US-08-630-118A-3	Sequence 3, Appl	663	61	2.1	2381	1	US-08-736-160-9	Sequence 9, Appl
591	63	2.2	2604	2	US-08-838-399-3	Sequence 3, Appl	664	61	2.1	2381	5	PCT-US94-01782-9	Sequence 9, Appl
592	63	2.2	2604	3	US-09-235-839-3	Sequence 3, Appl	665	61	2.1	2384	1	US-08-021-608D-1	Sequence 1, Appl
593	63	2.2	2604	3	US-09-327-035-3	Sequence 3, Appl	666	61	2.1	2384	1	US-08-726-160-1	Sequence 1, Appl
594	62	2.2	62	4	US-09-621-976-11091	Sequence 11091, A	667	61	2.1	2384	5	PCT-US94-01782-1	Sequence 1, Appl
595	62	2.2	62	4	US-09-621-976-14130	Sequence 14130, A	668	61	2.1	2483	1	US-09-205-258-68	Sequence 68, Appl
596	62	2.2	62	4	US-09-621-976-14936	Sequence 14936, A	669	61	2.1	2964	4	US-09-578-063-25	Sequence 25, Appl
597	62	2.2	91	3	US-09-404-879A-201	Sequence 201, App	670	60	2.1	60	3	US-09-457-959-8	Sequence 8, Appl
C 598	62	2.2	91	4	US-09-338-933-201	Sequence 201, App	671	60	2.1	60	4	US-09-621-976-12480	Sequence 12480, A
C 599	62	2.2	91	4	US-09-215-681-201	Sequence 201, App	672	60	2.1	60	4	US-09-621-976-13761	Sequence 13761, A
600	62	2.2	91	4	US-09-621-976-14925	Sequence 14925, A	673	60	2.1	60	4	US-09-621-976-14742	Sequence 14742, A
C 601	62	2.2	91	4	US-09-216-003A-201	Sequence 201, App	674	60	2.1	60	4	US-09-621-976-14884	Sequence 14884, A
C 602	62	2.2	91	4	US-09-667-857-201	Sequence 201, App	675	60	2.1	60	4	US-10-079-178-8	Sequence 8, Appl
603	62	2.2	145	4	US-09-621-976-16691	Sequence 16691, A	676	60	2.1	77	4	US-09-621-976-14176	Sequence 14176, A
604	62	2.2	146	4	US-09-621-976-16686	Sequence 16686, A	677	60	2.1	97	4	US-09-621-976-9086	Sequence 9086, Ap
605	62	2.2	214	4	US-09-621-976-9843	Sequence 9843, Ap	678	60	2.1	102	4	US-09-621-976-11436	Sequence 11436, A
606	62	2.2	332	4	US-09-621-976-16050	Sequence 16050, A	C 679	60	2.1	141	3	US-08-737-078A-1	Sequence 1, Appl
607	62	2.2	332	4	US-09-621-976-16053	Sequence 16053, A	C 680	60	2.1	141	5	PCT-US94-04706-1	Sequence 1, Appl
608	62	2.2	333	4	US-09-621-976-16032	Sequence 16032, A	681	60	2.1	150	4	US-09-621-976-8656	Sequence 8656, Ap
609	62	2.2	333	4	US-09-621-976-16045	Sequence 16045, A	682	60	2.1	204	4	US-09-621-976-1323	Sequence 1323, Ap
610	62	2.2	612	4	US-09-270-767-11643	Sequence 11643, A	683	60	2.1	235	4	US-09-621-976-16550	Sequence 16550, A
611	62	2.2	1579	4	US-09-403-463A-5	Sequence 5, Appl	684	60	2.1	255	4	US-09-621-976-9406	Sequence 9406, Ap

c 685	60	2.1	342	4	US-09-270-767-13044	Sequence 13044, A	c 758	58	2.0	509	3	US-09-439-313-202	Sequence 202, App
686	60	2.1	976	2	US-08-504-459-9	Sequence 9, Appli	c 759	58	2.0	509	3	US-09-352-616A-202	Sequence 202, App
687	60	2.1	1057	4	US-09-716-129-16	Sequence 16, Appl	c 760	58	2.0	509	3	US-09-232-149A-202	Sequence 202, App
688	60	2.1	1190	4	US-09-390-207-1	Sequence 1, Appli	c 761	58	2.0	509	4	US-09-159-812-202	Sequence 202, App
689	60	2.1	1813	5	PCT-US94-12883-3	Sequence 3, Appli	c 762	58	2.0	509	4	US-09-636-215-202	Sequence 202, App
690	60	2.1	1827	4	US-09-720-318A-9	Sequence 9, Appli	c 763	58	2.0	509	4	US-09-685-166A-202	Sequence 202, App
691	60	2.1	1842	4	US-09-482-273-90	Sequence 90, Appl	c 764	58	2.0	509	4	US-09-115-453-202	Sequence 202, App
692	60	2.1	1878	3	US-09-732-025-1	Sequence 1, Appli	c 765	58	2.0	509	4	US-09-688-489-202	Sequence 202, App
693	60	2.1	1882	4	US-09-419-679-3	Sequence 3, Appli	c 766	58	2.0	509	4	US-09-679-426-202	Sequence 202, App
694	60	2.1	1898	1	US-08-342-411A-1	Sequence 1, Appli	c 767	58	2.0	509	4	US-09-759-143-202	Sequence 202, App
695	60	2.1	1965	4	US-09-482-273-27	Sequence 27, Appli	c 768	58	2.0	509	4	US-09-651-236-202	Sequence 202, App
696	60	2.1	2431	1	US-07-847-743B-25	Sequence 25, Appl	769	58	2.0	530	4	US-09-461-325-28	Sequence 28, Appl
697	60	2.1	2431	1	US-08-456-201-25	Sequence 25, Appl	770	58	2.0	530	4	US-10-012-542-28	Sequence 28, Appl
698	60	2.1	2431	2	US-08-456-241-25	Sequence 25, Appl	771	58	2.0	530	4	US-10-115-123-28	Sequence 28, Appl
699	60	2.1	2431	5	PCT-US92-04295A-25	Sequence 25, Appl	c 772	58	2.0	530	3	US-09-313-300-6	Sequence 6, Appli
700	60	2.1	2485	4	US-09-889-463A-9	Sequence 9, Appli	773	58	2.0	748	1	US-08-361-467B-3	Sequence 3, Appli
701	60	2.1	5554	4	US-09-815-923-1	Sequence 1, Appli	774	58	2.0	748	1	US-08-484-332C-3	Sequence 3, Appli
702	60	2.1	6065	4	US-09-800-729-35	Sequence 35, Appl	775	58	2.0	795	4	US-09-270-767-14068	Sequence 14068, A
703	59	2.1	59	4	US-09-621-976-13084	Sequence 13084, A	776	58	2.0	1153	3	US-09-149-476-41	Sequence 41, Appl
704	59	2.1	59	4	US-09-621-976-13752	Sequence 13752, A	777	58	2.0	1154	3	US-08-651-136C-7	Sequence 7, Appli
705	59	2.1	146	4	US-09-621-976-16115	Sequence 16115, A	778	58	2.0	1154	3	US-09-229-911A-7	Sequence 7, Appli
706	59	2.1	162	4	US-09-621-976-18068	Sequence 18068, A	779	58	2.0	1166	5	PCT-US96-1129B-1	Sequence 1, Appli
707	59	2.1	232	4	US-09-621-976-17701	Sequence 17701, A	780	58	2.0	1405	4	US-09-244-111-9	Sequence 9, Appli
708	59	2.1	233	4	US-09-621-976-16559	Sequence 16559, A	781	58	2.0	1540	3	US-08-977-001-2	Sequence 2, Appli
709	59	2.1	234	4	US-09-621-976-16557	Sequence 16557, A	782	58	2.0	1958	3	US-08-665-034A-3	Sequence 3, Appli
710	59	2.1	249	4	US-09-621-976-19144	Sequence 19144, A	783	58	2.0	2230	3	US-08-378-313-24	Sequence 24, Appl
711	59	2.1	289	1	US-08-341-568-3	Sequence 3, Appli	784	58	2.0	2589	3	US-08-569-749-1	Sequence 1, Appli
712	59	2.1	289	2	US-08-911-020-3	Sequence 3, Appli	785	58	2.0	2589	4	US-09-689-366-1	Sequence 1, Appli
c 713	59	2.1	396	4	US-09-640-173-42	Sequence 42, Appl	786	58	2.0	2589	5	PCT-US96-12860-1	Sequence 1, Appli
c 714	59	2.1	396	4	US-09-713-550-42	Sequence 42, Appl	787	58	2.0	2790	3	US-08-800-291B-1	Sequence 1, Appli
c 715	59	2.1	396	4	US-09-825-294-42	Sequence 42, Appl	788	58	2.0	2908	4	US-09-904-615-35	Sequence 35, Appl
c 716	59	2.1	396	4	US-09-970-966-42	Sequence 42, Appl	789	58	2.0	3994	4	US-09-738-946-7	Sequence 7, Appli
717	59	2.1	491	4	US-09-311-021-191	Sequence 191, App	790	58	2.0	7859	1	US-07-854-596B-4	Sequence 4, Appli
718	59	2.1	570	1	US-07-885-970A-10	Sequence 10, Appl	791	58	2.0	7859	2	US-08-450-905B-15	Sequence 15, Appl
719	59	2.1	570	1	US-08-298-687A-10	Sequence 10, Appl	792	58	2.0	7859	2	US-07-982-759F-15	Sequence 15, Appl
720	59	2.1	570	1	US-08-298-829-10	Sequence 10, Appl	c 793	58	2.0	9472	4	US-08-150-204E-96	Sequence 96, Appl
c 721	59	2.1	609	1	US-08-530-797-9	Sequence 9, Appli	794	58	2.0	10660	2	US-08-267-803B-8	Sequence 8, Appli
c 722	59	2.1	609	2	US-08-787-335-9	Sequence 9, Appli	795	58	2.0	10660	3	US-09-041-886-16	Sequence 16, Appl
723	59	2.1	675	4	US-09-621-976-2461	Sequence 2461, Ap	796	58	2.0	57	4	US-09-621-976-11970	Sequence 11970, A
724	59	2.1	711	4	US-09-621-976-17854	Sequence 17854, A	797	57	2.0	57	4	US-09-621-976-13937	Sequence 13937, A
725	59	2.1	730	4	US-09-270-767-14600	Sequence 14600, A	798	57	2.0	70	4	US-09-621-976-14750	Sequence 14750, A
c 726	59	2.1	756	4	US-09-614-912-93	Sequence 93, Appl	799	57	2.0	134	4	US-09-621-976-18433	Sequence 18433, A
727	59	2.1	857	1	US-08-308-883-1	Sequence 1, Appli	800	57	2.0	157	4	US-09-621-976-10271	Sequence 10271, A
728	59	2.1	857	1	US-08-730-163-1	Sequence 1, Appli	801	57	2.0	160	4	US-09-621-976-18071	Sequence 18071, A
729	59	2.1	966	1	US-08-514-014-7	Sequence 7, Appli	802	57	2.0	249	4	US-09-621-976-16291	Sequence 16291, A
730	59	2.1	966	2	US-08-833-823-7	Sequence 7, Appli	803	57	2.0	249	4	US-09-621-976-16292	Sequence 16292, A
731	59	2.1	972	3	US-09-549-831-5	Sequence 5, Appli	804	57	2.0	272	4	US-09-621-976-16932	Sequence 16932, A
732	59	2.1	981	4	US-09-780-717-4	Sequence 4, Appli	805	57	2.0	304	4	US-09-621-976-16099	Sequence 16099, A
733	59	2.1	1315	3	US-09-164-193-1	Sequence 1, Appli	806	57	2.0	732	3	US-09-149-476-66	Sequence 66, Appl
734	59	2.1	1315	3	US-09-221-448A-1	Sequence 1, Appli	807	57	2.0	741	4	US-09-621-976-1894	Sequence 1894, Ap
735	59	2.1	1319	2	US-08-504-459-7	Sequence 7, Appli	808	57	2.0	857	3	US-08-256-799-1	Sequence 1, Appli
736	59	2.1	1358	4	US-09-949-016-463	Sequence 463, App	809	57	2.0	857	3	US-08-462-437-1	Sequence 1, Appli
737	59	2.1	1540	4	US-09-560-761B-3	Sequence 3, Appli	810	57	2.0	1039	4	US-09-464-535-23	Sequence 23, Appl
738	59	2.1	1639	2	US-08-737-524B-1	Sequence 1, Appli	811	57	2.0	1210	4	US-09-720-318A-3	Sequence 3, Appli
739	59	2.1	1963	4	US-09-482-273-91	Sequence 91, Appl	812	57	2.0	1503	4	US-09-907-794A-220	Sequence 220, App
740	59	2.1	2409	3	US-09-293-322C-8	Sequence 8, Appli	813	57	2.0	1503	4	US-09-905-125A-220	Sequence 220, App
741	59	2.1	2409	4	US-09-839-497A-8	Sequence 8, Appli	814	57	2.0	1503	4	US-09-902-775A-220	Sequence 220, App
742	59	2.1	2968	3	US-09-813-819-1	Sequence 1, Appli	815	57	2.0	1503	4	US-09-906-700-220	Sequence 220, App
743	59	2.1	2968	3	US-09-920-048-1	Sequence 1, Appli	816	57	2.0	1503	4	US-09-903-603A-220	Sequence 220, App
744	59	2.1	2968	4	US-10-014-501-1	Sequence 1, Appli	817	57	2.0	1503	4	US-09-904-920A-220	Sequence 220, App
745	59	2.1	3145	4	US-09-949-016-1149	Sequence 1149, Ap	818	57	2.0	1503	4	US-09-909-064-220	Sequence 220, App
746	59	2.1	4874	4	US-09-187-330-2	Sequence 2, Appli	819	57	2.0	1503	4	US-09-905-381A-220	Sequence 220, App
747	58	2.0	58	4	US-09-621-976-14827	Sequence 14827, A	820	57	2.0	1503	4	US-09-906-618-220	Sequence 220, App
748	58	2.0	72	4	US-09-621-976-15064	Sequence 15064, A	821	57	2.0	1505	2	US-08-909-965C-13	Sequence 13, Appl
749	58	2.0	194	4	US-09-621-976-15317	Sequence 15317, A	822	57	2.0	2301	3	US-09-232-191-8	Sequence 8, Appli
750	58	2.0	195	4	US-09-621-976-15314	Sequence 15314, A	823	57	2.0	2301	3	US-09-232-197-8	Sequence 8, Appli
c 751	58	2.0	253	2	US-08-520-678A-25	Sequence 25, Appl	824	57	2.0	2301	3	US-09-232-201-8	Sequence 8, Appli
c 752	58	2.0	253	2	US-08-897-126-25	Sequence 25, Appl	825	57	2.0	2301	3	US-09-232-195-8	Sequence 8, Appli
753	58	2.0	329	4	US-09-621-976-16012	Sequence 16012, A	826	57	2.0	2540	4	US-09-232-195-8	Sequence 8, Appli
754	58	2.0	332	4	US-09-621-976-16031	Sequence 16031, A	827	57	2.0	2540	4	US-09-949-016-431	Sequence 431, App
755	58	2.0	467	2	US-08-841-349-18	Sequence 18, Appl	828	57	2.0	2710	3	US-09-232-200-44	Sequence 44, Appl
c 756	58	2.0	467	4	US-09-431-184A-18	Sequence 18, Appl	829	57	2.0	2710	3	US-09-232-200-70	Sequence 70, Appl
c 757	58	2.0	509	3	US-09-030-607-202	Sequence 202, App	830	57	2.0	2710	3	US-09-232-197-44	Sequence 44, Appl

831	57	2.0	2710	3	US-09-232-137-70	Sequence 70, Appl	904	55	1.9	940	2	US-08-471-717-1	Sequence 1, Appli
832	57	2.0	2710	3	US-09-232-201-44	Sequence 44, Appl	905	55	1.9	1181	3	US-09-149-476-310	Sequence 310, App
833	57	2.0	2710	3	US-09-232-201-70	Sequence 70, Appl	906	55	1.9	1212	3	US-09-149-476-186	Sequence 186, App
834	57	2.0	2710	4	US-09-232-195-44	Sequence 44, Appl	907	55	1.9	1291	4	US-09-524-101D-5	Sequence 5, Appli
835	57	2.0	2710	4	US-09-232-195-70	Sequence 70, Appl	908	55	1.9	1653	3	US-09-345-469-2	Sequence 2, Appli
836	57	2.0	3300	3	US-09-336-643A-82	Sequence 82, Appl	909	55	1.9	1708	4	US-09-859-053-31	Sequence 31, Appl
837	57	2.0	4895	3	US-09-053-866-1	Sequence 1, Appli	910	55	1.9	1776	3	US-08-655-352-10	Sequence 10, Appl
838	57	2.0	4895	3	US-09-479-130-1	Sequence 1, Appli	911	55	1.9	1776	3	US-09-258-016-10	Sequence 10, Appl
839	57	2.0	4895	3	US-09-479-130A-1	Sequence 1, Appli	912	55	1.9	1776	3	US-09-257-825B-10	Sequence 10, Appl
840	57	2.0	8643	4	US-10-029-907-4	Sequence 4, Appli	913	55	1.9	1886	4	US-09-594-506-31	Sequence 31, Appl
841	56	2.0	56	4	US-09-621-976-12139	Sequence 12139, A	914	55	1.9	1897	1	US-08-184-632-1	Sequence 1, Appli
842	56	2.0	56	4	US-09-621-976-14556	Sequence 14556, A	915	55	1.9	1934	3	US-08-776-844-1	Sequence 1, Appli
843	56	2.0	81	4	US-09-513-999C-17324	Sequence 17324, A	916	55	1.9	1934	3	US-09-909-325-1	Sequence 1, Appli
844	56	2.0	87	4	US-09-621-976-14849	Sequence 14849, A	917	55	1.9	1934	4	US-09-909-326-1	Sequence 1, Appli
845	56	2.0	135	4	US-09-621-976-11087	Sequence 11087, A	918	55	1.9	2331	4	US-09-866-028-54	Sequence 54, Appl
846	56	2.0	156	4	US-09-621-976-9095	Sequence 9095, Ap	919	55	1.9	2331	4	US-09-944-457-54	Sequence 54, Appl
847	56	2.0	213	4	US-09-621-976-16536	Sequence 16536, A	920	55	1.9	2349	4	US-09-805-455-1	Sequence 1, Appli
848	56	2.0	246	4	US-09-621-976-16288	Sequence 16288, A	921	55	1.9	2695	4	US-09-706-137-3	Sequence 3, Appli
849	56	2.0	269	4	US-09-621-976-16936	Sequence 16936, A	922	55	1.9	2808	4	US-09-917-254-27	Sequence 27, Appl
850	56	2.0	334	4	US-09-621-976-16434	Sequence 16434, A	923	55	1.9	2821	4	US-09-702-705-1669	Sequence 1669, Ap
851	56	2.0	941	4	US-09-205-258-186	Sequence 186, App	924	55	1.9	2821	4	US-09-736-457-1669	Sequence 1669, Ap
852	56	2.0	1174	2	US-08-872-437-1	Sequence 1, Appli	925	55	1.9	2821	4	US-09-671-325-1669	Sequence 1669, Ap
853	56	2.0	1174	3	US-08-651-136C-11	Sequence 11, Appl	926	55	1.9	2821	4	US-09-658-824-1669	Sequence 1669, Ap
854	56	2.0	1174	3	US-09-229-911A-11	Sequence 11, Appl	927	55	1.9	3047	4	US-08-873-737A-1	Sequence 1, Appli
855	56	2.0	1454	4	US-09-614-912-63	Sequence 63, Appl	928	55	1.9	5503	2	US-08-726-012B-1	Sequence 1, Appli
856	56	2.0	1534	1	US-08-300-903A-6	Sequence 6, Appli	929	55	1.9	5503	4	US-09-023-655-989	Sequence 989, App
857	56	2.0	1534	4	US-08-988-197-6	Sequence 6, Appli	930	55	1.9	15450	4	US-09-470-661A-1	Sequence 1, Appli
858	56	2.0	1534	4	US-10-385-072-6	Sequence 6, Appli	931	55	1.9	139552	4	US-09-949-016-15300	Sequence 15300, A
859	56	2.0	1538	4	US-09-205-258-193	Sequence 193, App	932	55	1.9	192506	4	US-09-949-016-15830	Sequence 15830, A
860	56	2.0	1604	1	US-08-665-966-9	Sequence 9, Appli	933	54	1.9	54	4	US-08-621-976-14994	Sequence 14994, A
861	56	2.0	1604	3	US-09-041-780-9	Sequence 9, Appli	934	54	1.9	61	4	US-09-621-976-11967	Sequence 11967, A
862	56	2.0	1618	4	US-09-800-729-29	Sequence 29, Appli	935	54	1.9	80	3	US-09-284-627-15	Sequence 15, Appl
863	56	2.0	1804	2	US-08-504-459-5	Sequence 5, Appli	936	54	1.9	83	4	US-09-621-976-12087	Sequence 12087, A
864	56	2.0	2026	2	US-08-993-228-3	Sequence 3, Appli	937	54	1.9	83	4	US-09-621-976-12175	Sequence 12175, A
865	56	2.0	2280	3	US-08-813-150-1	Sequence 1, Appli	938	54	1.9	83	4	US-09-621-976-12429	Sequence 12429, A
866	56	2.0	2280	4	US-09-546-553-1	Sequence 1, Appli	939	54	1.9	83	4	US-09-621-976-12450	Sequence 12450, A
867	56	2.0	2285	2	US-08-967-101-136	Sequence 136, App	940	54	1.9	91	4	US-08-621-976-12161	Sequence 12161, A
868	56	2.0	2285	2	US-08-592-541-136	Sequence 136, App	941	54	1.9	257	2	US-08-520-678A-24	Sequence 24, Appl
869	56	2.0	2285	3	US-09-124-698-136	Sequence 136, App	942	54	1.9	257	3	US-08-897-126-24	Sequence 24, Appl
870	56	2.0	2285	3	US-09-127-480-136	Sequence 136, App	943	54	1.9	298	4	US-09-621-976-3871	Sequence 3871, Ap
871	56	2.0	2285	3	US-09-124-523-136	Sequence 136, App	944	54	1.9	365	4	US-09-621-976-14699	Sequence 14699, A
872	56	2.0	2285	4	US-09-636-736A-136	Sequence 136, App	945	54	1.9	1001	1	US-08-728-259A-10	Sequence 10, Appl
873	56	2.0	2797	4	US-09-482-273-74	Sequence 74, Appl	946	54	1.9	1001	2	US-08-473-486-10	Sequence 10, Appl
874	56	2.0	3350	2	US-08-663-566A-1	Sequence 1, Appli	947	54	1.9	1151	4	US-09-270-767-12633	Sequence 12633, A
875	56	2.0	3350	2	US-08-023-610-1	Sequence 1, Appli	948	54	1.9	1210	4	US-09-244-805-45	Sequence 45, Appli
876	56	2.0	3350	2	US-08-288-065A-1	Sequence 1, Appli	949	54	1.9	1230	4	US-09-244-805-6	Sequence 6, Appli
877	56	2.0	3350	2	US-08-362-240A-1	Sequence 1, Appli	950	54	1.9	1271	4	US-09-905-558D-1	Sequence 1, Appli
878	56	2.0	3350	5	PCT-US95-10245-1	Sequence 1, Appli	951	54	1.9	1302	4	US-09-322-409-31	Sequence 91, Appl
879	56	2.0	3871	2	US-08-599-455B-3	Sequence 3, Appli	952	54	1.9	1302	4	US-09-322-409-33	Sequence 93, Appl
880	56	2.0	3871	3	US-09-069-781B-3	Sequence 3, Appli	953	54	1.9	1302	4	US-09-451-527-91	Sequence 91, Appl
881	56	2.0	3871	3	US-09-137-132-3	Sequence 3, Appli	954	54	1.9	1302	4	US-09-451-527-93	Sequence 93, Appl
882	56	2.0	3871	3	US-08-864-564A-3	Sequence 3, Appli	955	54	1.9	1395	2	US-08-553-367A-1	Sequence 1, Appli
883	56	2.0	3871	3	US-09-094-410-3	Sequence 3, Appli	956	54	1.9	1395	3	US-09-295-306-1	Sequence 1, Appli
884	56	2.0	3871	4	US-08-708-123D-3	Sequence 3, Appli	957	54	1.9	1395	3	US-09-734-719-1	Sequence 1, Appli
885	56	2.0	3871	4	US-08-583-153A-3	Sequence 3, Appli	958	54	1.9	1705	4	US-09-205-258-216	Sequence 216, App
886	56	2.0	3871	4	US-08-570-142D-3	Sequence 3, Appli	959	54	1.9	1707	4	US-09-311-021-51	Sequence 51, Appl
887	56	2.0	3871	4	US-08-638-524B-3	Sequence 3, Appli	960	54	1.9	2296	3	US-08-496-841C-137	Sequence 137, App
888	56	2.0	670689	4	US-09-949-016-12505	Sequence 12505, A	961	54	1.9	2311	4	US-09-614-912-91	Sequence 91, Appl
889	56	2.0	670690	4	US-09-949-016-14207	Sequence 14207, A	962	54	1.9	2369	4	US-09-057-996-13	Sequence 13, Appl
890	55	1.9	55	4	US-09-621-976-14535	Sequence 14535, A	963	54	1.9	2406	4	US-09-594-506-37	Sequence 37, Appl
891	55	1.9	55	4	US-09-621-976-14535	Sequence 14535, A	964	54	1.9	2516	4	US-09-949-016-766	Sequence 766, App
892	55	1.9	159	4	US-09-621-976-17182	Sequence 17182, A	965	54	1.9	2668	3	US-09-370-838-156	Sequence 156, App
893	55	1.9	184	4	US-09-513-999C-36135	Sequence 36135, A	966	54	1.9	2668	4	US-09-854-133-156	Sequence 156, App
894	55	1.9	204	4	US-09-621-976-16458	Sequence 16458, A	967	54	1.9	3623	4	US-09-918-909A-23	Sequence 23, Appl
895	55	1.9	270	4	US-09-621-976-17927	Sequence 17927, A	968	54	1.9	3842	3	US-09-115-954-7	Sequence 7, Appli
896	55	1.9	276	4	US-09-621-976-18329	Sequence 18329, A	969	54	1.9	3912	3	US-09-115-954-1	Sequence 1, Appli
897	55	1.9	326	4	US-09-621-976-16024	Sequence 16024, A	970	54	1.9	5878	4	US-09-949-016-939	Sequence 939, App
898	55	1.9	339	4	US-09-621-976-16015	Sequence 16015, A	971	54	1.9	118143	4	US-09-949-016-17196	Sequence 17196, A
899	55	1.9	375	3	US-08-946-026-23	Sequence 23, Appl	972	53	1.9	53	4	US-09-621-976-12332	Sequence 12332, A
900	55	1.9	474	3	US-08-516-859A-97	Sequence 97, Appl	973	53	1.9	56	4	US-09-621-976-14989	Sequence 14989, A
901	55	1.9	474	3	US-08-586-472-97	Sequence 97, Appl	974	53	1.9	56	4	US-09-621-976-13461	Sequence 13461, A
902	55	1.9	474	3	US-09-528-706-97	Sequence 97, Appl	975	53	1.9	82	4	US-09-621-976-11689	Sequence 11689, A
903	55	1.9	487	3	US-09-257-179-22	Sequence 22, Appl	976	53	1.9	82	4	US-09-621-976-11841	Sequence 11841, A

977	53	1.9	82	4	US-09-621-976-11864	Sequence 11864, A	c1050	52	1.8	685	3	US-09-227-357-66	Sequence 66, Appl
978	53	1.9	82	4	US-09-621-976-11888	Sequence 11888, A	1051	52	1.8	1050	4	US-09-482-273-58	Sequence 58, Appl
979	53	1.9	82	4	US-09-621-976-11844	Sequence 11844, A	1052	52	1.8	1184	4	US-09-489-847-76	Sequence 76, Appl
980	53	1.9	82	4	US-09-621-976-11949	Sequence 11949, A	1053	52	1.8	1525	4	US-09-461-325-110	Sequence 110, App
981	53	1.9	82	4	US-09-621-976-12015	Sequence 12015, A	1054	52	1.8	1525	4	US-10-012-542-110	Sequence 110, App
982	53	1.9	82	4	US-09-621-976-12088	Sequence 12088, A	1055	52	1.8	1525	4	US-10-115-123-110	Sequence 110, App
983	53	1.9	82	4	US-09-621-976-12103	Sequence 12103, A	1056	52	1.8	1527	4	US-09-244-111-7	Sequence 7, Appl
984	53	1.9	82	4	US-09-621-976-12127	Sequence 12127, A	1057	52	1.8	1558	1	US-08-455-550-7	Sequence 7, Appl
985	53	1.9	82	4	US-09-621-976-12131	Sequence 12131, A	1058	52	1.8	1810	4	US-09-800-729-73	Sequence 73, Appl
986	53	1.9	82	4	US-09-621-976-12137	Sequence 12137, A	1059	52	1.8	1811	4	US-09-800-729-77	Sequence 77, Appl
987	53	1.9	82	4	US-09-621-976-12132	Sequence 12132, A	1060	52	1.8	2719	3	US-08-706-216-1	Sequence 1, Appl
988	53	1.9	82	4	US-09-621-976-12434	Sequence 12434, A	1061	52	1.8	2719	3	US-09-650-284-B	Sequence 1, Appl
989	53	1.9	82	4	US-09-621-976-13499	Sequence 13499, A	1062	52	1.8	2836	3	US-08-747-221B-24	Sequence 24, Appl
990	53	1.9	82	4	US-09-621-976-13499	Sequence 13499, A	1063	52	1.8	2836	3	US-08-747-221B-26	Sequence 26, Appl
991	53	1.9	83	4	US-09-621-976-13526	Sequence 13526, A	c1063	52	1.8	2836	3	US-09-005-051-24	Sequence 24, Appl
992	53	1.9	106	4	US-09-621-976-12195	Sequence 12195, A	1064	52	1.8	2836	3	US-09-005-051-26	Sequence 26, Appl
993	53	1.9	132	4	US-09-621-976-12079	Sequence 12079, A	c1065	52	1.8	2836	3	US-09-005-051-26	Sequence 26, Appl
994	53	1.9	140	4	US-09-621-976-13992	Sequence 13992, A	1066	52	1.8	2836	4	US-09-403-942F-24	Sequence 24, Appl
995	53	1.9	166	4	US-09-621-976-17449	Sequence 17449, A	c1067	52	1.8	2836	4	US-09-403-942F-26	Sequence 26, Appl
996	53	1.9	235	4	US-09-621-976-8455	Sequence 8455, Ap	1068	52	1.8	2837	2	US-08-993-228-11	Sequence 11, Appl
997	53	1.9	244	4	US-09-621-976-8455	Sequence 8455, Ap	1069	52	1.8	3136	4	US-09-680-728-1	Sequence 1, Appl
998	53	1.9	351	4	US-09-621-976-484	Sequence 484, App	1070	52	1.8	3136	4	US-10-017-066A-1	Sequence 1, Appl
999	53	1.9	443	4	US-09-621-976-16140	Sequence 16140, A	1071	51	1.8	57	4	US-09-621-976-12150	Sequence 12150, A
1000	53	1.9	773	3	US-09-621-976-17631	Sequence 17631, A	1072	51	1.8	61	4	US-09-621-976-14754	Sequence 14754, A
1001	53	1.9	872	3	US-09-248-335-63	Sequence 20, Appl	1073	51	1.8	63	4	US-09-621-976-12231	Sequence 12231, A
1002	53	1.9	882	2	US-08-909-965C-9	Sequence 9, Appl	1074	51	1.8	75	4	US-09-621-976-15073	Sequence 15073, A
1003	53	1.9	1013	1	US-07-920-519-30	Sequence 30, Appl	1075	51	1.8	327	4	US-09-621-976-16141	Sequence 16141, A
1004	53	1.9	1013	1	US-08-086-410-23	Sequence 23, Appl	1076	51	1.8	335	4	US-09-621-976-16038	Sequence 16038, A
1005	53	1.9	1013	1	US-08-314-586-30	Sequence 30, Appl	c1077	51	1.8	356	2	US-08-520-678A-22	Sequence 22, Appl
1006	53	1.9	1315	3	US-09-721-822A-10	Sequence 10, Appl	c1078	51	1.8	356	3	US-08-897-126-22	Sequence 22, Appl
1007	53	1.9	1375	4	US-09-489-847-120	Sequence 120, App	1079	51	1.8	371	4	US-09-621-976-16048	Sequence 16048, A
1008	53	1.9	1376	4	US-09-489-847-66	Sequence 66, Appl	c1080	51	1.8	495	4	US-09-220-132-186	Sequence 186, App
1009	53	1.9	1619	4	US-09-522-714-11	Sequence 11, Appl	1081	51	1.8	508	4	US-09-621-976-17886	Sequence 17886, A
1010	53	1.9	1722	4	US-09-482-273-102	Sequence 102, App	1082	51	1.8	742	1	US-07-847-010-12	Sequence 12, Appl
1011	53	1.9	1810	4	US-09-369-247-11	Sequence 11, Appl	1083	51	1.8	769	4	US-09-513-775B-5	Sequence 5, Appl
1012	53	1.9	1858	2	US-08-909-965C-11	Sequence 11, Appl	1084	51	1.8	780	2	US-08-540-804-36	Sequence 36, Appl
1013	53	1.9	1867	4	US-09-482-273-81	Sequence 81, Appl	1085	51	1.8	780	3	US-08-590-399-36	Sequence 36, Appl
1014	53	1.9	1949	4	US-09-461-325-26	Sequence 26, Appl	1086	51	1.8	785	4	US-09-518-036-9	Sequence 9, Appl
1015	53	1.9	1949	4	US-10-012-542-26	Sequence 26, Appl	1087	51	1.8	785	4	US-10-279-130-9	Sequence 9, Appl
1016	53	1.9	1949	4	US-10-115-123-26	Sequence 26, Appl	1088	51	1.8	803	4	US-09-800-729-60	Sequence 60, Appl
1017	53	1.9	2327	4	US-10-066-130-20	Sequence 20, Appl	1089	51	1.8	974	2	US-08-504-459-13	Sequence 13, Appl
1018	53	1.9	2648	3	US-09-417-455-6	Sequence 6, Appl	1090	51	1.8	1049	4	US-09-800-729-67	Sequence 67, Appl
1019	53	1.9	2648	3	US-09-348-942-6	Sequence 6, Appl	1091	51	1.8	1100	3	US-09-248-335-53	Sequence 53, Appl
1020	53	1.9	2648	3	US-09-457-626-6	Sequence 6, Appl	1092	51	1.8	1212	3	US-09-182-145-34	Sequence 34, Appl
1021	53	1.9	2648	4	US-09-576-008-6	Sequence 6, Appl	c1093	51	1.8	1212	3	US-09-182-145-35	Sequence 35, Appl
1022	53	1.9	2674	4	US-10-066-130-19	Sequence 19, Appl	1094	51	1.8	1215	4	US-09-646-693-1	Sequence 1, Appl
1023	53	1.9	2771	4	US-10-066-130-18	Sequence 18, Appl	1095	51	1.8	1332	3	US-09-333-423-1	Sequence 1, Appl
1024	53	1.9	2880	3	US-09-115-954-3	Sequence 3, Appl	1096	51	1.8	1375	3	US-03-372-422A-37	Sequence 37, Appl
1025	53	1.9	3108	4	US-09-937-521-11	Sequence 11, Appl	1097	51	1.8	1445	3	US-09-697-367-19	Sequence 19, Appl
1026	53	1.9	3268	4	US-09-688-188B-1	Sequence 1, Appl	1098	51	1.8	1445	4	US-09-918-909A-19	Sequence 19, Appl
1027	53	1.9	3268	4	US-09-291-417D-1	Sequence 1, Appl	1099	51	1.8	1577	3	US-08-821-994-59	Sequence 59, Appl
1028	53	1.9	5860	4	US-10-066-130-17	Sequence 17, Appl	1100	51	1.8	1699	3	US-09-152-060-19	Sequence 19, Appl
c1029	53	1.9	12980	3	US-08-811-566-5	Sequence 5, Appl	1101	51	1.8	1728	3	US-08-985-950-7	Sequence 7, Appl
c1030	53	1.9	12980	3	US-09-034-756-5	Sequence 5, Appl	1102	51	1.8	1728	3	US-09-546-049-7	Sequence 7, Appl
1031	52	1.8	52	4	US-09-621-976-13828	Sequence 13828, A	1103	51	1.8	1781	3	US-09-499-302A-1	Sequence 1, Appl
1032	52	1.8	58	4	US-09-621-976-8006	Sequence 8006, Ap	1104	51	1.8	1933	4	US-09-920-759-3	Sequence 3, Appl
1033	52	1.8	62	4	US-09-621-976-14825	Sequence 14825, A	1105	51	1.8	1976	4	US-09-920-759-10	Sequence 10, Appl
1034	52	1.8	81	4	US-09-621-976-12198	Sequence 12198, A	1106	51	1.8	1998	3	US-09-232-200-68	Sequence 68, Appl
1035	52	1.8	81	4	US-09-621-976-13601	Sequence 13601, A	1107	51	1.8	1998	3	US-09-232-197-68	Sequence 68, Appl
1036	52	1.8	85	4	US-09-621-976-14741	Sequence 14741, A	1108	51	1.8	1998	3	US-09-232-201-68	Sequence 68, Appl
1037	52	1.8	87	4	US-09-621-976-14560	Sequence 14560, A	1109	51	1.8	1998	4	US-09-232-195-68	Sequence 68, Appl
c1038	52	1.8	90	3	US-09-065-058-16	Sequence 16, Appl	1110	51	1.8	2028	2	US-09-211-930-12	Sequence 12, Appl
1039	52	1.8	164	4	US-09-621-976-8070	Sequence 8070, Ap	1111	51	1.8	2028	3	US-09-340-993-12	Sequence 12, Appl
1040	52	1.8	182	4	US-09-621-976-16234	Sequence 16234, A	1112	51	1.8	2028	3	US-09-468-442-12	Sequence 12, Appl
1041	52	1.8	223	3	US-09-792-594-11	Sequence 11, Appl	1113	51	1.8	2087	3	US-09-232-191-6	Sequence 6, Appl
1042	52	1.8	233	4	US-09-621-976-10675	Sequence 10675, A	1114	51	1.8	2087	3	US-09-232-200-6	Sequence 6, Appl
1043	52	1.8	272	4	US-09-621-976-8353	Sequence 8353, Ap	1115	51	1.8	2087	3	US-09-232-197-6	Sequence 6, Appl
1044	52	1.8	289	4	US-09-621-976-10009	Sequence 10009, A	1116	51	1.8	2087	3	US-09-232-201-6	Sequence 6, Appl
1045	52	1.8	347	4	US-09-621-976-16136	Sequence 16136, A	1117	51	1.8	2087	4	US-09-232-195-6	Sequence 6, Appl
1046	52	1.8	427	4	US-09-461-325-107	Sequence 107, App	1118	51	1.8	2202	4	US-09-396-149-3	Sequence 3, Appl
1047	52	1.8	427	4	US-10-012-542-107	Sequence 107, App	1119	51	1.8	2287	4	US-09-949-016-134	Sequence 134, App
1048	52	1.8	427	4	US-10-115-123-107	Sequence 123, App	1120	51	1.8	2288	4	US-09-800-729-24	Sequence 24, Appl
1049	52	1.8	472	4	US-09-270-767-12212	Sequence 12212, A	1121	51	1.8	3238	4	US-08-123-934A-5	Sequence 5, Appl
							1122	51	1.8	3238	4	US-09-874-628-5	Sequence 5, Appl

1123	51	1.8	3238	5	PCT-US94-10080-5	Sequence 5, Appli	1196	50	1.8	2103	4	US-09-489-847-40	Sequence 40, Appli
1124	51	1.8	3299	4	US-09-800-729-68	Sequence 68, Appli	1197	50	1.8	2114	1	US-07-803-622E-6	Sequence 6, Appli
1125	51	1.8	3375	3	US-09-511-625B-67	Sequence 67, Appli	1198	50	1.8	2196	3	US-09-149-476-163	Sequence 163, Appli
1126	51	1.8	9646	3	US-08-811-566-1	Sequence 1, Appli	1199	50	1.8	2202	3	US-09-388-743-1	Sequence 1, Appli
1127	51	1.8	9646	3	US-08-811-566-1	Sequence 1, Appli	1200	50	1.8	2202	3	US-10-044-543-1	Sequence 1, Appli
1128	51	1.8	13584	4	US-09-991-258-17	Sequence 17, Appli	1201	50	1.8	2345	3	US-09-149-476-193	Sequence 193, Appli
1129	51	1.8	64190	4	US-09-949-016-14712	Sequence 14712, A	1202	50	1.8	2567	3	US-08-993-260-4	Sequence 4, Appli
1130	51	1.8	64190	4	US-09-949-016-14713	Sequence 14713, A	1203	50	1.8	2610	3	US-09-545-814-1	Sequence 1, Appli
1131	51	1.8	86877	4	US-09-949-016-15491	Sequence 15491, A	1204	50	1.8	2610	3	US-09-545-814-3	Sequence 3, Appli
1132	51	1.8	86877	4	US-09-949-016-15492	Sequence 15492, A	1205	50	1.8	2677	4	US-09-733-643B-1	Sequence 1, Appli
1133	50	1.8	50	1	US-08-420-443-1	Sequence 1, Appli	1206	50	1.8	2908	3	US-09-930-181-1	Sequence 1, Appli
1134	50	1.8	50	4	US-09-621-976-14715	Sequence 14715, A	1207	50	1.8	3040	1	US-08-446-794A-1	Sequence 1, Appli
1135	50	1.8	61	3	US-09-457-959-7	Sequence 7, Appli	1208	50	1.8	3040	1	US-08-750-007-2	Sequence 2, Appli
1136	50	1.8	61	4	US-10-079-178-7	Sequence 7, Appli	1209	50	1.8	3040	2	US-08-945-024-1	Sequence 1, Appli
1137	50	1.8	71	4	US-09-816-089A-5	Sequence 5, Appli	1210	50	1.8	4704	2	US-08-476-062A-52	Sequence 52, Appli
1138	50	1.8	90	1	US-08-677-944-1	Sequence 1, Appli	1211	50	1.8	4704	4	US-09-023-655-1358	Sequence 17484, A
1139	50	1.8	90	1	US-08-677-944-2	Sequence 2, Appli	1212	50	1.8	92155	4	US-09-949-016-17484	Sequence 17484, A
1140	50	1.8	90	3	US-09-254-048A-1	Sequence 1, Appli	1213	49	1.7	104	4	US-09-621-976-9392	Sequence 9392, Ap
1141	50	1.8	90	3	US-09-921-203-1	Sequence 1, Appli	1214	49	1.7	110	4	US-09-621-976-12025	Sequence 12025, A
1142	50	1.8	90	4	US-09-816-089A-2	Sequence 2, Appli	1215	49	1.7	139	4	US-09-621-976-8632	Sequence 8632, Ap
1143	50	1.8	90	4	US-10-106-832-1	Sequence 1, Appli	1216	49	1.7	141	4	US-09-621-976-8705	Sequence 8705, Ap
1144	50	1.8	93	4	US-09-816-089A-8	Sequence 8, Appli	1217	49	1.7	153	4	US-09-621-976-18058	Sequence 18058, A
1145	50	1.8	100	3	US-08-991-789A-30	Sequence 30, Appli	1218	49	1.7	157	4	US-09-621-976-16781	Sequence 16781, A
1146	50	1.8	100	3	US-09-062-451-30	Sequence 30, Appli	1219	49	1.7	165	4	US-09-621-976-19195	Sequence 19195, A
1147	50	1.8	100	3	US-09-598-326-30	Sequence 30, Appli	1220	49	1.7	229	4	US-09-702-705-195	Sequence 195, App
1148	50	1.8	100	4	US-09-289-198-30	Sequence 30, Appli	1221	49	1.7	229	4	US-09-736-457-195	Sequence 195, App
1149	50	1.8	100	4	US-09-429-755-30	Sequence 30, Appli	1222	49	1.7	229	4	US-09-614-124B-195	Sequence 195, App
1150	50	1.8	100	4	US-09-699-295-30	Sequence 30, Appli	1223	49	1.7	229	4	US-09-671-325-195	Sequence 195, App
1151	50	1.8	105	2	US-08-735-381-2	Sequence 2, Appli	1224	49	1.7	229	4	US-09-589-184-195	Sequence 195, App
1152	50	1.8	105	3	US-09-183-619-1	Sequence 1, Appli	1225	49	1.7	229	4	US-09-658-824-195	Sequence 195, App
1153	50	1.8	105	3	US-09-201-674-2	Sequence 2, Appli	1226	49	1.7	273	4	US-09-809-545A-31	Sequence 31, Appli
1154	50	1.8	184	4	US-09-621-976-12893	Sequence 12893, A	1227	49	1.7	279	4	US-09-621-976-10220	Sequence 10220, A
1155	50	1.8	239	4	US-09-621-976-16632	Sequence 16632, A	1228	49	1.7	315	4	US-09-621-976-15329	Sequence 15329, A
1156	50	1.8	271	2	US-08-731-272A-29	Sequence 29, Appli	1229	49	1.7	341	4	US-09-621-976-11000	Sequence 11000, A
1157	50	1.8	351	4	US-09-270-767-11437	Sequence 11437, A	1230	49	1.7	396	4	US-09-640-173-18	Sequence 18, Appli
1158	50	1.8	399	1	US-07-885-970A-13	Sequence 13, Appli	1231	49	1.7	396	4	US-09-640-173-57	Sequence 57, Appli
1159	50	1.8	399	1	US-08-298-687A-13	Sequence 13, Appli	1232	49	1.7	396	4	US-09-713-550-18	Sequence 18, Appli
1160	50	1.8	399	1	US-08-530-797-12	Sequence 12, Appli	1233	49	1.7	396	4	US-09-713-550-57	Sequence 57, Appli
1161	50	1.8	399	1	US-08-298-829-13	Sequence 13, Appli	1234	49	1.7	396	4	US-09-825-294-18	Sequence 18, Appli
1162	50	1.8	399	2	US-08-787-335-12	Sequence 12, Appli	1235	49	1.7	396	4	US-09-825-294-57	Sequence 57, Appli
1163	50	1.8	406	4	US-09-621-976-15107	Sequence 15107, A	1236	49	1.7	396	4	US-09-970-966-18	Sequence 18, Appli
1164	50	1.8	540	4	US-09-313-434C-15	Sequence 15, Appli	1237	49	1.7	396	4	US-09-970-966-57	Sequence 57, Appli
1165	50	1.8	577	3	US-09-149-476-313	Sequence 313, App	1238	49	1.7	458	1	US-08-524-757-1	Sequence 1, Appli
1166	50	1.8	615	3	US-09-105-542A-2	Sequence 2, Appli	1239	49	1.7	568	1	US-08-582-257-20	Sequence 20, Appli
1167	50	1.8	741	2	US-08-975-316-58	Sequence 58, Appli	1240	49	1.7	619	4	US-08-582-398-20	Sequence 20, Appli
1168	50	1.8	741	3	US-09-615-192A-58	Sequence 58, Appli	1241	49	1.7	619	4	US-09-489-847-58	Sequence 58, Appli
1169	50	1.8	741	3	US-09-169-789-58	Sequence 58, Appli	1242	49	1.7	636	4	US-09-534-506-27	Sequence 27, Appli
1170	50	1.8	788	3	US-09-615-192A-96	Sequence 96, Appli	1243	49	1.7	728	3	US-09-091-097-5	Sequence 5, Appli
1171	50	1.8	788	4	US-09-169-789-96	Sequence 96, Appli	1244	49	1.7	740	2	US-08-713-000-8	Sequence 8, Appli
1172	50	1.8	873	3	US-09-475-316A-20	Sequence 20, Appli	1245	49	1.7	740	2	US-08-975-316-8	Sequence 8, Appli
1173	50	1.8	873	4	US-09-704-640-20	Sequence 20, Appli	1246	49	1.7	740	2	US-09-211-710-8	Sequence 8, Appli
1174	50	1.8	888	3	US-09-188-930-13	Sequence 13, Appli	1247	49	1.7	740	3	US-09-615-192A-8	Sequence 8, Appli
1175	50	1.8	888	4	US-09-312-283C-13	Sequence 13, Appli	1248	49	1.7	740	3	US-09-169-789-8	Sequence 8, Appli
1176	50	1.8	959	4	US-09-578-030-5	Sequence 5, Appli	1249	49	1.7	835	4	US-09-311-021-71	Sequence 71, Appli
1177	50	1.8	1134	3	US-09-248-335-29	Sequence 29, Appli	1250	49	1.7	971	4	US-09-800-729-49	Sequence 49, Appli
1178	50	1.8	1144	4	US-09-904-615-20	Sequence 20, Appli	1251	49	1.7	1223	3	US-09-154-874-4	Sequence 4, Appli
1179	50	1.8	1242	3	US-08-413-974-1	Sequence 1, Appli	1252	49	1.7	1223	4	US-08-931-668-4	Sequence 4, Appli
1180	50	1.8	1242	3	US-08-434-418-1	Sequence 1, Appli	1253	49	1.7	1223	4	US-09-468-175-4	Sequence 4, Appli
1181	50	1.8	1242	3	US-08-433-288-1	Sequence 1, Appli	1254	49	1.7	1281	4	US-09-436-521A-5	Sequence 5, Appli
1182	50	1.8	1242	3	US-08-174-739A-1	Sequence 1, Appli	1255	49	1.7	1478	4	US-09-216-393B-7	Sequence 7, Appli
1183	50	1.8	1242	3	US-08-434-256-1	Sequence 1, Appli	1256	49	1.7	1721	5	FCT-US96-00994-3	Sequence 4, Appli
1184	50	1.8	1307	4	US-09-641-612-3	Sequence 3, Appli	1257	49	1.7	1790	4	US-09-866-028-31	Sequence 31, Appli
1185	50	1.8	1386	2	US-08-897-340-1	Sequence 1, Appli	1258	49	1.7	1790	4	US-09-944-457-31	Sequence 31, Appli
1186	50	1.8	1386	3	US-09-252-329-1	Sequence 1, Appli	1259	49	1.7	1825	3	US-09-461-697-75	Sequence 75, Appli
1187	50	1.8	1483	3	US-09-262-749-1	Sequence 1, Appli	1260	49	1.7	1921	4	US-09-057-996-7	Sequence 7, Appli
1188	50	1.8	1530	4	US-09-811-361-19	Sequence 19, Appli	1261	49	1.7	1931	3	US-09-019-942-2	Sequence 2, Appli
1189	50	1.8	1576	1	US-08-157-101A-6	Sequence 6, Appli	1262	49	1.7	1931	3	US-09-099-041A-1	Sequence 1, Appli
1190	50	1.8	1666	3	US-09-822-862-1	Sequence 1, Appli	1263	49	1.7	1931	3	US-09-245-281-1	Sequence 1, Appli
1191	50	1.8	1683	3	US-09-347-803-11	Sequence 11, Appli	1264	49	1.7	1931	3	US-09-470-271-2	Sequence 2, Appli
1192	50	1.8	1865	3	US-09-370-253-5	Sequence 5, Appli	1265	49	1.7	1931	4	US-09-207-359B-1	Sequence 1, Appli
1193	50	1.8	1883	4	US-09-419-679-13	Sequence 13, Appli	1266	49	1.7	1931	4	US-09-340-620A-1	Sequence 1, Appli
1194	50	1.8	1929	3	US-09-146-950-1	Sequence 1, Appli	1267	49	1.7	1931	4	US-09-865-364-1	Sequence 1, Appli
1195	50	1.8	2017	4	US-09-690-454-45	Sequence 45, Appli	1268	49	1.7	1931	4	US-09-748-537-2	Sequence 2, Appli

1269	49	1.7	2025	3	US-09-149-476-316	Sequence 316, App	1342	48	1.7	1910	2	US-09-009-438-1	Sequence 1, Appli
1270	49	1.7	2182	4	US-09-214-619-3	Sequence 3, Appli	1343	48	1.7	1910	3	US-09-207-493-1	Sequence 1, Appli
1271	49	1.7	2182	4	US-09-555-820A-11	Sequence 11, Appl	1344	48	1.7	1951	3	US-09-465-558-35	Sequence 35, Appl
1272	49	1.7	2611	4	US-09-800-729-66	Sequence 66, Appl	1345	48	1.7	2060	4	US-09-345-473E-5	Sequence 5, Appli
1273	49	1.7	2325	3	US-09-245-041-18	Sequence 18, Appl	1346	48	1.7	2065	2	US-08-968-751-1	Sequence 1, Appli
1274	49	1.7	2625	4	US-09-358-055B-18	Sequence 18, Appl	1347	48	1.7	2134	4	US-08-629-222A-23	Sequence 23, Appl
1275	49	1.7	2625	4	US-09-893-238-18	Sequence 18, Appl	1348	48	1.7	2152	4	US-09-629-222A-1	Sequence 1, Appli
c1276	49	1.7	2760	1	US-08-101-593-1	Sequence 1, Appli	1349	48	1.7	2152	4	US-09-629-222A-25	Sequence 25, Appl
c1277	49	1.7	2760	1	US-08-101-593-3	Sequence 3, Appli	1350	48	1.7	2152	4	US-09-629-222A-26	Sequence 26, Appl
c1278	49	1.7	3001	4	US-09-539-333D-153	Sequence 153, App	1351	48	1.7	2152	4	US-09-629-222A-27	Sequence 27, Appl
1279	49	1.7	3007	4	US-09-810-268-1	Sequence 1, Appli	1352	48	1.7	2269	4	US-10-262-083-17	Sequence 17, Appl
1280	49	1.7	4765	3	US-08-936-135-21	Sequence 21, Appl	1353	48	1.7	2575	4	US-08-716-129-25	Sequence 25, Appl
1281	49	1.7	4765	4	US-09-439-711C-21	Sequence 21, Appl	1354	48	1.7	2581	4	US-09-369-247-51	Sequence 51, Appl
1282	49	1.7	4780	3	US-08-936-135-23	Sequence 23, Appl	1355	48	1.7	2584	4	US-08-716-129-47	Sequence 47, Appl
1283	49	1.7	4780	4	US-09-439-711C-23	Sequence 23, Appl	1356	48	1.7	2643	2	US-08-750-134A-10	Sequence 10, Appl
1284	49	1.7	5325	4	US-10-164-595-17	Sequence 17, Appl	1357	48	1.7	2643	3	US-09-363-745-10	Sequence 10, Appl
1285	49	1.7	5334	4	US-10-164-595-21	Sequence 21, Appl	1358	48	1.7	2643	3	US-09-023-655-897	Sequence 897, App
1286	49	1.7	5581	4	US-10-164-595-19	Sequence 19, Appl	1359	48	1.7	2643	4	US-09-949-016-365	Sequence 365, App
1287	49	1.7	9704	3	US-09-814-951A-3	Sequence 3, Appli	1360	48	1.7	2822	4	US-09-907-794A-48	Sequence 48, Appl
c1288	49	1.7	31739	4	US-09-949-016-16226	Sequence 16226, A	1361	48	1.7	2822	4	US-09-905-125A-48	Sequence 48, Appl
1289	49	1.7	48994	4	US-09-949-016-14091	Sequence 14091, A	1362	48	1.7	2822	4	US-09-902-775A-48	Sequence 48, Appl
1290	49	1.7	53562	4	US-09-949-016-16286	Sequence 16286, A	1363	48	1.7	2822	4	US-09-906-700-48	Sequence 48, Appl
1291	49	1.7	193303	4	US-09-497-855A-37	Sequence 37, Appl	1364	48	1.7	2822	4	US-09-903-603A-48	Sequence 48, Appl
1292	49	1.7	193303	4	US-09-497-855A-44	Sequence 44, Appl	1365	48	1.7	2822	4	US-09-904-920A-48	Sequence 48, Appl
c1293	49	1.7	524032	4	US-09-949-016-16928	Sequence 16928, A	1366	48	1.7	2822	4	US-09-909-064-48	Sequence 48, Appl
c1294	49	1.7	524032	4	US-09-949-016-16929	Sequence 16929, A	1367	48	1.7	2822	4	US-09-905-381A-48	Sequence 48, Appl
c1295	49	1.7	524032	4	US-09-949-016-16930	Sequence 16930, A	1368	48	1.7	2822	4	US-09-906-618-48	Sequence 48, Appl
c1296	49	1.7	524032	4	US-09-949-016-16931	Sequence 16931, A	1369	48	1.7	5894	3	US-08-665-259-24	Sequence 24, Appl
c1297	49	1.7	528885	4	US-09-949-016-14340	Sequence 14340, A	1370	48	1.7	5894	3	US-08-762-500-74	Sequence 24, Appl
c1298	49	1.7	528885	4	US-09-949-016-14341	Sequence 14341, A	1371	48	1.7	6525	3	US-08-762-500-74	Sequence 74, Appl
c1299	49	1.7	528885	4	US-09-949-016-14342	Sequence 14342, A	1372	48	1.7	12116	4	US-09-949-016-12831	Sequence 12831, A
c1300	49	1.7	528885	4	US-09-949-016-14343	Sequence 14343, A	c1373	48	1.7	12116	4	US-09-949-016-12991	Sequence 12991, A
c1301	49	1.7	528885	4	US-09-949-016-14344	Sequence 14344, A	1374	48	1.7	15722	4	US-09-949-016-16709	Sequence 16709, A
c1302	49	1.7	528885	4	US-09-949-016-14345	Sequence 14345, A	1375	48	1.7	28257	4	US-09-949-016-13076	Sequence 13076, A
c1303	49	1.7	528885	4	US-09-949-016-14346	Sequence 14346, A	1376	48	1.7	28257	4	US-09-949-016-13076	Sequence 13076, A
c1304	49	1.7	528885	4	US-09-949-016-14347	Sequence 14347, A	1377	48	1.7	38479	4	US-09-949-016-16730	Sequence 16730, A
1305	48	1.7	56	4	US-09-513-999C-17929	Sequence 17929, A	c1378	48	1.7	146095	4	US-09-949-016-12872	Sequence 12872, A
1306	48	1.7	77	4	US-09-621-976-12266	Sequence 12266, A	c1379	48	1.7	146104	4	US-09-949-016-13239	Sequence 13239, A
1307	48	1.7	138	4	US-09-621-976-8112	Sequence 8112, Ap	c1380	48	1.7	173787	4	US-09-949-016-12542	Sequence 12542, A
1308	48	1.7	191	4	US-09-621-976-18332	Sequence 18332, A	1381	48	1.7	173791	4	US-09-949-016-17302	Sequence 17302, A
1309	48	1.7	216	1	US-08-686-878A-34	Sequence 34, Appl	c1382	48	1.7	818128	4	US-09-949-016-14546	Sequence 14546, A
1310	48	1.7	216	3	US-09-175-928-34	Sequence 34, Appl	c1383	48	1.7	818128	4	US-09-949-016-14547	Sequence 14547, A
1311	48	1.7	237	4	US-09-621-976-10277	Sequence 10277, A	c1384	48	1.7	818128	4	US-09-949-016-14548	Sequence 14548, A
1312	48	1.7	289	4	US-09-621-976-15142	Sequence 15142, A	c1385	48	1.7	818128	4	US-09-949-016-14549	Sequence 14549, A
1313	48	1.7	382	4	US-09-621-976-18855	Sequence 18855, A	c1386	48	1.7	818128	4	US-09-949-016-14550	Sequence 14550, A
1314	48	1.7	391	4	US-09-621-976-18858	Sequence 18858, A	c1387	48	1.7	818128	4	US-09-949-016-14551	Sequence 14551, A
1315	48	1.7	399	4	US-09-621-976-9484	Sequence 9484, Ap	c1388	48	1.7	818128	4	US-09-949-016-14552	Sequence 14552, A
1316	48	1.7	614	3	US-08-688-988-44	Sequence 44, Appl	c1389	48	1.7	818128	4	US-09-949-016-14553	Sequence 14553, A
1317	48	1.7	624	4	US-09-902-540-1318	Sequence 1318, Ap	c1390	48	1.7	818128	4	US-09-949-016-14554	Sequence 14554, A
1318	48	1.7	658	4	US-09-270-767-13424	Sequence 13424, A	c1391	48	1.7	818128	4	US-09-949-016-14555	Sequence 14555, A
1319	48	1.7	753	4	US-09-465-559-1	Sequence 1, Appli	c1392	48	1.7	818128	4	US-09-949-016-14556	Sequence 14556, A
1320	48	1.7	832	4	US-09-902-331B-9	Sequence 9, Appli	c1393	48	1.7	818128	4	US-09-949-016-14557	Sequence 14557, A
1321	48	1.7	879	1	US-08-158-682A-1	Sequence 1, Appli	c1394	48	1.7	818128	4	US-09-949-016-14558	Sequence 14558, A
1322	48	1.7	879	1	US-08-158-682A-1	Sequence 1, Appli	c1395	48	1.7	818128	4	US-09-949-016-14559	Sequence 14559, A
1323	48	1.7	890	4	US-08-015-203-1	Sequence 1, Appli	c1396	48	1.7	818128	4	US-09-949-016-14560	Sequence 14560, A
1324	48	1.7	890	4	US-09-621-976-2725	Sequence 2725, Ap	c1397	48	1.7	818128	4	US-09-949-016-14561	Sequence 14561, A
1325	48	1.7	1115	4	US-09-949-016-539	Sequence 539, App	c1398	48	1.7	818128	4	US-09-949-016-14562	Sequence 14562, A
1326	48	1.7	1115	4	US-09-949-016-539	Sequence 539, App	c1399	48	1.7	818128	4	US-09-949-016-14564	Sequence 14564, A
1327	48	1.7	1146	3	US-09-452-239-3	Sequence 3, Appli	c1400	48	1.7	818128	4	US-09-949-016-14565	Sequence 14565, A
1328	48	1.7	1159	3	US-09-410-464-14	Sequence 14, Appl	c1401	48	1.7	818128	4	US-09-949-016-14566	Sequence 14566, A
1329	48	1.7	1192	4	US-09-439-554-23	Sequence 23, Appl	c1402	48	1.7	818128	4	US-09-949-016-14567	Sequence 14567, A
1330	48	1.7	1277	4	US-09-187-999-30	Sequence 30, Appl	1403	47	1.7	69	1	US-08-702-344-22	Sequence 22, Appl
1331	48	1.7	1364	1	US-08-265-087-3	Sequence 3, Appli	1404	47	1.7	120	1	US-08-153-051B-28	Sequence 28, Appl
1332	48	1.7	1364	1	US-08-621-493-3	Sequence 3, Appli	1405	47	1.7	120	1	US-08-060-952C-44	Sequence 44, Appl
1333	48	1.7	1364	2	US-08-965-688-3	Sequence 3, Appli	1406	47	1.7	120	2	US-08-151-477A-28	Sequence 28, Appl
1334	48	1.7	1364	3	US-09-260-173-3	Sequence 3, Appli	1407	47	1.7	120	3	US-08-819-867A-58	Sequence 58, Appl
1335	48	1.7	1493	4	US-09-668-097A-15	Sequence 15, Appl	1408	47	1.7	120	3	US-08-464-011B-44	Sequence 44, Appl
1336	48	1.7	1493	6	5340934-5	Patent No. 5340934	1409	47	1.7	120	4	US-09-378-535-58	Sequence 58, Appl
1337	48	1.7	1493	6	5340934-5	Patent No. 5340934	1410	47	1.7	159	4	US-09-621-976-8623	Sequence 8623, Ap
1338	48	1.7	1596	3	US-09-146-950-17	Sequence 17, Appl	1411	47	1.7	159	4	US-09-621-976-8655	Sequence 8655, Ap
1339	48	1.7	1605	3	US-09-149-476-187	Sequence 187, App	1412	47	1.7	208	1	US-08-686-878A-37	Sequence 37, Appl
1340	48	1.7	1670	4	US-09-023-655-980	Sequence 980, App	1413	47	1.7	208	3	US-09-175-928-37	Sequence 37, Appl
1341	48	1.7	1748	4	US-08-635-967-1	Sequence 1, Appli	1414	47	1.7	269	4	US-09-621-976-17610	Sequence 17610, A

Db 385 |||||TTTGTAAACA|||CTCCTATGTTCTTAGTGGCAATGAGAAAAGAACTTGCAGCAGAAATGGAG 444
Qy 1026 AGTGGTCAGGGAAACAGCCCATCTGCATAAAGCCTGCGGAGAACCAAGAATTTTCAGACC 1085
Db 445 AGTGGTCAGGGAAACAGCCCATCTGCATAAAGCCTGCGGAGAACCAAGAATTTTCAGACC 504
Qy 1086 TGGTGAGAAAGAGAGTTCTTCGAGTGCAGGTTTCAGTCAAGGGAGACACCATTTACACCAGC 1145
Db 505 TGGTGAGAAAGAGAGTTCTTCGAGTGCAGGTTTCAGTCAAGGGAGACACCATTTACACCAGC 564
Qy 1146 TATATCTACGGCGCTTCAGCAAGCAGAACTGCGAGTGCCTTACCAAGAAGCCAGCCCC 1205
Db 565 TATATCTACGGCGCTTCAGCAAGCAGAACTGCGAGTGCCTTACCAAGAAGCCAGCCCC 624
Qy 1206 TTCCCTTTGGAGATCTGCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGT 1265
Db 625 TTCCCTTTGGAGATCTGCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGT 684
Qy 1266 GCATCTACCCCTTCTACCGCGCTTGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGA 1325
Db 685 GCATCTACCCCTTCTACCGCGCTTGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGA 744
Qy 1326 AGTGGAGTGGCGGCGCACCATCTGCATPCCCTATCTGCGGAAAAATTGAGAACATCACTG 1385
Db 745 AGTGGAGTGGCGGCGCACCATCTGCATPCCCTATCTGCGGAAAAATTGAGAACATCACTG 804
Qy 1386 CTCMAAGACCAAGGGTTGGCTTGGCGTGGCAGGAGGACCATCTACAGGAGGACCAAGC 1445
Db 805 CTCMAAGACCAAGGGTTGGCTTGGCGTGGCAGGAGGACCATCTACAGGAGGACCAAGC 864
Qy 1446 GGGTGATGACGGCAGCCTACACAAGGAGGAGTGTCTTAAGTCTGCGAGCGTGCCCTGG 1505
Db 865 GGGTGATGACGGCAGCCTACACAAGGAGGAGTGTCTTAAGTCTGCGAGCGTGCCCTGG 924
Qy 1506 TGAATGACGCGACATGTGTGTGGTGCGCCACTGTGTACTGACCTGGGGAAAGTTCACCA 1565
Db 925 TGAATGACGCGACATGTGTGTGGTGCGCCACTGTGTACTGACCTGGGGAAAGTTCACCA 984
Qy 1566 TGATCAAGACAGCAGACCTGAAAGTGTGTGGGAAATTTCTACGGGATGATGACCGGG 1625
Db 985 TGATCAAGACAGCAGACCTGAAAGTGTGTGGGAAATTTCTACCGGGATGATGACCGGG 1044
Qy 1626 ATGAGAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCATCCCAACTATGACC 1685
Db 1045 ATGAGAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCATCCCCAACTATGACC 1104
Qy 1686 CCATCCTGCTTGTATGCTGACATCGCCATCCTGAAAGCTCCTAGACAAGGCCCGTATCAGCA 1745
Db 1105 CCATCCTGCTTGTATGCTGACATCGCCATCCTGAAAGCTCCTAGACAAGGCCCGTATCAGCA 1164
Qy 1746 CCGAGTCCAGCCCATCTGCTCGCTGCGTGCAGTGGGATCTCAGCACTTCTTCAGAGAGT 1805
Db 1165 CCGAGTCCAGCCCATCTGCTCGCTGCGTGCAGTGGGATCTCAGCACTTCTTCAGAGAGT 1224
Qy 1806 CCCACATCACTGTGCTGCGCTGGGATGTCCTGGCAGAGCTGAGGAGCCCTGCGTTCAGA 1865
Db 1225 CCCACATCACTGTGCTGCGCTGGGATGTCCTGGCAGAGCTGAGGAGCCCTGCGTTCAGA 1284
Qy 1866 ACGACACACTGCGCTCTGGGGTGGTTCAGTGTGGTGAATCGCTGCTGTGTGAGGAGCAGC 1925
Db 1285 ACGACACACTGCGCTCTGGGGTGGTTCAGTGTGGTGAATCGCTGCTGTGTGAGGAGCAGC 1344
Qy 1926 ATGAGGACCATGGCATCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1985
Db 1345 ATGAGGACCATGGCATCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1404
Qy 1986 CCATGCCCCCTTCTGATATCTGCATGCGCTGCGAGACAGGAGGATCGCGCTGTGCTTCC 2045
Db 1405 CCATGCCCCCTTCTGATATCTGCATGCGCTGCGAGACAGGAGGATCGCGCTGTGCTTCC 1464
Qy 2046 CCGGACGAGCATCTCCTGAGCAGCCTGGCATCTGATGGGACTGCTGAGCTGGAGCTATG 2105

Db 1465 CGGACGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATG 1524
Qy 2106 ATAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2165
Db 1525 ATAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1584
Qy 2166 GGATTTGAAAGAAATATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 2225
Db 1585 GGATTTGAAAGAAATATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1644
Qy 2226 ATCCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2285
Db 1645 ATCCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1704
Qy 2286 TGAATTTGGCTGTGCTGAGGCTTCTGACTTTCAGGAGCAAAACTCAGTGAAGGGTGAGTAG 2345
Db 1705 TGAATTTGGCTGTGCTGAGGCTTCTGACTTTCAGGAGCAAAACTCAGTGAAGGGTGAGTAG 1764
Qy 2346 ACCTCCATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2405
Db 1765 ACCTCCATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1824
Qy 2406 CAGGGCTTGCAGAAAGTAAAGTTTCTTCAAGAGACCAATATACAAAACCTCTCCACTCCA 2465
Db 1825 CAGGGCTTGCAGAAAGTAAAGTTTCTTCAAGAGACCAATATACAAAACCTCTCCACTCCA 1884
Qy 2466 CTGACCTGGTGGTCTTCCCAACTTTTCAGTTATAGATGATGATGATGATGATGATGATGATG 2525
Db 1885 CTGACCTGGTGGTCTTCCCAACTTTTCAGTTATAGATGATGATGATGATGATGATGATGATG 1944
Qy 2526 GATCTGGGCTTTCATGAGGCGCCCTTTTGAAGGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGA 2585
Db 1945 GATCTGGGCTTTCATGAGGCGCCCTTTTGAAGGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGA 2004
Qy 2586 CAGCCGAGGCGAGCAGAGCTGGGATGTGTGATGATGATGATGATGATGATGATGATGATGATG 2645
Db 2005 CAGCCGAGGCGAGCAGAGCTGGGATGTGTGATGATGATGATGATGATGATGATGATGATGATG 2064
Qy 2646 GTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTTAAATAAAGGTTGGCTTC 2705
Db 2065 GTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTTAAATAAAGGTTGGCTTC 2124
Qy 2706 TGAATCTACAAAAAATAAAAA 2725
Db 2125 TGAATCTACAAAAAATAAAAA 2144

RESULT 2
US-09-620-312D-1006
; Sequence 1006, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D

```
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; FILING DATE: 2000-01-21
; NUMBER OF SEQ. ID NOS: 1105
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 1006
; LENGTH: 2142
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (528)..(1604)
; US-09-620-312D-1006

Query Match      64.2%; Score 1827; DB 4; Length 2142;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1877; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 846 TCCTTGAAGAAAGAACTGCTCAGACCCCTGGGGGCCCAAGTCAATGGGTACCGAAAAATAA 905
Db 265 TCCTTGAAGAAAGAACTGCTCAGACCCCTGGGGGCCCAAGTCAATGGGTACCGAAAAATAA 324
Qy 906 CAGGGGGCCCTGGGGCTTATCAACGGACGCCCATGCTAAATTTGGACACCGTGTGCTTTCT 965
Db 325 CAGGGGGCCCTGGGGCTTATCAACGGACGCCCATGCTAAATTTGGACACCGTGTGCTTTCT 384
Qy 966 TTTCTTAACAACCTCTATGTTCTTAGTGGCAATGAGAAAGAACTTGGCCAGCAGAAATGGAG 1025
Db 385 TTTGTAAACAACCTCTATGTTCTTAGTGGCAATGAGAAAGAACTTGGCCAGCAGAAATGGAG 444
Qy 1026 AGTGGTCAGGGAAACAGCCCATCTGCTATATAAGGCTGCCGAGAACCAAGATTTTCAGACC 1085
Db 445 AGTGGTCAGGGAAACAGCCCATCTGCTATATAAGGCTGCCGAGAACCAAGATTTTCAGACC 504
Qy 1086 TGGTGAGAGAGAGATTTCTTCGATGACAGGTTTCAGTCAAGGAGACACCATTAACACAGC 1145
Db 505 TGGTGAGAGAGAGATTTCTTCGATGACAGGTTTCAGTCAAGGAGACACCATTAACACAGC 564
Qy 1146 TATACTCAGCGGCTTCAGCAAGCAGCAAACTGCAAGTGGCCCTTACCAGAAAGCCAGCC 1205
Db 565 TATACTCAGCGGCTTCAGCAAGCAGCAAACTGCAAGTGGCCCTTACCAGAAAGCCAGCC 624
Qy 1206 TTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGT 1265
Db 625 TTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGT 684
Qy 1266 GCATCTCACCTTTACCGCGCTGGGCGAGCAGCAGGAGACATGTCTGAGGACTGGGA 1325
Db 685 GCATCTCACCTTTACCGCGCTGGGCGAGCAGCAGGAGACATGTCTGAGGACTGGGA 744
Qy 1326 AGTGGAGTGGGGGGCCACCATCTGCACTCCCTATCTGGGGGAAATTCAGAACATCACTG 1385
Db 745 AGTGGAGTGGGGGGCCACCATCTGCACTCCCTATCTGGGGGAAATTCAGAACATCACTG 804
Qy 1386 CTCCAAAGACCAAGGGTTGGCTGGCGTGGCAGGAGCCATCTACAGGAGGACCCAGCG 1445
Db 805 CTCCAAAGACCAAGGGTTGGCTGGCGTGGCAGGAGCCATCTACAGGAGGACCCAGCG 864
Qy 1446 GGGTGCAATGACGGCAGCCTACACAAGGAGCGTGGTTCCTAGTCTGCAGCGGTGCCCTGG 1505
Db 865 GGGTGCAATGACGGCAGCCTACACAAGGAGCGTGGTTCCTAGTCTGCAGCGGTGCCCTGG 924
Qy 1506 TGAATGAGCGCACTGTGTGTGTGGCTGCCCATCTGTGTTACTGACCTGGGGAGGTCAACA 1565
Db 925 TGAATGAGCGCACTGTGTGTGTGGCTGCCCATCTGTGTTACTGACCTGGGGAGGTCAACA 984
Qy 1566 TGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAATTTCTACCGGATCATGACCGGG 1625
Db 985 TGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAATTTCTACCGGATCATGACCGGG 1044
Qy 1626 ATGAGAAGACCATCCAGAGCCTACAGATTTTCTGCTATCATTTCTGCACTCCCAACTATGACC 1685
```

```
||||| 1045 ATGAGAAAGACCAATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCAATCCCAACTATGACC 1104
Qy 1686 CCATCTCTGCTTGTAGTCTGACATCGCCATCTCTGAAAGCTCTTAGACAAGGCCCGTATCAGCA 1745
Db 1105 CCATCTCTGCTTGTAGTCTGACATCGCCATCTCTGAAAGCTCTTAGACAAGGCCCGTATCAGCA 1164
Qy 1746 CCGAGTCCAGCCCATCTGCTCGCTGCGAGTGGGATCTCAGCACTCTCTTCAGGAGT 1805
Db 1165 CCGAGTCCAGCCCATCTGCTCGCTGCGAGTGGGATCTCAGCACTCTCTTCAGGAGT 1224
Qy 1806 CCACATCACTGTGGCTGGCTGGAATGTCCTGGCAGACGTGAGGAGCCCTGGCTTCAAGA 1865
Db 1225 CCACATCACTGTGGCTGGCTGGAATGTCCTGGCAGACGTGAGGAGCCCTGGCTTCAAGA 1284
Qy 1866 ACACACACTGCTGCGCTCTGGGGTGGTCAAGTGTGGTGGACTCGCTCTGTGTGAGGAGCAGC 1925
Db 1285 ACACACACTGCTGCGCTCTGGGGTGGTCAAGTGTGGTGGACTCGCTCTGTGTGAGGAGCAGC 1344
Qy 1926 ATGAGGACCATGGGCATCCCAAGTGTGCTGACTGATTAACATGTTCTGTGCCAGCTGGGAAC 1985
Db 1345 ATGAGGACCATGGGCATCCCAAGTGTGCTGACTGATTAACATGTTCTGTGCCAGCTGGGAAC 1404
Qy 1986 CCATGCCCCCTTCTGATATCTGCACTGCAAGACAGGAGCAGCAGGCTCGCGCTGTGCTTCC 2045
Db 1405 CCATGCCCCCTTCTGATATCTGCACTGCAAGACAGGAGCAGCAGGCTCGCGCTGTGCTTCC 1464
Qy 2046 CGGAGCAGCATCTCTGAGCACCGCTGGCATCTGATGGGACTGGTCAAGCTGGGAGCTATG 2105
Db 1465 CGGAGCAGCATCTCTGAGCACCGCTGGCATCTGATGGGACTGGTCAAGCTGGGAGCTATG 1524
Qy 2106 ATAAAAATGAGCAGCAGGCTCTCCACTGCTCTCAACAGGCTGCTGCTTTTAAAGACT 2165
Db 1525 ATAAAAATGAGCAGCAGGCTCTCCACTGCTCTCAACAGGCTGCTGCTTTTAAAGACT 1584
Qy 2166 GGATTGAAGAAATATGAATGAACCATGCTCATGCACTCTCTCAGAGTGTGTTTGGCCTG 2225
Db 1585 GGATTGAAGAAATATGAATGAACCATGCTCATGCACTCTCTCAGAGTGTGTTTGGCCTG 1644
Qy 2226 ATCCGCTCTGTACGCTGTCTATTGGCTGAAGCAGTGTGGGCTGAAAGTGTGTTTGGCCTG 2285
Db 1645 ATCCGCTCTGTACGCTGTCTATTGGCTGAAGCAGTGTGGGCTGAAAGTGTGTTTGGCCTG 1704
Qy 2286 TGAATCTGGCTGTGCCAGGGCTTCTGACTTCAGGGGACAAAACCTCAGTGAAGGGTGAAGTAG 2345
Db 1705 TGAATCTGGCTGTGCCAGGGCTTCTGACTTCAGGGGACAAAACCTCAGTGAAGGGTGAAGTAG 1764
Qy 2346 ACCTCCATCTGCTGTAGGCTGATGCCGGTCCACTACTAGGACAGCCAAATTTGGAGATGC 2405
Db 1765 ACCTCCATCTGCTGTAGGCTGATGCCGGTCCACTACTAGGACAGCCAAATTTGGAGATGC 1824
Qy 2406 CAGGGCTTGAAGAAATGAAGTTTCTTCAAGAAGACCAATATACAAAACCTCTCCACTCCA 2465
Db 1825 CAGGGCTTGAAGAAATGAAGTTTCTTCAAGAAGACCAATATACAAAACCTCTCCACTCCA 1884
Qy 2466 CTGACCTGGTGGTCTTCCCAACTTTTCAGTTATACGAATGCCATCAGCTTCAACAGGAA 2525
Db 1885 CTGACCTGGTGGTCTTCCCAACTTTTCAGTTATACGAATGCCATCAGCTTCAACAGGAA 1944
Qy 2526 GATCTGGGCTTCATGAGGCCCTTTTGAAGGCTCTCAAGTCTTAGAGAGCTGCTGTGGGA 2585
Db 1945 GATCTGGGCTTCATGAGGCCCTTTTGAAGGCTCTCAAGTCTTAGAGAGCTGCTGTGGGA 2004
Qy 2586 CAGCCCAAGGCGAGCAGAGCTGGGATGTGGTCACTGCTCTTGTATACATGGGCCACAGTACA 2645
Db 2005 CAGCCCAAGGCGAGCAGAGCTGGGATGTGGTCACTGCTCTTGTATACATGGGCCACAGTACA 2064
Qy 2646 GTCTGGTCTCTTTTCCCTTCCCATCTTCTGTACACATTTTAAATAAAGGGTTGGCTTC 2705
Db 2065 GTCTGGTCTCTTTTCCCTTCCCATCTTCTGTACACATTTTAAATAAAGGGTTGGCTTC 2124
Qy 2706 TGAATCAAAAAA 2723
|||||
```


Db 2125 TGAACACAAAAA 2142

RESULT 3

US-10-067-422-2

; Sequence 2, Application US/10067422

; Patent No. 6743613

; GENERAL INFORMATION:

; APPLICANT: Ni et al.

; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and

; TITLE OF INVENTION: Antibodies

; FILE REFERENCE: PT004P1

; CURRENT APPLICATION NUMBER: US/10/067,422

; CURRENT FILING DATE: 2002-02-07

; PRIOR FILING DATE: 2000-10-11

; PRIOR APPLICATION NUMBER: 09/685,899

; PRIOR FILING DATE: 2000-04-06

; PRIOR APPLICATION NUMBER: PCT/US00/09028

; PRIOR FILING DATE: 2000-04-06

; PRIOR APPLICATION NUMBER: 60/152,933

; PRIOR FILING DATE: 1999-09-09

; PRIOR APPLICATION NUMBER: 60/147,020

; PRIOR FILING DATE: 1999-08-03

; PRIOR APPLICATION NUMBER: 60/131,672

; PRIOR FILING DATE: 1999-04-29

; PRIOR APPLICATION NUMBER: 60/130,693

; PRIOR FILING DATE: 1999-04-23

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn ver. 2.0

; SEQ ID NO 2

; LENGTH: 2259

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-067-422-2

Query Match 62.8%; Score 1787; DB 4; Length 2259;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1887; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 846 TCCTTGAAGAAGAACTGCTCAGACCCTGGGGCCAGTCAATGGGTACAGAAATAA 905

Db 371 TCCTTGAAGAAGAACTGCTCAGACCCTGGGGCCAGTCAATGGGTACAGAAATAA 430

Qy 906 CAGGGGCGCTGGGCTTATCAACGAGCCCATGCTTAAATTTGGACCGTGGTCTTTCT 965

Db 431 CAGGGGCGCTGGGCTTATCAACGAGCCCATGCTTAAATTTGGACCGTGGTCTTTCT 490

Qy 966 TTTGTAAACACTCCCTATGTTCTTAGTGCAATGAGAAAGAACTTGCAGCAGATGGAG 1025

Db 491 TTTGTAAACACTCCCTATGTTCTTAGTGCAATGAGAAAGAACTTGCAGCAGATGGAG 550

Qy 1026 AGTGGTCAGGAAACAGCCCATCTGCATAAAGCTGCGAGAACCAAGATTTTCAGACC 1085

Db 551 AGTGGTCAGGAAACAGCCCATCTGCATAAAGCTGCGAGAACCAAGATTTTCAGACC 610

Qy 1086 TGGTGAGAAGGAGAGTTCTTCGGATGACAGTTTCAGTCAAGGAGACACCATTAACACGAG 1145

Db 611 TGGTGAGAAGGAGAGTTCTTCGGATGACAGTTTCAGTCAAGGAGACACCATTAACACGAG 670

Qy 1146 TATACCTACGCGCCTTCAGCAAGCAGAAACTGCAAGTGCCTTACCAAGAGCCAGCCC 1205

Db 671 TATACCTACGCGCCTTCAGCAAGCAGAAACTGCAAGTGCCTTACCAAGAGCCAGCCC 730

Qy 1206 TTCCCTTTGGAGATCTGCCCATGGATACCAACATCTGCATACCCAGTCCAGTATGAGT 1265

Db 731 TTCCCTTTGGAGATCTGCCCATGGATACCAACATCTGCATACCCAGTCCAGTATGAGT 790

Qy 1266 GCATCTCACCTTCTTACCGCGCTGGGCGAGCAGGAGGACATGTTCTGAGGACTGGGA 1325

Db 791 GCATCTCACCTTCTTACCGCGCTGGGCGAGCAGGAGGACATGTTCTGAGGACTGGGA 850

Qy 1326 AGTGGAGTGGGCGGCACCATCTGCATCCCTATCTGCGGGAAATTCAGAACATCACTG 1385

Db 851 AGTGGAGTGGGCGGCACCATCTGCATCCCTATCTGCGGGAAATTCAGAACATCACTG 910

Qy 1386 CTCCAAAGACCCAAAGGTTTGGCTGGCGTGGCAGGAGCCATCTACAGAGGAGCCAGCG 1445

Db 911 CTCCAAAGACCCAAAGGTTTGGCTGGCGTGGCAGGAGCCATCTACAGAGGAGCCAGCG 970

Qy 1446 GGGTGCATGACGGCAGCCTACACAAGGAGCGTGGTTCCTAGTCTGACGCGGTGCGCTGG 1505

Db 971 GGGTGCATGACGGCAGCCTACACAAGGAGCGTGGTTCCTAGTCTGACGCGGTGCGCTGG 1030

Qy 1506 TGAATGAGCGACATGTTGGTGGCTGCCACCTGTGTACTGACCTGGGAGAGTCCACCA 1565

Db 1031 TGAATGAGCGACATGTTGGTGGCTGCCACCTGTGTACTGACCTGGGAGAGTCCACCA 1090

Qy 1566 TGATCAAGACAGCAGACCTGAAAGTGTGTTTGGGGAATTTCTACCGGATGATCACCGGG 1625

Db 1091 TGATCAAGACAGCAGACCTGAAAGTGTGTTTGGGGAATTTCTACCGGATGATCACCGGG 1150

Qy 1626 ATGAGAAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTCTGATCCCAATATGACC 1685

Db 1151 ATGAGAAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTCTGATCCCAATATGACC 1210

Qy 1686 CCATCCTGCTTGATGCTGACATCGGCATCTGAAAGTCTCTAGACCTCCGATCAGCA 1745

Db 1211 CCATCCTGCTTGATGCTGACATCGGCATCTGAAAGTCTCTAGACCTCCGATCAGCA 1270

Qy 1746 CCGAGTCCAGCCCATCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 1805

Db 1271 CCGAGTCCAGCCCATCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 1330

Qy 1806 CCCACATCACTGTGGCTGGCTGGAATGTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGA 1865

Db 1331 CCCACATCACTGTGGCTGGCTGGAATGTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGA 1390

Qy 1866 ACGACACACTGCGCTCTGGGGTGGTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1925

Db 1391 ACGACACACTGCGCTCTGGGGTGGTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1450

Qy 1926 ATGAGGACCATGGCATCCAGTGAAGTGTCACTGAATAACATGTTCTGTGCCAGCTGGGAAC 1985

Db 1451 ATGAGGACCATGGCATCCAGTGAAGTGTCACTGAATAACATGTTCTGTGCCAGCTGGGAAC 1510

Qy 1986 CCACTGCGCTTCTGATATCTGCACTGCAAGACAGGAGGATCGCGCTGTGCTCTTCC 2045

Db 1511 CCACTGCGCTTCTGATATCTGCACTGCAAGACAGGAGGATCGCGCTGTGCTCTTCC 1570

Qy 2046 CGGACGAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGCTCAGCTGGAGCTATG 2105

Db 1571 CGGACGAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGCTCAGCTGGAGCTATG 1630

Qy 2106 ATAAACATGACGACACAGGCTCTCCACTGCTTCAACCAAGGTGCTGCTTTTAAAGACT 2165

Db 1631 ATAAACATGACGACACAGGCTCTCCACTGCTTCAACCAAGGTGCTGCTTTTAAAGACT 1690

Qy 2166 GGATTTGAAAGAAATATGAAATGAAACCATGCTCATGCACTCTTGAAGAGTGTTCGTAT 2225

Db 1691 GGATTTGAAAGAAATATGAAATGAAACCATGCTCATGCACTCTTGAAGAGTGTTCGTAT 1750

Qy 2226 ATCCGTCTGATGCTGTGCTGATGAGCAGTGTGGGCTGAGTGTGATTTGGCCTG 2285

Db 1751 ATCCGTCTGATGCTGTGCTGATGAGCAGTGTGGGCTGAGTGTGATTTGGCCTG 1810

Qy 2286 TGAATCTGGCTGTGCGCAGGGCTTCTGACTTCAAGGACAAACACTCAGTCAAGGGTGAAGTAG 2345

Db 1811 TGAATCTGGCTGTGCGCAGGGCTTCTGACTTCAAGGACAAACACTCAGTCAAGGGTGAAGTAG 1870

Qy 2346 ACCTCCATGCTGTGATGCTGATGCGCGTCCATCTAGGACAGCCAAATTTGGAAGATGC 2405

Db 1871 ACCTCCATGCTGTGATGCTGATGCGCGTCCATCTAGGACAGCCAAATTTGGAAGATGC 1930

Qy 2406 CAGGCTTGGCAAGAGTAAAGTTTCTTCAAGAGACCATATACAAAACCTCTCCACTCCA 2465

Db 1931 CAGGCTTGGCAAGAGTAAAGTTTCTTCAAGAGACCATATACAAAACCTCTCCACTCCA 1990

QY 2466 CTGACCTGGTGGTCTTCCCAACTTTTCAGTTATACGAATGCATCAGCTTGACAGGGAA 2525
|
Db 1991 CTGACCTGGTGGTCTTCCCAACTTTTCAGTTATACGAATGCATCAGCTTGACAGGGAA 2050
|
QY 2526 GATCTGGGCTTCATGAGGCCCTTTTGAAGGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGA 2585
|
Db 2051 GATCTGGGCTTCATGAGGCCCTTTTGAAGGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGA 2110
|
QY 2586 CAGCCAGGGCAGCAGAGCTGGATGTGGTGATGCCCTTTGTGTACATGGCCACAGTACA 2645
|
Db 2111 CAGCCAGGGCAGCAGAGCTGGATGTGGTGATGCCCTTTGTGTACATGGCCACAGTACA 2170
|
QY 2646 GTCTGGTCTTTCTCTCCCATCTCTGTGTACACATTTTAAATAAAGGTTGGCTTC 2705
|
Db 2171 GTCTGGTCTTTCTCTCCCATCTCTGTGTACACATTTTAAATAAAGGTTGGCTTC 2230
|
QY 2706 TGAACACAAAAAATAAAAAAATAAAAAA 2734
|
Db 2231 TGAACACAAAAAATAAAAAAATAAAAAA 2259
|
RESULT 4
US-09-280-116-179
; Sequence 179, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: astacin/m 12a metalloproteases
US-09-280-116-179

Query Match 13.0%; Score 370; DB 3; Length 505;
Best Local Similarity 99.8%; Pred. No. 5.8e-134; Mismatches 1; Indels 0; Gaps 0;
Matches 420; Conservative 0;
QY 381 GCTGTACGAGGAGACTGCATGCCATGTGGCCAGGTTCTGCGACCCCAAGGTCAGA 440
|
Db 51 GCTGTACGAGGAGACTGCATGCCATGTGGCCAGGTTCTGCGACCCCAAGGTCAGA 110
|
QY 441 TTTTGTTCGAAAGCTATCCCTTAAATGCTACTGTGAATGGACCAATCATGCTAAACCTG 500
|
Db 111 TTTTGTTCGAAAGCTATCCCTTAAATGCTACTGTGAATGGACCAATCATGCTAAACCTG 170
|
QY 501 GGTGTGTCATCCCACTAGATTTGTCATGTTGAGTCTGGATTTGACTACATGTGCCAGT 560
|
Db 171 GGTGTGTCATCCCACTAGATTTGTCATGTTGAGTCTGGATTTGACTACATGTGCCAGT 230
|
QY 561 ATGACTATGTTGAGGTTCTGTATGAGACAAACCGGATGGCCAGATCATCAAGCGTGTCT 620
|
Db 231 ATGACTATGTTGAGGTTCTGTATGAGACAAACCGGATGGCCAGATCATCAAGCGTGTCT 290
|
QY 621 GTGGCAACGAGCGGCAGCTCTTATCCAGAGCATAGGATTCCTCACTCAAGCTCTTCTCC 680
|
Db 291 GTGGCAACGAGCGGCAGCTCTTATCCAGAGCATAGGATTCCTCACTCAAGCTCTTCTCC 350
|
QY 681 ACTCGATGGCTCCAAAGATTTTGACGGTTTCCATGCCATTTATGAGGATCACAGCAT 740
|
Db 351 ACTCGATGGCTCCAAAGATTTTGACGGTTTCCATGCCATTTATGAGGATCACAGCAT 410
|
QY 741 GCTCTCATCCCTGTTTCCATGACGCGCTGCTTGACAAAGCTGTGATCTTACA 800
|
Db 411 GCTCTCATCCCTGTTTCCATGACGCGCTGCTTGACAAAGCTGTGATCTTACA 470
|

QY 801 A 801
|
Db 471 A 471
|
RESULT 5
US-09-280-116-104
; Sequence 104, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
; LENGTH: 2886
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
; NAME/KEY: misc feature
; LOCATION: (1)..(2886)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-104
Query Match 11.6%; Score 329; DB 3; Length 2886;
Best Local Similarity 99.8%; Pred. No. 3.6e-118; Mismatches 0; Indels 1; Gaps 1;
Matches 449; Conservative 0;
QY 686 GATGGCTCCAAAGAAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCATGCTCC 745
|
Db 815 GATGGCTCCAAAGAAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCATGCTCC 874
|
QY 746 TCATCCCTCTGTTTCCATGACGGCAGTGGCTCTTGACAAAGCTGGATCTTACAAGTGT 805
|
Db 875 TCATCCCTCTGTTTCCATGACGGCAGTGGCTCTTGACAAAGCTGGATCTTACAAGTGT 934
|
QY 806 GCCTGCTTGGCAGGC-TATACCTGGGCGAGCGCTGTGAAATCTCTCTTGAAGAAAGAACTG 864
|
Db 935 GCCTGCTTGGCAGGC-TATACCTGGGCGAGCGCTGTGAAATCTCTCTTGAAGAAAGAACTG 994
|
QY 865 CTCAGACCTCTGGGGGCCAGTCAATGGGTACCAAGAAATAACAGGGGCCCTTGGGCTTAT 924
|
Db 995 CTCAGACCTCTGGGGGCCAGTCAATGGGTACCAAGAAATAACAGGGGCCCTTGGGCTTAT 1054
|
QY 925 CAACGGACGCCATGCTAAATTTGGCACCGTGGTGTCTTTCTTTGTAACTCCTATGT 984
|
Db 1055 CAACGGACGCCATGCTAAATTTGGCACCGTGGTGTCTTTCTTTGTAACTCCTATGT 1114
|
QY 985 TCTTAGTGGCAATGAGAAAGAACTTGCACAGAAATGAGAGTGGTCAGGGAACAGCC 1044
|
Db 1115 TCTTAGTGGCAATGAGAAAGAACTTGCACAGAAATGAGAGTGGTCAGGGAACAGCC 1174
|
QY 1045 CATCTGATAAAGCTCTGCCAGAAACCAAGATTTTCAGACCTGTGTGAGAGAGAGTTCT 1104
|
Db 1175 CATCTGATAAAGCTCTGCCAGAAACCAAGATTTTCAGACCTGTGTGAGAGAGAGTTCT 1234
|
QY 1105 TCCGATGAGGTTTCAAGTCAAGGGAGACCC 1134
|
Db 1235 TCCGATGAGGTTTCAAGTCAAGGGAGACCC 1264
|
RESULT 6
US-09-537-654-3
; Sequence 3, Application US/09537654
; Patent No. 6720478
; GENERAL INFORMATION:
; APPLICANT: Mahajan, Pramod B.
; APPLICANT: Shi, Jinrui

; TITLE OF INVENTION: A No. 6720478e1 Maize Rad51-Like Gene and Uses
; FILE REFERENCE: 1107
; CURRENT APPLICATION NUMBER: US/09/537,654
; CURRENT FILING DATE: 2000-03-29
; EARLIER APPLICATION NUMBER: 60/132,582
; EARLIER FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1459
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (169)...(1011)
US-09-537-654-3

Query Match 4.7%; Score 134; DB 4; Length 1459;
Best Local Similarity 100.0%; Pred. No. 1.4e-42;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2713 CAAAAA... 2846
DB 1314 CAAAAA... 1373

QY 2773 AAAAAA... 2832
DB 1374 AAAAAA... 1433

QY 2833 AAAAAA... 2846
DB 1434 AAAAAA... 1447

RESULT 7
US-09-370-838-151
; Sequence 151, Application US/09370838
; Patent No. 644425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roadoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: LONG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 151
; LENGTH: 3275
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-370-838-151

Query Match 4.7%; Score 134; DB 3; Length 3275;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2713 CAAAAA... 2772
DB 3128 CAAAAA... 3187

QY 2773 AAAAAA... 2832
DB 3188 AAAAAA... 3247

QY 2833 AAAAAA... 2846

Db 3248 AAAAAAAAAAAAAA 3261

RESULT 8
US-09-854-133-151
; Sequence 151, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roadoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 151
; LENGTH: 3275
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-854-133-151

Query Match 4.7%; Score 134; DB 4; Length 3275;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2713 CAAAAA... 2772
DB 3128 CAAAAA... 3187

QY 2773 AAAAAA... 2832
DB 3188 AAAAAA... 3247

QY 2833 AAAAAA... 2846
DB 3248 AAAAAA... 3261

RESULT 9
US-08-628-417-6
; Sequence 6, Application US/08628417
; Patent No. 5627054
; GENERAL INFORMATION:
; APPLICANT: GILLESPIE, DAVID
; TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
; STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
; CITY: ABERDEEN PROVING GROUND
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,417
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BIFFONI, ULYSSES J
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 398-94

```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 6:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 240 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: oligodeoxynucleotide
;
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
;
; US-08-628-417-6

```

[illegible]

```

RESULT 10
US-09-640-173-53/c
; Sequence 53, Application US/09640173
; Patent No. 6613515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 210121.484C2
; CURRENT APPLICATION NUMBER: US/09/640,173
; CURRENT FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-640-173-53

```

	Query Match	4.7%; Score 133; DB 4; Length 396;
	Best Local Similarity 100.0%; Pred. No. 4e-42;	
	Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	2714 AA 2773	
Dd	222 AA 163	
Qy	2774 AA 2833	
Dd	162 AA 103	
Qy	2834 AAAAAAAAAAAAAAAAAA 2846	
Dd	102 AAAAAAAAAAAAAAA 90	

RESULT 11

```

US-09-713-550-53/c
; Sequence 53, Application US/09713550
; Patent No. 6617109
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT OF OVARIAN CANCER
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN
; CANCER
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-53

```

	Query Match	4.7%	Score 133;	DB 4;	Length 396;
	Best Local Similarity	100.0%;	Pred. No. 4e-42;		
	Matches 133;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	2714	AAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAA	2773
Dd	222	AAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAA	163
Qy	2774	AAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAA	2833
Dd	162	AAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAA	103
Qy	2834	AAAAAAAAAAAAAAAAAAA	A2846		
Dd	102	AAAAAAAAAAAAAAAAAA	90		

```

RESULT 12
US-09-825-294-53/c
; Sequence 53, Application US/09825294
; Patent No. 6710170
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stoik, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITL OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-53

```

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 9, 2005, 20:53:28 ; Search time 8260 Seconds
(without alignments)
4223.699 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 3945
Sequence: 1 MELGCTWQLGLTFLQLLLIS.....LSTAFKTVLPFKDWIERNMK 720

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2 1/USPTO.spool/US10063692/runat_09052005_122254_4863/app_query.fasta_1.903
-Db=GenEmbl -QFMT=fastap -SUPPLX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blom62 -TRANS=human40.cdi -LIST=1500
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10063692 @CGN 1 1 5469 @runat_09052005_122254_4863 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGIOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3945	100.0	2846	6	AR252533 Sequence
2	3945	100.0	2846	6	AX092306 Sequence
3	3945	100.0	2846	6	AX376102 Sequence
4	3945	100.0	2846	6	AX403343 Sequence

5	3945	100.0	2846	9	AY358346	AY358346 Homo sapi
6	3941	99.9	2768	9	HSMB03699	AL832391 Homo sapi
7	3939	99.8	2306	6	AX084209	AX084209 Sequence
8	3939	99.8	2306	6	AX133839	AX133839 Sequence
9	3921.5	99.4	2289	6	BD012236	BD012236 A novel g
10	3921.5	99.4	2784	6	BD157134	BD157134 Primer fo
11	3921.5	99.4	2784	6	AX878296	AX878296 Sequence
12	3921.5	99.4	2784	6	BD012234	BD012234 A novel g
13	3921.5	99.4	2784	9	AK027841	AK027841 Homo sapi
14	3612	91.6	2244	6	BD012235	BD012235 A novel g
15	3612	91.6	2841	10	BC031841	BC031841 Mus muscu
16	3612	91.6	2841	10	BC057685	BC057685 Mus muscu
17	3500.5	88.7	2632	6	AX704692	AX704692 Sequence
18	3450.5	87.5	2886	6	AX263926	AX263926 Sequence
19	3132.5	79.4	1867	6	AX084207	AX084207 Sequence
20	2987	75.7	1669	6	CQ723377	CQ723377 Sequence
21	2977.5	75.5	2350	9	BC038457	BC038457 Homo sapi
22	2946.5	74.7	2259	6	AR541687	AR541687 Sequence
23	2823	71.6	5735	5	BC075430	BC075430 Xenopus t
24	2678.5	67.9	2142	6	AR339515	AR339515 Sequence
25	2678.5	67.9	2144	6	AR339478	AR339478 Sequence
26	1413.5	35.8	142522	9	AC090625	AC090625 Homo sapi
27	1396.5	35.4	141818	2	AL133389	AL133389 Homo sapi
28	1386.5	35.1	208659	2	AC067845	AC067845 Homo sapi
29	1298	32.9	217777	2	AC113891	AC113891 Rattus no
30	1296	32.9	188958	10	AL844605	AL844605 Mouse DNA
31	1295	32.8	222330	2	AC096255	AC096255 Rattus no
32	1191	30.2	705	6	BD150061	BD150061 Primer fo
33	1191	30.2	705	6	AX869999	AX869999 Sequence
34	1124.5	28.5	246369	2	AC125707	AC125707 Rattus no
35	949	24.1	1088	9	HSMB00511	AR050214 Homo sapi
36	893	22.6	505	6	AR264001	AR264001 Sequence
37	824	20.9	421	6	CQ723379	CQ723379 Sequence
38	755	19.1	106657	9	AL354921	AL354921 Human DNA
39	681.5	17.3	657	5	CR387267	CR387267 Gallus ga
40	672	17.2	3060	3	AF467804	AF467804 Tachypieu
41	672	17.0	3467	3	TATLFC1	D90271 Tachypieu
42	665	16.9	3438	6	S77063	S77063 factor C=cn
43	665	16.9	3448	6	AR028519	AR028519 Sequence
44	665	16.9	3448	6	AR086513	AR086513 Sequence
45	665	16.9	3448	6	I88008	I88008 Sequence 3
46	665	16.9	3448	6	AR429665	AR429665 Sequence
47	665	16.9	3448	6	AX492795	AX492795 Sequence
48	665	16.9	3448	6	AX112199	AX112199 Sequence
49	665	16.9	4182	3	S77064	S77064 factor C=cn
50	665	16.9	4182	6	AR028518	AR028518 Sequence
51	665	16.9	4182	6	AR086512	AR086512 Sequence
52	665	16.9	4182	6	I88007	I88007 Sequence 1
53	665	16.9	4182	6	AR429664	AR429664 Sequence
54	665	16.9	4182	6	AR492794	AR492794 Sequence
55	665	16.9	4182	6	AX112197	AX112197 Sequence
56	608.5	15.4	2695	3	AB089267	AB089267 Branchios
57	597	15.1	2782	3	AB089268	AB089268 Branchios
58	580	14.7	340	6	BD076812	BD076812 5' EST of
59	512.5	13.0	3305	5	BC073178	BC073178 Xenopus l
60	490.5	12.4	3636	5	AY567829	AY567829 Gallus ga
61	489.5	12.4	2550	5	D83276	D83276 Xenopus lae
62	483	12.2	2108	10	RNO277423	AJ277423 Rattus no
63	482.5	12.2	5112	10	RNO457084	AJ457084 Rattus no
64	482	12.2	2787	9	HUMWASP	D28593 Human mRNA
65	482	12.2	4457	5	AB078636	AB078636 Xenopus l
66	476	12.1	4489	9	D17525	D17525 Human mRNA
67	475	12.0	2752	6	CQ714371	CQ714371 Sequence
68	475	12.0	5135	10	MUSCRARF	D16492 Mouse mRNA
69	471	11.9	3895	6	AX156466	AX156466 Sequence
70	469.5	11.9	4696	5	AB078637	AB078637 Xenopus l
71	468	11.9	3895	9	AF284421	AF284421 Homo sapi
72	461	11.7	3863	6	AX254423	AX254423 Sequence
73	459.5	11.6	369	5	AX395272	AX395272 Sequence
74	457	11.6	2407	5	AB009074	AB009074 Triakis s
75	455	11.5	3713	9	HSMB07381	EX647237 Homo sapi
76	452	11.5	3736	10	AB049755	AB049755 Mus muscu
77	450.5	11.4	2217	5	BC084139	BC084139 Xenopus t

78	448	11.4	3229	5	AB009073	AB009073 Cyprinus	151	335.5	8.5	3147	6	AX207945	AX207945 Sequence
79	447	11.3	2449	5	AY567828	Gallus ga	152	335.5	8.5	3147	9	AF057145	Homo sapi
80	436.5	11.1	3255	5	AB089265	Lethenter	153	335	8.5	4989	3	AY380790	Manuoca s
81	435	11.0	162877	2	CR318591	Danio rer	154	334	8.5	1662	5	AF515270	Danio rer
82	429	10.9	2416	10	AF148216	Mus muscu	155	333	8.4	3073	9	AK055183	Homo sapi
83	428	10.8	2409	10	BC004637	Mus muscu	156	331.5	8.4	3696	6	AX207959	Sequence
84	425.5	10.8	3950	10	RN0487622	Rattus no	157	331.5	8.4	3696	6	AX677073	Sequence
85	425	10.8	2282	5	AB009072	Xenopus l	158	331.5	8.4	3696	9	HSU09860	Human enter
86	424	10.7	2037	10	RN0277747	Rattus no	159	331	8.4	1182	9	AB036334	Homo sapi
87	420	10.6	1937	10	RN018572	Rattus norv	160	331	8.4	2616	9	HSC1S	Homo sapi
88	417	10.6	3070	10	BC013893	Mus muscu	161	330.5	8.4	3586	4	PIGENPR	Human mRNA
89	416.5	10.6	2166	10	AF459018	Mus muscu	162	329.5	8.4	10944	9	AY017307	Sus scrofa
90	412	10.4	2090	10	AB009459	Mus muscu	163	329.5	8.4	11580	9	AF333704	Homo sapi
91	406.5	10.3	3202	5	BC079773	Xenopus l	164	329	8.3	11221	10	AY017475	Mus muscu
92	404	10.2	2450	9	HSMA5P2	H. sapiens m	165	328.5	8.3	5598	6	AX306886	Sequence
93	404	10.2	2455	9	HSMA5P2PR	Homo sapien	166	328.5	8.3	5667	6	AX306889	Sequence
94	403.5	10.2	2386	6	AX250080	Sequence	167	328.5	8.3	6145	6	AX306887	Sequence
95	403.5	10.2	2386	9	HSC1R	Human mRNA	168	328.5	8.3	6409	6	AX306888	Sequence
96	403.5	10.2	2492	6	AR130745	Sequence	169	328.5	8.3	7323	6	AX306890	Sequence
97	403.5	10.2	2492	6	AR448569	Sequence	170	328.5	8.3	8034	6	AX306891	Sequence
98	403.5	10.2	2492	6	BD080942	Detection	171	324	8.2	2900	6	AR081725	Sequence
99	403.5	10.2	2493	6	AX302547	Sequence	172	324	8.2	2900	6	AR229705	Sequence
100	403.5	10.2	2493	6	AX409609	Sequence	173	324	8.2	2900	6	AR430931	Sequence
101	403.5	10.2	2493	9	HUMC1R	Human compl	174	324	8.2	2900	9	HSU20428	Human SMC19
102	403.5	10.2	2526	9	BC035220	Homo sapi	175	324	8.2	3490	9	AK126857	Homo sapi
103	403.5	10.2	1490	10	GPI457086	Cavia por	176	324	8.2	12525	6	AX374893	Sequence
104	401.5	10.2	2051	6	QD827400	Sequence	177	323	8.2	8010	6	AX685959	Sequence
105	400.5	10.2	2555	3	D88204	Halocynthia	178	323	8.2	10136	6	AX685957	Sequence
106	399.5	10.1	2449	6	Q0720832	Sequence	179	323	8.2	13113	9	AY210418	Homo sapi
107	398.5	10.1	2550	5	AB042609	Cyprinus	180	322.5	8.2	1499	10	MUSCP	Mouse mRNA
108	395	10.0	3170	5	AB089266	Lethenter	181	322.5	8.2	2249	5	BC081673	Danio rer
109	386	9.8	2135	5	AY349426	Sus scrofa	182	322.5	8.2	2589	6	COQ729246	Rattus no
110	385.5	9.8	3708	5	AB009075	Lampetra	183	321.5	8.1	2568	10	AB037898	Rattus no
111	384	9.7	2662	10	AF459020	Mus muscu	184	321.5	8.1	3174	10	AB049189	Rattus no
112	382.5	9.7	2507	3	D88205	Halocynthia	185	321	8.1	1386	6	AX149646	Sequence
113	380	9.6	2534	3	AK112393	Ciona int	186	320.5	8.1	2212	9	AK025309	Homo sapi
114	378.5	9.6	2711	10	MACASP	Mesocricetu	187	320.5	8.1	10433	6	AX374896	Sequence
115	376	9.5	1898	10	RN018564	Rattus norv	188	320.5	8.1	10673	6	AX374891	Sequence
116	371.5	9.4	1657	10	RN018566	Rattus norv	189	319.5	8.1	1580	10	AF318182	Mus muscu
117	368	9.3	2249	5	AB042610	Cyprinus	190	319.5	8.1	1603	10	BC013896	Mus muscu
118	365	9.3	208659	2	AC067845	Homo sapi	191	318.5	8.1	3106	6	AX395268	Sequence
119	364	9.2	2830	10	AF459019	Mus muscu	192	318.5	8.1	3106	10	AF042822	Mus muscu
120	364	9.2	2855	10	BC018319	Mus muscu	193	318.5	8.1	3248	10	BC005496	Mus muscu
121	364	9.2	2915	10	BC022123	Mus muscu	194	318	8.1	32808	2	AC111821	Rattus no
122	361.5	9.2	3519	9	AK024951	Homo sapi	195	317.5	8.0	2581	6	164576	Sequence 1
123	361	9.2	4628	5	XLU81290	Cyprinus	196	317.5	8.0	2581	6	AR544611	Sequence
124	357	9.0	2225	5	AY643493	Cyprinus	197	317.5	8.0	3860	4	BTU09859	Bos taurus
125	351	8.9	2647	6	COQ76438	Sequence	198	315.5	8.0	1386	6	AX149643	Sequence
126	351	8.9	2647	6	AX409458	Sequence	199	315.5	8.0	1680	5	BC053182	Danio rer
127	351	8.9	2647	9	HUMC1RS	Human compl	200	315	8.0	1386	6	AX149645	Sequence
128	351	8.9	9378	3	AB089507	Branchios	201	315	8.0	1619	4	OCU77477	Oryctolagus
129	349	8.8	2582	9	HUMC1SAB	Human compl	202	314.5	8.0	2246	5	CHRVAP	Gallus gall
130	345	8.7	2407	5	OMY519930	Oncorhync	203	314	8.0	1386	6	AX149644	Sequence
131	342	8.7	2915	10	BC027183	Mus muscu	204	314	8.0	3173	5	AB042611	Cyprinus
132	340.5	8.6	561	11	G91095	S210P6215RE	205	312.5	7.9	1843	6	AR390799	Sequence
133	340.5	8.6	2908	6	AX401672	Sequence	206	312.5	7.9	1843	6	AX411026	Sequence
134	340.5	8.6	2908	10	D88250	Rattus norv	207	312.5	7.9	1843	9	HSPROTC	Human liver
135	340.5	8.6	2910	10	BC062042	Rattus no	208	312	7.9	1386	6	AX207787	Sequence
136	340.5	8.6	3128	9	AB030036	Homo sapi	209	312	7.9	1386	6	AX212334	Sequence
137	340.5	8.6	3273	9	BC030532	Homo sapi	210	311.5	7.9	2580	6	AX748409	Sequence
138	337.5	8.6	2790	9	BC056903	Homo sapi	211	311.5	7.9	2580	9	AK094009	Homo sapi
139	336.5	8.5	2139	9	BC056902	Homo sapi	212	311	7.9	1341	10	AF532184	Rattus no
140	336.5	8.5	2955	6	BD274670	Matritpas	213	311	7.9	1386	6	AX207785	Sequence
141	336.5	8.5	3120	9	AF133086	Homo sapi	214	311	7.9	1386	6	AX207788	Sequence
142	336.5	8.5	3149	6	BD274671	Matritpas	215	310.5	7.9	1245	6	BD232213	Human pro
143	336.5	8.5	3149	9	AF118224	Homo sapi	216	310.5	7.9	1257	6	CQ821347	Sequence
144	335.5	8.5	2838	6	AX921703	Sequence	217	310.5	7.9	1257	6	AX427736	Sequence
145	335.5	8.5	3147	6	AR081724	Sequence	218	310.5	7.9	1260	6	BD246882	Protein C
146	335.5	8.5	3147	6	AR229704	Sequence	219	310.5	7.9	1260	6	I00579	Sequence 1
147	335.5	8.5	3147	6	AR229712	Sequence	220	310.5	7.9	1260	6	AR404691	Sequence
148	335.5	8.5	3147	6	AR430930	Sequence	221	310.5	7.9	1260	6	AX044041	Sequence
149	335.5	8.5	3147	6	AR430938	Sequence	222	310.5	7.9	1260	6	AX149639	Sequence
150	335.5	8.5	3147	6	AX207897	Sequence	223	310.5	7.9	1260	6	AX207783	Sequence

224	310.5	7.9	1260	6	AX212330	Sequence	AX212330	Sequence	297	290.5	7.4	1260	6	E00961	cdNA encodi
225	310.5	7.9	1383	6	CQ757487	Sequence	CQ757487	Sequence	298	290.5	7.4	1557	6	I00300	Sequence 5
226	310.5	7.9	1383	6	CQ821348	Sequence	CQ821348	Sequence	299	290.5	7.4	1557	6	I09486	Sequence 2
227	310.5	7.9	1383	6	AX427734	Sequence	AX427734	Sequence	300	290.5	7.4	2544	9	BC007231	Homo sapi
228	310.5	7.9	1386	6	AR070468	Sequence	AR070468	Sequence	301	289.5	7.3	1774	6	I00296	Sequence 1
229	310.5	7.9	1386	6	BD246883	Protein C	BD246883	Protein C	302	289.5	7.3	1834	6	I01047	Sequence 1
230	310.5	7.9	1386	6	BD246884	Protein C	BD246884	Protein C	303	289.5	7.3	1834	6	I02179	Sequence 1
231	310.5	7.9	1386	6	E01708	DNA sequenc	E01708	DNA sequenc	304	289.5	7.3	2151	6	A04842	H.sapiens T
232	310.5	7.9	1386	6	I06643	Sequence 1	I06643	Sequence 1	305	289.5	7.3	2151	6	E00654	cdNA encodi
233	310.5	7.9	1386	6	I08112	Sequence 1	I08112	Sequence 1	306	289.5	7.3	2153	6	A11976	Synthetic n
234	310.5	7.9	1386	6	AR044692	Sequence	AR044692	Sequence	307	289.5	7.3	2162	6	AR017909	Sequence
235	310.5	7.9	1386	6	AR044042	Sequence	AR044042	Sequence	308	289.5	7.3	2162	6	AR017931	Sequence 3
236	310.5	7.9	1386	6	AX044043	Sequence	AX044043	Sequence	309	289.5	7.3	2162	6	I18796	Sequence 3
237	310.5	7.9	1386	6	AX149640	Sequence	AX149640	Sequence	310	289.5	7.3	2170	6	E08757	cdNA of tis
238	310.5	7.9	1386	6	AX149641	Sequence	AX149641	Sequence	311	289.5	7.3	2509	6	E02027	Sequence 2
239	310.5	7.9	1386	6	AX149642	Sequence	AX149642	Sequence	312	289.5	7.3	2509	6	AX787057	Sequence
240	310.5	7.9	1386	6	AX207784	Sequence	AX207784	Sequence	313	289.5	7.3	2509	6	HSTPAR	Human fetal
241	310.5	7.9	1386	6	AX212331	Sequence	AX212331	Sequence	314	289.5	7.3	2519	6	A07251	Artificial
242	310.5	7.9	1755	6	AR363767	Sequence	AR363767	Sequence	315	289.5	7.3	2519	6	AX427760	Sequence
243	310.5	7.9	1756	6	CQ730237	Sequence	CQ730237	Sequence	316	289.5	7.3	2519	6	AX427760	Sequence
244	310.5	7.9	1756	6	I05477	Sequence 12	I05477	Sequence 12	317	289.5	7.3	2519	9	HUMPLAT	Human tissu
245	310.5	7.9	1756	6	E01189	cdNA encodi	E01189	cdNA encodi	318	289.5	7.3	2544	6	I09136	Sequence 4
246	310.5	7.9	1792	9	BC034377	Homo sapi	BC034377	Homo sapi	319	289.5	7.3	2544	6	AR353675	Sequence
247	310.5	7.9	1386	6	AR404695	Sequence	AR404695	Sequence	320	289.5	7.3	2546	9	BC013968	Homo sapi
248	310.5	7.9	1386	6	AR404696	Sequence	AR404696	Sequence	321	289.5	7.3	2546	9	BC013968	Homo sapi
249	310.5	7.9	1386	6	AX207786	Sequence	AX207786	Sequence	322	289.5	7.3	2560	6	A01465	H.sapiens c
250	309.5	7.8	1386	6	BD246885	Protein C	BD246885	Protein C	323	289.5	7.3	2672	6	AX207905	Sequence
251	309.5	7.8	1386	6	BD246886	Protein C	BD246886	Protein C	324	289.5	7.3	3104	6	AX207903	Sequence
252	309.5	7.8	1386	6	AX044044	Sequence	AX044044	Sequence	325	289	7.3	7360	6	I26927	Sequence 1
253	309.5	7.8	1386	6	AX044045	Sequence	AX044045	Sequence	326	288.5	7.3	2409	6	AX360098	Sequence
254	309.5	7.8	3142	10	BC205764	Mus muscu	BC205764	Mus muscu	327	288.5	7.3	2475	6	CQ716095	Sequence
255	309.5	7.8	3183	10	AY240929	Mus muscu	AY240929	Mus muscu	328	288.5	7.3	2475	6	CQ716095	Sequence
256	309.5	7.8	3183	10	BC029645	Mus muscu	BC029645	Mus muscu	329	288.5	7.3	3143	6	CQ767701	Sequence
257	309	7.8	1386	6	AR404693	Sequence	AR404693	Sequence	330	288.5	7.3	3143	9	AX358206	Sequence
258	309	7.8	1386	6	AX212332	Sequence	AX212332	Sequence	331	288.5	7.3	3547	6	BD217672	Choline a
259	308.5	7.8	1389	6	E02492	DNA encodin	E02492	DNA encodin	332	288	7.3	1689	6	I06609	Sequence 44
260	308	7.8	1386	6	AR404694	Sequence	AR404694	Sequence	333	288	7.3	2547	6	E01092	cdNA encodi
261	308	7.8	1386	6	AX212333	Sequence	AX212333	Sequence	334	288	7.3	2547	6	E01163	cdNA encodi
262	306	7.8	1383	6	E02246	DNA sequenc	E02246	DNA sequenc	335	288	7.3	2547	6	I07841	Sequence 1
263	305.5	7.7	1671	5	AY040345	Danio rer	AY040345	Danio rer	336	288	7.3	2547	6	I07989	Sequence 1
264	305.5	7.7	5994	6	CQ723917	Sequence	CQ723917	Sequence	337	288	7.3	2547	6	I09622	Sequence 1
265	304	7.7	4215	10	MMU73378	Mus musculu	U73378	Mus musculu	338	288	7.3	2549	6	E01055	DNA encodin
266	303.5	7.7	2409	9	BC002795	Homo sapi	BC002795	Homo sapi	339	287.5	7.3	1366	6	AR474607	Sequence
267	302.5	7.7	1869	10	BC061149	Mus muscu	BC061149	Mus muscu	340	287.5	7.3	1366	9	HUNPRC	Human prote
268	301.5	7.6	1383	6	E01914	DNA encodin	E01914	DNA encodin	341	287.5	7.3	2449	9	HS319876	Homo sapi
269	301.5	7.6	2078	12	AF272773	Synthetic	AF272773	Synthetic	342	287.5	7.3	3194	9	AY055384	Homo sapi
270	300.5	7.6	1850	10	MMU44795	Mus musculu	U44795	Mus musculu	343	287	7.3	1586	6	E01273	DNA encodin
271	300.5	7.6	2219	5	AY631238	Pseudonaj	AY631238	Pseudonaj	344	287	7.3	2294	5	BC056804	Danio rer
272	300.5	7.6	2459	6	E01466	DNA encodin	E01466	DNA encodin	345	287	7.3	2359	9	HUMTPARN	Homo sapien
273	300.5	7.6	2459	9	HSTPAL	Human mRNA	X02901	Human mRNA	346	287	7.3	2582	3	AK116731	Ciona int
274	299.5	7.6	2231	5	AY631239	Pseudonaj	AY631239	Pseudonaj	347	287	7.3	7533	6	E01324	Recombinant
275	299	7.6	3645	10	AY251285	Rattus no	AY251285	Rattus no	348	286	7.2	1689	6	A14927	tPA-DNA fro
276	298.5	7.6	2466	5	BC061654	Xenopus l	BC061654	Xenopus l	349	286	7.2	1689	6	A14930	tPA-DNA fro
277	297.5	7.5	1428	5	AF465276	Takifugu	AF465276	Takifugu	350	286	7.2	1689	6	A34204	Human t-PA
278	297	7.5	1514	4	AF191307	Sus scrof	AF191307	Sus scrof	351	286	7.2	1689	6	A34205	Human t-PA
279	297	7.5	2459	6	E00880	DNA encodin	E00880	DNA encodin	352	286	7.2	1689	6	E01665	cdNA encodi
280	296.5	7.5	1387	4	AC364387	Sequence	AR364387	Sequence	353	286	7.2	1689	6	E02663	DNA encodin
281	296	7.5	1558	4	OCU49933	Oryctolagus	U49933	Oryctolagus	354	286	7.2	1689	6	I08637	Sequence 1
282	296	7.5	65326	2	AC124815	Mus muscu	AC124815	Mus muscu	355	286	7.2	1689	6	I08789	Sequence 3
283	295.5	7.5	1326	5	AF465273	Takifugu	AF465273	Takifugu	356	286	7.2	1689	6	AX427761	Sequence
284	295.5	7.5	1537	4	BTCFX1	Bovine mRNA	X00673	Bovine mRNA	357	286	7.2	1689	9	BT007060	Homo sapi
285	295.5	7.5	1554	6	A73583	Sequence 1	A73583	Sequence 1	358	286	7.2	1689	12	BT007513	Synthetic c
286	295.5	7.5	1554	6	AR001423	Sequence	AR001423	Sequence	359	286	7.2	1738	6	AR363266	Sequence
287	295	7.5	1278	5	AF465268	Gallus ga	AF465268	Gallus ga	360	286	7.2	1955	6	AR086682	Sequence
288	294.5	7.5	1543	6	AX401899	Sequence	AX401899	Sequence	361	286	7.2	1974	6	A07195	Artificial
289	294.5	7.5	1543	10	RMPROC	Rattus norv	X64336	Rattus norv	362	286	7.2	1974	6	A27425	DNA sequenc
290	294	7.5	1535	10	BC078879	Rattus no	BC078879	Rattus no	363	286	7.2	1974	6	AR059984	Sequence
291	293	7.4	1293	5	AF465275	Takifugu	AF465275	Takifugu	364	286	7.2	1989	6	I01256	Sequence 2
292	293	7.4	1689	6	E02664	DNA encodin	E02664	DNA encodin	365	286	7.2	2100	6	A07197	H.sapiens m
293	293	7.4	1738	6	I08077	Sequence 1	I08077	Sequence 1	366	286	7.2	2100	6	A27429	cdNA sequen
294	292	7.4	2550	6	I08531	Sequence 2	I08531	Sequence 2	367	286	7.2	2100	6	E01934	DNA encodin
295	291.5	7.4	1193	4	AY349421	Sus scrof	AY349421	Sus scrof	368	286	7.2	2101	6	AR059986	Sequence
296	291	7.4	1738	6	I06376	Sequence 37	I06376	Sequence 37	369	286	7.2	2310	6	A03776	H.sapiens m

370	286	7.2	2434	6	E02025	E02025 DNA sequenc	443	279	7.1	1689	6	E01666	E01666 cDNA encodi
371	286	7.2	2457	6	E00896	E00896 cDNA encodi	444	279	7.1	2460	4	AF364605	AF364605 Sus scrofa
372	286	7.2	2457	6	E01221	E01221 cDNA human	445	279	7.1	2913	6	AX360086	AX360086 Sequence
373	286	7.2	2457	6	AR364602	AR364602 Sequence	446	279	7.1	3522	6	CQ819022	CQ819022 Sequence
374	286	7.2	2460	6	I09411	I09411 Sequence 1	447	278.5	7.1	877	6	AX704801	AX704801 Sequence
375	286	7.2	2461	9	HUMUPAA	M18182 Human plasm	448	278.5	7.1	1221	6	E62998	E62998 Hemocoagula
376	286	7.2	2482	6	E06629	E06629 DNA encodin	449	278.5	7.1	1440	6	AR112953	AR112953 Sequence
377	286	7.2	2544	6	I08530	I08530 Sequence 1	450	278.5	7.1	1440	6	AR112969	AR112969 Sequence
378	286	7.2	7533	6	I08638	I08638 Sequence 2	451	278.5	7.1	1440	6	BD194674	BD194674 Tissue fa
379	285.5	7.2	1874	6	I01184	I01184 Sequence 1	452	278.5	7.1	1440	6	I19358	I19358 Sequence 3
380	285.5	7.2	2869	4	DOGFIX	M21757 Canis famil	453	278.5	7.1	1440	6	I19360	I19360 Sequence 3
381	285.5	7.2	3080	4	DOCFIXA	M33826 Canine bloo	454	278.5	7.1	1491	10	MMCOAGULX	AJ222677 Mus muscu
382	285	7.2	1689	6	E02448	E02448 DNA encodin	455	278.5	7.1	2236	4	VMPBAA2A	M63988 Desmodus ro
383	285	7.2	1689	9	AY221101	AY221101 Homo sapi	456	278.5	7.1	2257	6	A07244	A07244 Artificial
384	284.5	7.2	1800	6	E04506	E04506 DNA encodin	457	278.5	7.1	2459	6	CQ723338	CQ723338 Sequence
385	284.5	7.2	1800	6	E05896	E05896 DNA sequenc	458	278.5	7.1	2462	6	AR095304	AR095304 Sequence
386	284.5	7.2	2512	6	A19618	A19618 Mammalian c	459	278.5	7.1	2462	6	AR103988	AR103988 Sequence
387	284.5	7.2	2520	10	BC061508	BC061508 Mus muscu	460	278.5	7.1	2462	6	AX335083	AX335083 Sequence
388	284.5	7.2	2542	10	BC057967	BC057967 Mus muscu	461	278.5	7.1	2462	6	AX409604	AX409604 Sequence
389	284.5	7.2	2585	10	BC061565	BC061565 Rattus no	462	278.5	7.1	2462	9	HUMFVII	M13232 Human facto
390	284.5	7.2	4864	10	AB013874	AB013874 Mus muscu	463	278.5	7.1	2483	6	E01076	E01076 cDNA sequen
391	284	7.2	1598	6	I08550	I08550 Sequence 1	464	278.5	7.1	2483	6	I07990	I07990 Sequence 3
392	284	7.2	2537	5	BC073613	BC073613 Xenopus l	465	278.5	7.1	2691	9	CR456446	CR456446 Homo sapi
393	284	7.2	3028	5	AB070367	AB070367 Bufo japo	466	278	7.0	1302	5	AF465270	AF465270 Gallus ga
394	283.5	7.2	1486	10	AF087644	AF087644 Mus muscu	467	278	7.0	1467	6	CQ723339	CQ723339 Sequence
395	283.5	7.2	1497	10	RNFXRAT	X79807 R.norvegicu	468	278	7.0	1507	6	AX774765	AX774765 Sequence
396	283.5	7.2	1500	4	AF003200	AF003200 Oryctolag	469	278	7.0	1517	9	HUMFACX	M57285 Human coagu
397	283.5	7.2	1925	10	BC003877	BC003877 Mus muscu	470	278	7.0	1517	9	AY318867	AY318867 Homo sapi
398	283.5	7.2	2519	6	AX305289	AX305289 Sequence	471	278	7.0	1541	9	BC046125	BC046125 Homo sapi
399	283.5	7.2	2519	10	MUSTPA	J03520 Mouse tisseu	472	278	7.0	1569	6	CQ614289	CQ614289 Sequence
400	283	7.2	1630	6	E00994	E00994 cDNA encodi	473	278	7.0	1573	9	BC040125	BC040125 Homo sapi
401	283	7.2	1689	6	I06614	I06614 Sequence 46	474	278	7.0	1707	3	AX071128	AX071128 Drosophil
402	283	7.2	1780	6	A06611	A06611 Synthetic n	475	278	7.0	1836	6	E01176	E01176 DNA encodin
403	283	7.2	1780	6	A10226	A10226 Synthetic D	476	278	7.0	1836	6	I01581	I01581 Sequence 1
404	282	7.1	1373	4	BOVPBC	K02435 Bovine prot	477	278	7.0	1981	6	I01583	I01583 Sequence 1
405	282	7.1	1599	4	AF275654	AF275654 Ornithorh	478	278	7.0	2009	6	E01177	E01177 DNA encodin
406	281.5	7.1	901	6	BD209910	BD209910 Human nuc	479	277	7.0	1327	6	CQ767703	CQ767703 Sequence
407	281.5	7.1	901	6	AX014224	AX014224 Sequence	480	277	7.0	1327	6	AX538208	AX538208 Sequence
408	281.5	7.1	1221	6	E63000	E63000 Hemocoagula	481	277	7.0	1338	6	CQ798455	CQ798455 Sequence
409	281.5	7.1	1838	5	BC074475	BC074475 Xenopus l	482	277	7.0	1338	6	CQ880376	CQ880376 Sequence
410	281.5	7.1	2172	10	AB177406	AB177406 Rattus no	483	277	7.0	1338	6	AX211659	AX211659 Sequence
411	281.5	7.1	2190	10	AK128915	AK128915 Mus muscu	484	277	7.0	1338	6	AX951866	AX951866 Sequence
412	281.5	7.1	2445	10	RATPATISS	M23697 Rat tissue-	485	277	7.0	1357	6	CQ880378	CQ880378 Sequence
413	281	7.1	1443	9	HUMFPM	K03194 Human facto	486	277	7.0	1357	6	AX211661	AX211661 Sequence
414	281	7.1	1467	6	A86859	A86859 Sequence 43	487	276.5	7.0	1620	6	I08184	I08184 Sequence 4
415	281	7.1	1467	6	A86886	A86886 Sequence 26	488	276.5	7.0	1725	4	VMPPTA	J05082 Vampire bat
416	281	7.1	1467	6	AR316969	AR316969 Sequence	489	276.5	7.0	1727	6	AR363981	AR363981 Sequence
417	281	7.1	1467	6	AR340866	AR340866 Sequence	490	276.5	7.0	2033	6	E07591	E07591 DNA encodin
418	281	7.1	1467	6	AX082959	AX082959 Sequence	491	276.5	7.0	2033	6	I15469	I15469 Sequence 14
419	281	7.1	1467	6	BD070392	BD070392 Factor X-	492	276.5	7.0	2033	6	I69315	I69315 Sequence 14
420	281	7.1	1467	6	BD070435	BD070435 Factor X	493	276.5	7.0	2036	6	AX333070	AX333070 Sequence
421	281	7.1	1605	6	AR363979	AR363979 Sequence	494	276.5	7.0	2036	6	AX408965	AX408965 Sequence
422	281	7.1	2130	4	VMPBAP	M63989 Desmodus ro	495	276.5	7.0	2036	9	HUMHGFAP	D14012 Homo sapien
423	281	7.1	2137	6	A07246	A07246 Artificial	496	276.5	7.0	2040	6	CQ768744	CQ768744 Sequence
424	280.5	7.1	922	9	BC063475	BC063475 Homo sapi	497	276.5	7.0	2040	6	AF272774	AF272774 Homo sapi
425	280.5	7.1	928	9	BC039716	BC039716 Homo sapi	498	276.5	7.0	7427	6	CQ768745	CQ768745 Sequence
426	280.5	7.1	1169	6	CQ723499	CQ723499 Sequence	499	276.5	7.0	1505	6	AX523898	AX523898 Sequence
427	280.5	7.1	1184	6	AX337830	AX337830 Sequence	500	276	7.0	2119	10	BC031775	BC031775 Mus muscu
428	280.5	7.1	1184	6	AX774731	AX774731 Sequence	501	275.5	7.0	889	5	AX935351	AX935351 Gallus ga
429	280.5	7.1	1184	9	HSCHVPRO	X71877 H.sapiens m	502	275.5	7.0	899	5	AX935315	AX935315 Gallus ga
430	280.5	7.1	2438	6	I07991	I07991 Sequence 6	503	275.5	7.0	899	5	AX936273	AX936273 Gallus ga
431	280.5	7.1	2747	10	BC057186	BC057186 Mus muscu	504	275.5	7.0	911	5	AX933638	AX933638 Gallus ga
432	280.5	7.1	2771	10	BC014773	BC014773 Mus muscu	505	275.5	7.0	937	5	CR352633	CR352633 Gallus ga
433	280.5	7.1	5996	9	HSMB06659	BS641029 Homo sapi	506	275.5	7.0	1221	6	E62997	E62997 Hemocoagula
434	280.5	7.1	10774	9	AB067481	AB067481 Homo sapi	507	275.5	7.0	1646	5	AF515271	AF515271 Danio rer
435	280	7.1	1605	12	SYNHUMTPAA	M26666 Synthetic h	508	275.5	7.0	2177	6	E01075	E01075 cDNA sequen
436	280	7.1	1689	6	E01667	E01667 cDNA encodi	509	275.5	7.0	2230	4	AB022425	AB022425 Sus scrof
437	279.5	7.1	2106	6	CQ768741	CQ768741 Sequence	510	275.5	7.0	2402	4	BTTPA	X85800 B.taurus mr
438	279.5	7.1	2540	10	BC011256	BC011256 Mus muscu	511	275.5	7.0	2422	6	AR030786	AR030786 Sequence
439	279.5	7.1	2604	6	I05002	I05002 Sequence 4	512	275.5	7.0	2422	6	AR045090	AR045090 Sequence
440	279.5	7.1	7493	6	CQ768742	CQ768742 Sequence	513	275.5	7.0	2422	6	AR052946	AR052946 Sequence
441	279	7.1	889	5	AX933670	AX933670 Gallus ga	514	275.5	7.0	2422	6	AR122899	AR122899 Sequence
442	279	7.1	1206	6	E63002	E63002 Hemocoagula	515	275.5	7.0	2422	6	AR127821	AR127821 Sequence

516	275.5	7.0	2720	10	MUSPLGN	J04766 Mouse plasma	589	267.5	6.8	1404	6	A93124	A93124 Sequence 15
517	275.5	7.0	4436	6	AX249945	AX249945 Sequence	590	267.5	6.8	1414	9	HUMCFX	M22613 Human blood
518	275.5	7.0	6098	6	AX565990	AX565990 Sequence	591	267	6.8	835	5	AX931595	AX931595 Human blood
519	275	7.0	1683	6	BD177602	BD177602 Detection	592	267	6.8	841	5	AX931604	AX931604 Gallus ga
520	275	7.0	1683	6	BD177603	BD177603 Detection	593	267	6.8	841	5	AX931627	AX931627 Gallus ga
521	275	7.0	1683	6	AX383954	AX383954 Sequence	594	267	6.8	841	5	AX935230	AX935230 Gallus ga
522	275	7.0	1683	6	AX383955	AX383955 Sequence	595	267	6.8	842	5	AX931598	AX931598 Gallus ga
523	275	7.0	2005	4	BOVTHBNM	J00041 Bovine prot	596	267	6.8	844	5	AX933624	AX933624 Gallus ga
524	275	7.0	2251	9	BC031412	BC031412 Homo sapi	597	267	6.8	1027	10	RNO18565	Y18565 Rattus Norv
525	275	7.0	2408	9	S83182	S83182 hyaluronan-	598	267	6.8	1389	6	AX431491	AX431491 Sequence
526	275	7.0	3008	6	AX409021	AX409021 Sequence	599	267	6.8	1437	6	AR095305	AR095305 Sequence
527	275	7.0	3008	6	HUMGEFAL	D49742 Human mRNA	600	267	6.8	1437	6	AR103989	AR103989 Sequence
528	274.5	7.0	1911	6	A08501	A08501 Artificial	601	267	6.8	1437	9	HUMFIX	J00136 Human facto
529	274.5	7.0	2060	4	AY532633	AY532633 Canis fam	602	267	6.8	1437	5	BC054968	BC054968 Xenopus l
530	274.5	7.0	2200	3	AK112434	AK112434 Ciona int	603	266.5	6.8	1749	5	LCRCFB	D13568 Lampetra ja
531	274.5	7.0	3943	3	AY831414	AY831414 Ciona int	604	266	6.7	1473	6	E02114	E02114 cDNA sequen
532	274.5	7.0	12486	9	AB210419	AB210419 Homo sapi	605	266	6.7	1473	6	E08289	E08289 Synthetic D
533	274.5	7.0	13040	9	AB114605	AB114605 Homo sapi	606	266	6.7	2561	4	AY029518	AY029518 Oryctolag
534	274.5	7.0	13148	9	AB114604	AB114604 Homo sapi	607	266	6.7	4933	5	BC082854	BC082854 Xenopus l
535	274	6.9	1500	9	BC015525	BC015525 Homo sapi	608	265.5	6.7	753	6	CQ596802	CQ596802 Sequence
536	274	6.9	1503	9	AY318869	AY318869 Homo sapi	609	265.5	6.7	1359	6	AX451990	AX451990 Sequence
537	274	6.9	1839	5	AF465278	AF465278 Takifugu	610	265.5	6.7	3094	6	BD242873	BD242873 Secreted
538	274	6.9	4276	6	AX249946	AX249946 Sequence	611	265.5	6.7	3118	6	AX250079	AX250079 Sequence
539	273.5	6.9	1722	5	AF515269	AF515269 Danio rer	612	265.5	6.7	3345	9	AF178985	AF178985 Homo sapi
540	273	6.9	929	9	AY318870	AY318870 Homo sapi	613	285	6.7	2078	5	U75331	U75331 Gallus gall
541	273	6.9	1112	10	RNO18571	Y18571 Rattus Norv	614	285	6.7	3689	5	XLH81291	XLH81291 Sequence
542	273	6.9	1206	6	E63001	E63001 Hemococculu	615	265	6.7	5532	6	AR105803	AR105803 Sequence
543	273	6.9	9120	10	AK122567	AK122567 Mus muscu	616	264.5	6.7	1236	6	E02710	E02710 Human prour
544	272.5	6.9	1533	9	MPFIX	X65473 M.fascicula	617	264.5	6.7	1236	6	E02710	E02710 DNA sequenc
545	271.5	6.9	732	6	I95869	I95869 Sequence 2	618	264.5	6.7	1393	6	CQ722424	CQ722424 Sequence
546	271.5	6.9	735	9	BT006852	BT006852 Homo sapi	619	264.5	6.7	1981	6	I01586	I01586 Sequence 6
547	271.5	6.9	735	12	BT008102	BT008102 Synthetic	620	264.5	6.7	1998	10	BC013662	BC013662 Mus muscu
548	271.5	6.9	1221	6	E62999	E62999 Hemococculu	621	264.5	6.7	2010	6	E01178	E01178 DNA encodin
549	271.5	6.9	1419	9	D78203	D78203 Homo sapien	622	264.5	6.7	2031	10	WMPTHROM	X52308 Mouse mRNA
550	271.5	6.9	1438	6	E13202	E13202 Human gene	623	264.5	6.7	256455	2	AC129138	AC129138 Rattus no
551	271.5	6.9	1451	6	CQ874887	CQ874887 Sequence	624	264	6.7	2035	10	AF099017	AF099017 Mus muscu
552	271.5	6.9	1451	6	CQ874963	CQ874963 Sequence	625	284	6.7	2063	10	AF224724	AF224724 Mus muscu
553	271.5	6.9	1451	9	AF013988	AF013988 Homo sapi	626	264	6.7	2300	6	BC055574	BC055574 Synthetic H
554	271.5	6.9	1506	6	CQ720601	CQ720601 Sequence	627	263.5	6.7	875	5	BC055574	BC055574 Danio rer
555	271.5	6.9	1506	6	CQ874889	CQ874889 Sequence	628	263.5	6.7	1398	10	AF456428	AF456428 Mus muscu
556	271.5	6.9	1506	6	CQ874965	CQ874965 Sequence	629	263.5	6.7	1667	6	AX250017	AX250017 Sequence
557	271.5	6.9	1506	6	AX329982	AX329982 Sequence	630	263.5	6.7	1891	6	AX250019	AX250019 Sequence
558	271.5	6.9	1506	6	AX326503	AX326503 Sequence	631	263.5	6.7	1726	10	BC070472	BC070472 Mus muscu
559	271.5	6.9	1506	6	AX951756	AX951756 Sequence	632	263	6.7	1296	6	BD183647	BD183647 Anti-HIV
560	271.5	6.9	1506	6	AX960034	AX960034 Sequence	633	263	6.7	1296	6	E02577	E02577 DNA encodin
561	271.5	6.9	1506	6	HSU62801	U62801 Human prote	634	263	6.7	1296	6	E02647	E02647 DNA sequenc
562	271	6.9	1443	6	E02473	E02473 DNA encodin	635	263	6.7	1296	6	E02649	E02649 DNA sequenc
563	271	6.9	1443	6	E08290	E08290 Synthetic D	636	263	6.7	1296	6	E02711	E02711 DNA sequenc
564	271	6.9	1549	4	AY122285	AY122285 Oryctolag	637	263	6.7	1296	6	E06064	E06064 DNA encodin
565	271	6.9	1689	6	E02360	E02360 DNA sequenc	638	263	6.7	1296	6	AX512750	AX512750 Sequence
566	271	6.9	2350	4	AY029517	AY029517 Oryctolag	639	263	6.7	1296	9	BT007391	BT007391 Homo sapi
567	271	6.9	2358	4	AB087224	AB087224 Oryctolag	640	263	6.7	1394	12	AY335599	AY335599 Synthetic
568	271	6.9	3016	3	AK116923	AK116923 Ciona int	641	263	6.7	1394	6	E00421	E00421 cDNA coding
569	270.5	6.9	2803	3	AB030007	AB030007 Polyandro	642	263	6.7	1474	6	E00924	E00924 cDNA encodi
570	270	6.8	200	6	AX395273	AX395273 Sequence	643	263	6.7	1474	6	E01238	E01238 cDNA encodi
571	270	6.8	1605	6	I06014	I06014 Sequence 6	644	263	6.7	1474	6	E01559	E01559 cDNA sequen
572	270	6.8	2245	4	MPFAA1A	M63987 Desmodus ro	645	263	6.7	1474	6	E01580	E01580 cDNA encodi
573	270	6.8	2252	6	A07242	A07242 Artificial	646	263	6.7	1474	6	E02095	E02095 DNA sequenc
574	270	6.8	2252	4	A07250	A07250 Artificial	647	263	6.7	1475	6	BD226054	BD226054 Compound
575	270	6.8	2266	4	MPFAA1S	M63986 Desmodus ro	648	263	6.7	1475	6	BD275725	BD275725 COMPOUNDS
576	269.5	6.8	3610	5	BC071077	BC071077 Xenopus l	649	263	6.7	1475	6	E01560	E01560 cDNA sequen
577	269	6.8	795	5	BX931589	BX931589 Gallus ga	650	263	6.7	1475	6	AR220510	AR220510 Sequence
578	269	6.8	1032	6	CQ578484	CQ578484 Sequence	651	263	6.7	1475	6	AR255504	AR255504 Sequence
579	269	6.8	1186	3	AB020543	AB020543 Haemaphys	652	263	6.7	1475	6	AR281074	AR281074 Sequence
580	269	6.8	1209	6	BD001742	BD001742 Tick vacc	653	263	6.7	1475	6	AR437865	AR437865 Sequence
581	269	6.8	1589	5	BC076035	BC076035 Danio rer	654	263	6.7	1475	6	AR476401	AR476401 Sequence
582	269	6.8	2310	6	A03777	A03777 H.sapiens m	655	263	6.7	1475	6	AR486592	AR486592 Sequence
583	269	6.8	2737	10	RNO242649	AJ72649 Rattus no	656	263	6.7	1475	6	AR541095	AR541095 Sequence
584	269	6.8	3136	3	AF059284	AF059284 Strongylo	657	263	6.7	1475	9	HUMUKM1	AX365729 Sequence
585	268	6.8	1689	6	A04051	A04051 H.sapiens t	658	263	6.7	1475	9	HUMUKM1	K03226 Human prepr
586	268	6.8	4464	9	HOSA18286	Y18286 Homo sapien	659	263	6.7	1500	6	A10915	A10915 Artificial
587	268	6.8	4465	9	HOSA18287	Y18287 Homo sapien	660	263	6.7	1500	6	A10916	A10916 Artificial
588	267.5	6.8	974	5	BC072795	BC072795 Xenopus l	661	263	6.7	1964	6	A18397	A18397 Human uPA c

662	263	6.7	1964	6	AX402384 Sequence	735	259.5	6.6	2375	4	SSUPAR	X02724 Porcine mRN
663	263	6.7	1964	6	AX451989 Sequence	736	259.5	6.6	16984	3	AGTRY1C	222930 A.Gambiae A
664	263	6.7	2067	10	BC019376 Sequence	737	259	6.6	1575	6	E01670	E01670 CDNA encodi
665	263	6.7	2293	6	A11978	738	259	6.6	1746	3	AF149789	AF149789 Strongylo
666	263	6.7	2294	6	A09202 Artificial	739	259	6.6	2304	5	BC084671	BC084671 Xenopus l
667	263	6.7	2294	6	BD226055 Compound	740	258.5	6.6	1236	6	E02493	E02493 CDNA encodi
668	263	6.7	2294	6	BD275726 COMPOUNDS	741	258.5	6.6	1236	6	E02832	E02832 DNA encodin
669	263	6.7	2294	6	AR220511 Sequence	742	258.5	6.6	1236	6	E02833	E02833 DNA encodin
670	263	6.7	2294	6	AR255505 Sequence	743	258.5	6.6	1236	6	E03359	E03359 CDNA encodi
671	263	6.7	2294	6	AR281075 Sequence	744	258.5	6.6	1236	6	AR380382	AR380382 Sequence
672	263	6.7	2294	6	AR281075 Sequence	745	258.5	6.6	1236	9	HUMUPAB	D11143 Human RNA f
673	263	6.7	2294	6	AR380672 Sequence	746	258.5	6.6	1455	6	E03404	E03404 DNA encodin
674	263	6.7	2294	6	AR437866 Sequence	747	258.5	6.6	1455	6	E03405	E03405 DNA encodin
675	263	6.7	2294	6	AR476402 Sequence	748	258.5	6.6	1548	6	AR008972	AR008972 Sequence
676	263	6.7	2294	6	AR486593 Sequence	749	258.5	6.6	1548	6	I24420	I24420 Sequence 15
677	263	6.7	2294	6	AR541096 Sequence	750	258.5	6.6	2594	3	AY119618	AY119618 Drosophil
678	263	6.7	2294	6	AX365730 Sequence	751	258.5	6.6	3736	6	CQ612939	CQ612939 Sequence
679	263	6.7	2294	11	D00244 Homo sapien	752	258.5	6.6	3749	3	DROSTURBLE	L11451 Drosophila
680	263	6.7	2294	6	G27040 SHGC-31374	753	258	6.5	869	9	GM0242521	AJ242521 Gadus mor
681	263	6.7	2296	6	A35395 H.sapiens u	754	258	6.5	1597	9	PCUOKIN	X51935 Papio cynoc
682	263	6.7	2299	6	CQ718477 Sequence	755	257.5	6.5	1236	6	E04897	E04897 gDNA encodi
683	263	6.7	2300	6	A21571 pro-Urokina	756	257.5	6.5	1236	6	E05128	E05128 DNA sequenc
684	263	6.7	2301	6	E01467	757	257.5	6.5	139312	5	EX571739	EX571739 Zebrafish
685	263	6.7	2303	6	I07013 Sequence 4	758	257	6.5	2413	3	AY118964	AY118964 Drosophil
686	263	6.7	2304	6	I08092 Sequence 1	759	256.5	6.5	898	10	AB016228	AB016228 Mus muscu
687	263	6.7	2304	6	E00178 CDNA encodi	760	256.5	6.5	156011	6	I56011	I56011 Sequence 2
688	263	6.7	2304	6	I03932 Sequence 6	761	256.5	6.5	1335	12	ASHPAAB	X54317 Synthetic g
689	263	6.7	2304	9	I04632 Sequence 1	762	256.5	6.5	1335	12	ASHPAAB	BC009305 Homo sapi
690	263	6.7	2333	3	M15476 Human pro-u	763	256.5	6.5	2717	9	BC009305	BC002593 Homo sapi
691	262.5	6.7	1389	6	BC013575 Homo sapi	764	256.5	6.5	2738	9	BC002593	BC032105 Homo sapi
692	262.5	6.7	1389	6	AF486486 Aurelia a	765	255.5	6.5	2740	9	BC032105	BC005385 Homo sapi
693	262.5	6.7	1389	6	A07407 H.sapiens D	766	255.5	6.5	915	5	BC005385	BC080976 Xenopus t
694	262.5	6.7	1389	6	A93125 Sequence 16	767	255.5	6.5	967	5	BC080976	BC02708 DNA sequenc
695	262.5	6.7	1413	9	AR365693 Sequence	768	255	6.5	1236	6	E02708	AB002407 Sarcophag
696	262.5	6.7	1533	9	AX379343 Sequence	769	255	6.5	1244	3	AB002407	I08788 Sequence 1
697	262.5	6.7	1548	6	X65472 P.trogodyt	770	255	6.5	1296	6	I08788	X02760 Human mRNA
698	262.5	6.7	1610	6	AR009140 Sequence	771	255	6.5	1340	5	BC077104	BC077104 Danio rer
699	262.5	6.7	1610	6	AR202300 Sequence	772	255	6.5	2610	5	BC077104	U50330 Human proco
700	262.5	6.7	1639	6	A01819	773	255	6.5	3546	9	U50330	AX577979 Sequence
701	262.5	6.7	1639	6	A13997 H.sapiens m	774	255	6.5	3552	6	AX393311	AX393311 Sequence
702	262.5	6.7	1639	6	A14017 H.sapiens m	775	254.5	6.5	3557	6	AX393311	AF465269 Gallus ga
703	262.5	6.7	1639	9	HUMFIXA	776	254.5	6.5	1416	5	AF465269	AF465269 Gallus ga
704	262.5	6.7	1823	5	BC060330	777	254.5	6.5	1467	5	E03403	E03403 DNA encodin
705	262.5	6.7	2038	6	CQ718548 Sequence	778	254	6.5	3311	5	BC059801	BC059801 Danio rer
706	262.5	6.7	2075	6	AR178034 Sequence	779	254	6.4	714	6	AX763031	AX763031 Sequence
707	262.5	6.7	2775	6	CQ714145 Sequence	780	254	6.4	1372	6	AR363528	AR363528 Sequence
708	262.5	6.7	2775	9	HUMCIX	781	254	6.4	2045	10	RNPROTH	X52835 Rattus norv
709	262.5	6.7	2775	11	G28615 human STS S	782	254	6.4	2249	6	A07209	A07209 Artificial
710	262.5	6.7	2781	6	HSPACIXM	783	254	6.4	3405	6	CQ859271	CQ859271 Sequence
711	262.5	6.7	2802	6	A47227 Sequence 1	784	254	6.4	167208	2	AC034190	AC034190 Homo sapi
712	262.5	6.7	2804	6	CQ882048 Sequence	785	253.5	6.4	937	5	EX935330	EX935330 Gallus ga
713	262.5	6.7	2804	6	AR452580 Sequence	786	253.5	6.4	946	5	EX935330	EX935330 Gallus ga
714	262.5	6.7	2804	6	BD217671 Choline a	787	253.5	6.4	947	5	EX935330	EX935330 Gallus ga
715	262.5	6.7	4933	6	AX207957 Sequence	788	253.5	6.4	947	5	EX935332	EX935332 Gallus ga
716	262.5	6.7	4933	6	AF133845	789	253.5	6.4	948	5	EX935360	EX935360 Gallus ga
717	262.5	6.7	5753	6	BD270196 Complex o	790	253.5	6.4	948	5	EX935221	EX935221 Gallus ga
718	262.5	6.7	5753	6	CQ871378 Sequence	791	253.5	6.4	950	5	EX933671	EX933671 Gallus ga
719	262.5	6.7	5753	6	AX033474 Sequence	792	253.5	6.4	951	5	EX933648	EX933648 Gallus ga
720	262.5	6.7	5753	6	AX253513 Sequence	793	253.5	6.4	957	5	EX933648	EX933648 Gallus ga
721	262.5	6.7	5905	6	BD270207 Complex o	794	253.5	6.4	962	5	CR338996	CR338996 Gallus ga
722	262.5	6.7	5905	6	AX033486 Sequence	795	253.5	6.4	969	5	EX933689	EX933689 Gallus ga
723	262.5	6.7	6052	6	BD270208 Complex o	796	253.5	6.4	975	5	EX933686	EX933686 Gallus ga
724	262.5	6.7	6052	6	AX033487 Sequence	797	253.5	6.4	976	5	EX9336261	EX9336261 Gallus ga
725	262	6.6	1316	6	A20747 Artificial	798	253.5	6.4	983	5	EX935254	EX935254 Gallus ga
726	262	6.6	3858	6	AB078908 Sequence	799	253.5	6.4	2006	5	BC073504	BC073504 Xenopus l
727	261.5	6.6	1236	6	E02578 DNA encodin	800	253.5	6.4	2487	6	I78454	I78454 Sequence 1
728	261	6.6	2228	4	BTUPA	801	253.5	6.4	2487	6	I78454	M22488 Human bone
729	261	6.6	2355	4	BOVUKPA	802	253.5	6.4	2500	6	I08629	I08629 Sequence 30
730	260.5	6.6	798	10	AB020757 Rattus no	803	253.5	6.4	3289	9	AB067477	AB067477 Homo sapi
731	260.5	6.6	1680	6	I06432 Sequence 42	804	253.5	6.4	3715	9	AY358174	AY358174 Homo sapi
732	260.5	6.6	2387	6	AX743686 Sequence	805	253.5	6.4	4161	3	ACU57369	U57369 Aplysia cal
733	260	6.6	1607	6	CQ729780 Sequence	806	253.5	6.4	173534	2	AC007920	AC007920 Homo sapi
734	259.5	6.6	1236	6	E02709 DNA sequenc	807	253.5	6.4	207841	2	AC072019	AC072019 Homo sapi

808	253	6.4	1680	6	I06422	106422 Sequence 40	881	248	6.3	2902	10	BC063079	BC063079 Mus muscu
809	253	6.4	2055	4	AB022426	AB022426 Sus scrofa	882	248	6.3	3705	10	BC066062	BC066062 Mus muscu
810	253	6.4	2697	10	MUSFIX	M23109 Mouse coagu	883	247.5	6.3	749	6	CQ592056	CQ592056 Sequence
811	253	6.4	4140	6	CQ575613	CQ575613 Sequence	884	247.5	6.3	937	5	AX933662	AX933662 Gallus ga
812	252.5	6.4	1419	6	A27725	A27725 DNA sequenc	885	247.5	6.3	954	5	AX935323	AX935323 Gallus ga
813	252.5	6.4	1419	6	E01944	E01944 Synthetic D	886	247.5	6.3	957	5	CR338993	CR338993 Gallus ga
814	252.5	6.4	1440	6	E01668	E01668 cDNA encodi	887	247.5	6.3	969	5	AX933653	AX933653 Gallus ga
815	252	6.4	881	5	BC081638	BC081638 Danio rer	888	247.5	6.3	1323	10	BC055854	BC055854 Mus muscu
816	252	6.4	947	5	BC064277	BC064277 Xenopus t	889	247.5	6.3	1494	6	AX814647	AX814647 Sequence
817	252	6.4	1506	6	E02247	E02247 cDNA sequen	890	247.5	6.3	1787	6	BD139221	BD139221 Soluble i
818	252	6.4	2099	6	A07207	A07207 Artificial	891	247.5	6.3	1810	9	AF280546	AF280546 Homo sapi
819	252	6.4	2901	5	BC076742	BC076742 Xenopus l	892	247.5	6.3	2976	10	MUSEBPIA	L24755 Mus musculu
820	251.5	6.4	959	5	EX931608	EX931608 Gallus ga	893	247	6.3	826	4	RAETHRO	M81396 Oryctolagus
821	251.5	6.4	3180	9	HS488946	AJ488946 Homo sapi	894	247	6.3	995	4	DOGCTRPA	M24664 Dog mast ce
822	251.5	6.4	3387	6	AX360082	AX360082 Sequence	895	247	6.3	1095	6	CQ600633	CQ600633 Sequence
823	251.5	6.4	3711	6	AX786888	AX786888 Sequence	896	247	6.3	2804	6	CQ592055	CQ592055 Sequence
824	251	6.4	888	10	AY149996	AY149996 Rattus no	897	247	6.3	3095	6	CQ600632	CQ600632 Sequence
825	251	6.4	1614	5	AF465277	AF465277 Takifugu	898	247	6.3	3146	6	AX685997	AX685997 Sequence
826	251	6.4	2152	6	AR379612	AR379612 Sequence	899	247	6.3	4674	6	CQ590238	CQ590238 Sequence
827	250.5	6.3	1243	4	AF372520	AF372520 Oryctolag	900	247	6.3	6119	3	AY075422	AY075422 Drosophil
828	250	6.3	1321	10	AB010778	AB010778 Mus muscu	901	247	6.3	11095	2	AC017524	AC017524 Drosophil
829	250	6.3	1341	6	A30593	A30593 DNA for tis	902	247	6.3	56080	2	AC018086	AC018086 Drosophil
830	250	6.3	2017	5	AB028871	AB028871 Struthio	903	247	6.3	86884	3	AC004366	AC004366 Drosophil
831	250	6.3	2267	6	AX335042	AX335042 Sequence	904	247	6.3	155553	3	AC007802	AC007802 Drosophil
832	250	6.3	2267	6	AX409602	AX409602 Sequence	905	247	6.3	155553	3	AC007802	AC007802 Drosophil
833	250	6.3	2267	3	HUMPPKFA	M13143 Nucleotide	906	247	6.3	198244	3	AC007803	AC007803 Drosophil
834	249.5	6.3	1887	9	TATCFBP	D14701 Tachyples	907	247	6.3	291250	3	AE003455	AE003455 Drosophil
835	249.5	6.3	2695	9	HSBMP15	Y08724 H.sapiens m	908	246.5	6.2	291250	3	AE003455	AE003455 Drosophil
836	249.5	6.3	2770	4	BTPLASMIN	X79402 B.taurus mR	909	246.5	6.2	813	5	NEWTHRO	M81395 Cynops pyr
837	249.5	6.3	3344	9	HSNEUROTR	AJ001531 Homo sapi	910	246.5	6.2	885	6	AR108139	AR108139 Sequence
838	249.5	6.3	3350	6	AX83630	A83630 Sequence 1	911	246.5	6.2	1072	6	BD189695	BD189695 A method
839	249	6.3	708	6	AX207901	AX207901 Sequence	912	246.5	6.2	1139	6	AR076901	AR076901 Sequence
840	249	6.3	792	6	AX360081	AX360081 Sequence	913	246.5	6.2	1139	6	AR167292	AR167292 Sequence
841	249	6.3	792	6	BT007356	BT007356 Homo sapi	914	246.5	6.2	1259	10	RAA5642	AJ005642 Rattus ra
842	249	6.3	792	12	BT007599	BT007599 Synthetic	915	246.5	6.2	1409	6	CQ613929	CQ613929 Sequence
843	249	6.3	865	9	HUMCTRP	M24400 Human chymo	916	246.5	6.2	1869	6	AX58753	AX58753 Sequence 7
844	249	6.3	873	9	AK131056	AK131056 Homo sapi	917	246.5	6.2	1869	6	AR102461	AR102461 Sequence
845	249	6.3	909	10	BC061083	BC061083 Mus muscu	918	246.5	6.2	1947	6	AR095303	AR095303 Sequence
846	249	6.3	960	9	BC073145	BC073145 Homo sapi	919	246.5	6.2	1947	6	AR103987	AR103987 Sequence
847	249	6.3	1823	9	BC018146	BC018146 Homo sapi	920	246.5	6.2	1947	6	I16618	I16618 Sequence 2
848	249	6.3	2038	6	AX511622	AX511622 Sequence	921	246.5	6.2	1947	6	I19057	I19057 Sequence 2
849	249	6.3	2447	9	S67310	S67310 Homo sapien	922	246.5	6.2	1947	6	I22331	I22331 Sequence 2
850	249	6.3	2483	6	AR034619	AR034619 Sequence	923	246.5	6.2	1947	6	AX774839	AX774839 Sequence
851	249	6.3	2555	9	AK130533	AK130533 Homo sapi	924	246.5	6.2	1947	9	HSTHR1	V00595 Homo sapien
852	249	6.3	2733	6	AR447886	AR447886 Sequence	925	246.5	6.2	1988	6	AR105746	AR105746 Sequence
853	248.5	6.3	1314	6	A27435	A27435 DNA sequenc	926	246.5	6.2	1988	6	I14101	I14101 Sequence 15
854	248.5	6.3	1314	6	A27437	A27437 DNA sequenc	927	246.5	6.2	1997	6	CQ717780	CQ717780 Sequence
855	248.5	6.3	1314	6	A27441	A27441 DNA sequenc	928	246.5	6.2	1998	9	BC051332	BC051332 Homo sapi
856	248.5	6.3	1314	6	AR059989	AR059989 Sequence	929	246	6.2	2178	10	BC026555	BC026555 Mus muscu
857	248.5	6.3	1314	6	AR059990	AR059990 Sequence	930	246	6.2	2470	11	BV178314	BV178314 sqm99805
858	248.5	6.3	1314	6	AR059992	AR059992 Sequence	931	245.5	6.2	3430	5	XELXTLDP	D83476 Xenopus lae
859	248.5	6.3	1314	6	AR059993	AR059993 Sequence	932	245.5	6.2	1494	6	AX814649	AX814649 Sequence
860	248.5	6.3	1314	6	E01937	E01937 Synthetic D	933	245.5	6.2	1801	3	AF357226	AF357226 Panulirus
861	248.5	6.3	1314	6	E01938	E01938 Synthetic D	934	245.5	6.2	4380	6	CQ850562	CQ850562 Sequence
862	248.5	6.3	1314	6	E01940	E01940 Synthetic D	935	245	6.2	4380	6	AK127722	AK127722 Homo sapi
863	248.5	6.3	1314	6	E01941	E01941 Synthetic D	936	245	6.2	854	5	BC073555	BC073555 Xenopus l
864	248.5	6.3	2096	3	AY061936	AY061936 Bombyx mo	937	245	6.2	1440	6	E01669	E01669 cDNA encodi
865	248.5	6.3	2345	9	HSBF	X72875 H.sapiens m	938	245	6.2	2398	10	BC026555	L23338 Strongyloce
866	248.5	6.3	2388	6	CQ730887	CQ730887 Sequence	939	245	6.2	2398	5	AB038498	AB038498 Xenopus l
867	248.5	6.3	2388	6	AX330489	AX330489 Sequence	940	245	6.2	3487	5	AB038498	AB038498 Xenopus l
868	248.5	6.3	2388	6	AX409518	AX409518 Sequence	941	245	6.2	6717	9	AB023149	AB023149 Homo sapi
869	248.5	6.3	2388	6	HUMCOMPACB	LI5702 Human compl	942	244.5	6.2	6753	6	CQ873941	CQ873941 Sequence
870	248.5	6.3	2503	9	BC004143	BC004143 Homo sapi	943	244.5	6.2	807	6	AX1220086	AX1220086 Sequence
871	248.5	6.3	2503	9	BC007990	BC007990 Homo sapi	944	244.5	6.2	807	6	AX150967	AX150967 Sequence
872	248	6.3	860	5	BC078367	BC078367 Danio rer	945	244.5	6.2	842	6	AX375290	AX375290 Sequence
873	248	6.3	861	6	AX800024	AX800024 Sequence	946	244.5	6.2	989	6	I08551	I08551 Sequence 3
874	248	6.3	869	5	AY179345	AY179345 Panlo rer	947	244.5	6.2	1317	12	SYNUTUPA	M69037 Synthetic h
875	248	6.3	885	6	BD209905	BD209905 Human nuc	948	244.5	6.2	1488	6	AX814651	AX814651 Sequence
876	248	6.3	885	6	AB014219	AB014219 Sequence	949	244.5	6.2	1739	6	AR034820	AR034820 Sequence
877	248	6.3	907	5	AB029753	AB029753 Paralicht	950	244.5	6.2	3024	9	AK055872	AK055872 Homo sapi
878	248	6.3	1419	6	AR059996	AR059996 Sequence	951	244.5	6.2	65326	2	AC124815	AC124815 Mus muscu
879	248	6.3	1575	6	E01671	E01671 cDNA encodi	952	244	6.2	216636	2	AC117672	AC117672 Mus muscu
880	248	6.3	1621	5	AY216598	AY216598 Meleagris	953	244	6.2	1128	10	AB049453	AB049453 Mus muscu
										1329	5	AF465274	AF465274 Takifugu

954	244	6.2	1521	6	AX814631	Sequence	1027	239.5	6.1	1468	6	CQ414741	Sequence
955	244	6.2	1987	3	AGA675	Sequence	1028	239.5	6.1	3989	6	CQ849871	Sequence
956	244	6.2	2174	6	CQ720386	Sequence	1029	239.5	6.1	3989	6	AK126936	Sequence
957	244	6.2	2728	10	RNO487623	Sequence	1030	239.5	6.1	11230	6	AR435510	Sequence
958	244	6.2	2753	10	MUSPKA	Sequence	1031	239.5	6.1	11230	6	AX375163	Sequence
959	244	6.2	276258	2	AC136872	Sequence	1032	239.5	6.1	11289	10	AF206329	Sequence
960	243.5	6.2	991	12	AB053399	Sequence	1033	239.5	6.1	152909	10	AL929406	Sequence
961	243.5	6.2	2362	9	HSBMP14	Sequence	1034	239	6.1	987	6	AX360076	Sequence
962	243	6.2	869	4	OAR18224	Sequence	1035	239	6.1	1170	6	AR059998	Sequence
963	243	6.2	1979	6	CQ845801	Sequence	1036	239	6.1	3215	11	BV176814	Sequence
964	243	6.2	1979	9	AK131261	Sequence	1037	239	6.1	3658	6	CQ596606	Sequence
965	243	6.2	2810	10	AX13552852	Sequence	1038	238.5	6.0	875	5	AB029754	Sequence
966	243	6.2	2991	6	AX577904	Sequence	1039	238.5	6.0	900	3	PLAJ658	Sequence
967	243	6.2	3584	6	CQ613928	Sequence	1040	238.5	6.0	1188	6	E06063	Sequence
968	243	6.2	5021	6	BD225401	Mammalian	1041	238.5	6.0	1207	3	BC058031	Sequence
969	243	6.2	5021	6	AR343520	Sequence	1042	238.5	6.0	1501	3	TATPROCL0T	Sequence
970	243	6.2	5021	9	AF059516	Homo sapi	1043	238.5	6.0	1739	10	RNHEPA	Sequence
971	243	6.2	28628	2	AC020159	Sequence	1044	238.5	6.0	1776	4	AY569316	Sequence
972	243	6.2	184272	3	AC009211	Drosophil	1045	238.5	6.0	2444	3	AK115605	Sequence
973	243	6.2	247955	3	AB003698	Sequence	1046	238.5	6.0	5463	9	AB067471	Sequence
974	242.5	6.1	929	3	AGTRYLA	Sequence	1047	238	6.0	820	10	RATTHRO	Sequence
975	242.5	6.1	1068	6	I62336	Sequence 7	1048	238	6.0	828	6	E40571	Sequence
976	242.5	6.1	1176	6	E01673	Human facto	1049	238	6.0	882	4	DOGCTRP	Sequence
977	242.5	6.1	1571	9	HUMCFX11B	Sequence	1050	238	6.0	1047	4	AB038652	Sequence
978	242.5	6.1	1605	6	AR085656	Sequence	1051	238	6.0	1230	9	HSHPALIS	Sequence
979	242.5	6.1	1724	3	AF499913	Ilyanassa	1052	238	6.0	1234	9	HUMHPALB	Sequence
980	242.5	6.1	2457	6	AR162262	Sequence	1053	238	6.0	1485	3	AX814628	Sequence
981	242.5	6.1	2457	6	AR317164	Sequence	1054	238	6.0	1487	3	AGA250916	Sequence
982	242.5	6.1	4796	5	XLXOLL	Sequence	1055	238	6.0	1497	6	AX814642	Sequence
983	242	6.1	1176	6	E01672	Sequence	1056	238	6.0	1663	3	AY061564	Sequence
984	242	6.1	1497	6	AX814639	Sequence	1057	238	6.0	1831	6	CQ613029	Sequence
985	242	6.1	1848	6	CQ730299	Sequence	1058	238	6.0	2419	5	XEUBMPIA	Sequence
986	242	6.1	1959	6	AX774785	Sequence	1059	238	6.0	2625	6	AR164818	Sequence
987	242	6.1	1959	9	HUMCFX11A	Sequence	1060	238	6.0	2625	6	AR490618	Sequence
988	242	6.1	1980	9	HUMF12A	Sequence	1061	238	6.0	2625	6	AR532392	Sequence
989	241.5	6.1	840	10	AF305425	Mus muscu	1062	238	6.0	3507	5	AB038497	Sequence
990	241.5	6.1	1044	10	AF442819	Mus muscu	1063	238	6.0	4037	6	CQ614288	Sequence
991	241.5	6.1	1248	6	AX262412	Sequence	1064	238	6.0	4072	6	AR164817	Sequence
992	241.5	6.1	1618	3	AY075233	Drosophil	1065	238	6.0	4072	6	AR490617	Sequence
993	241.5	6.1	1639	6	CQ414399	Sequence	1066	238	6.0	4072	6	AR532391	Sequence
994	241.5	6.1	1641	6	AX262410	Sequence	1067	238	6.0	4510	9	MACAPOA	Sequence
995	241.5	6.1	1872	6	AX254430	Sequence	1068	238	6.0	8589	6	AR490616	Sequence
996	241.5	6.1	2320	9	HSBMP16	H.sapiens m	1069	238	6.0	8589	6	AR532390	Sequence
997	241.5	6.1	2658	9	HSM804478	Sequence	1070	238	6.0	8589	2	AC017357	Sequence
998	241.5	6.1	2663	9	HSM806070	Homo sapi	1071	238	6.0	69485	2	AC017357	Sequence
999	241.5	6.1	3210	3	AK112764	Sequence	1072	238	6.0	154160	3	AC046154	Sequence
1000	241.5	6.1	3440	10	AY135525S2	Mus muscu	1073	238	6.0	169863	3	AC069458	Sequence
1001	241.5	6.1	3915	6	CQ734404	Sequence	1074	238	6.0	183948	3	AC009376	Sequence
1002	241	6.1	1065	6	AR27447	DNA sequence	1075	238	6.0	289990	3	AE003516	Sequence
1003	241	6.1	1065	6	AR059995	Sequence	1076	237.5	6.0	960	6	CQ735672	Sequence
1004	241	6.1	1065	6	E01943	Synthetic D	1077	237.5	6.0	1068	6	E05898	Sequence
1005	241	6.1	1076	10	AB006130	Mesocric	1078	237.5	6.0	1798	3	AY119095	Sequence
1006	241	6.1	1497	6	AX814644	Sequence	1079	237.5	6.0	2531	5	XLMP1	Sequence
1007	241	6.1	3546	6	AR162263	Sequence	1080	237.5	6.0	2585	5	BC080382	Sequence
1008	241	6.1	3546	6	AR317165	Sequence	1081	237.5	6.0	3819	9	AF106861	Sequence
1009	241	6.1	4493	4	AF531101	Sequence	1082	237.5	6.0	11152	6	AX686198	Sequence
1010	240.5	6.1	833	5	AB029751	Paralich	1083	237.5	6.0	11158	6	AX686196	Sequence
1011	240.5	6.1	846	6	AX254967	Sequence	1084	237	6.0	818	10	TRU25747	Sequence
1012	240.5	6.1	1068	6	AR363691	Sequence	1085	237	6.0	819	10	MUSTHRO	Sequence
1013	240.5	6.1	1233	6	I48917	Sequence 1	1086	237	6.0	923	9	AF113248	Sequence
1014	240.5	6.1	2388	5	AF089860	Oncorhinc	1087	237	6.0	1700	5	BC056849	Sequence
1015	240.5	6.1	3350	6	AX685995	Sequence	1088	237	6.0	2320	5	EPTTHROM	Sequence
1016	240.5	6.1	10878	6	AR435509	Sequence	1089	237	6.0	4771	6	AR170997	Sequence
1017	240.5	6.1	10878	6	AX375161	Sequence	1090	237	6.0	4771	6	AR170997	Sequence
1018	240	6.1	877	5	PWTRYPS1N	Sequence	1091	237	6.0	4883	6	CQ720933	Sequence
1019	240	6.1	1521	6	AX814634	Sequence	1092	237	6.0	1065	6	I62333	Sequence
1020	240	6.1	2801	6	CQ727939	Sequence	1093	236.5	6.0	1065	6	I62333	Sequence
1021	240	6.1	2949	6	CQ737049	Sequence	1094	236.5	6.0	1065	6	AX431270	Sequence
1022	239.5	6.1	832	5	AB041929	Engraulis	1095	236.5	6.0	1065	6	AX431270	Sequence
1023	239.5	6.1	832	6	BD056354	Novel DNA	1096	236.5	6.0	1068	6	A00762	Synthetic t
1024	239.5	6.1	1397	9	HUMHPAB	Human hapto	1097	236.5	6.0	1068	6	A00762	Synthetic t
1025	239.5	6.1	1411	9	L29394	Homo sapien	1098	236.5	6.0	1068	6	A27431	DNA sequenc
1026	239.5	6.1	1441	6	BD276276	Serine pr	1099	236.5	6.0	1068	6	A27433	DNA sequenc

1100	236.5	6.0	1068	6	A27445	A27445 DNA sequenc	1173	235	6.0	9177	10	AJ584850	AJ584850 Mus muscu
1101	236.5	6.0	1068	6	AR059987	AR059987 Sequence	1174	234.5	5.9	1185	9	AF260825	AF260825 Homo sapi
1102	236.5	6.0	1068	6	AR059988	AR059988 Sequence	1175	234.5	5.9	1566	3	BT011129	BT011129 Drosophi
1103	236.5	6.0	1068	6	AR059994	AR059994 Sequence	1176	234.5	5.9	2231	10	BC019485	BC019485 Mus muscu
1104	236.5	6.0	1068	6	E01935	E01935 Synthetic D	1177	234	5.9	785	6	AX921749	AX921749 Sequence
1105	236.5	6.0	1068	6	E01936	E01936 Synthetic D	1178	234	5.9	1701	6	AX814625	AX814625 Sequence
1106	236.5	6.0	1068	6	E01942	E01942 Synthetic D	1179	234	5.9	2394	10	BC005451	BC005451 Mus muscu
1107	236.5	6.0	1068	6	E18744	E18744 Sequence 2	1180	233.5	5.9	867	5	CMPRECT	X78490 G.morhua mR
1108	236.5	6.0	1068	6	I62334	I62334 Sequence 3	1181	233.5	5.9	870	6	AX226513	AX226513 Sequence
1109	236.5	6.0	1067	6	AR080456	AR080456 Sequence	1182	233.5	5.9	1163	6	AR076898	AR076898 Sequence
1110	236.5	6.0	1097	10	RATRMCT	D38455 Rat mRNA fo	1183	233.5	5.9	1163	6	AR167289	AR167289 Sequence
1111	236.5	6.0	1128	6	AX431268	AX431268 Sequence	1184	233.5	5.9	1803	6	AX814646	AX814646 Sequence
1112	236.5	6.0	1128	6	AX431271	AX431271 Sequence	1185	233.5	5.9	2363	6	AR220138	AR220138 Sequence
1113	236.5	6.0	1137	6	AR175771	AR175771 Sequence	1186	233.5	5.9	2363	6	AX336397	AX336397 Sequence
1114	236.5	6.0	1137	6	AR232006	AR232006 Sequence	1187	233.5	5.9	2363	6	AX411046	AX411046 Sequence
1115	236.5	6.0	1137	6	AX136012	AX136012 Sequence	1188	233.5	5.9	2363	6	AX511632	AX511632 Sequence
1116	236.5	6.0	1137	6	AX136781	AX136781 Sequence	1189	233.5	5.9	2363	9	HSRPSH	X07732 Human hepat
1117	236.5	6.0	1137	6	AX137832	AX137832 Sequence	1190	233.5	5.9	6567	10	AK172967	AK172967 Mus muscu
1118	236.5	6.0	1137	6	BD000154	BD000154 Process f	1191	233.5	5.9	6609	10	AY688677	AY688677 Mus muscu
1119	236.5	6.0	1137	6	BD010886	BD010886 Process f	1192	233	5.9	1002	4	OAR18223	Y18223 Ovis aries
1120	236.5	6.0	1170	6	A27727	A27727 DNA sequenc	1193	233	5.9	1077	6	AX780068	AX780068 Sequence
1121	236.5	6.0	1170	6	E01945	E01945 Synthetic D	1194	233	5.9	2385	10	AF537098	AF537098 Rattus no
1122	236.5	6.0	1173	6	E01674	E01674 cDNA -encodi	1195	232.5	5.9	1283	6	CO797981	CO797981 Sequence
1123	236.5	6.0	1179	6	A00137	A00137 Synthetic g	1196	232.5	5.9	1283	9	AF283670	AF283670 Homo sapi
1124	236.5	6.0	1179	6	A00140	A00140 Synthetic g	1197	232.5	5.9	1500	6	AR024194	AR024194 Sequence
1125	236.5	6.0	1179	6	AI4893	AI4893 Plasmidogen	1198	232.5	5.9	3125	5	BC068636	BC068636 Xenopus l
1126	236.5	6.0	1179	6	E02397	E02397 DNA encodin	1199	232.5	5.9	3517	3	CG1431705	AJ431705 Crassostr
1127	236.5	6.0	1616	6	I06017	I06017 Sequence 9	1200	232.5	5.9	3919	6	AR085400	AR085400 Sequence
1128	236.5	6.0	1724	6	AR363268	AR363268 Sequence	1201	232.5	5.9	3919	6	AR170998	AR170998 Sequence
1129	236.5	6.0	1781	10	AF030065	AF030065 Mus muscu	1202	232.5	5.9	3919	9	HSU91963	U91963 Human tolo
1130	236.5	6.0	1950	4	S70164	S70164 Hageman fac	1203	232.5	5.9	4284	10	AB062913	AB062913 Mesocrice
1131	236.5	6.0	2331	4	AF395821	AF395821 Oryctolag	1204	232.5	5.9	5139	9	AF282732	AF282732 Homo sapi
1132	236.5	6.0	2499	10	RNU0311671	AJ311671 Rattus no	1205	232.5	5.9	5145	6	AR096487	AR096487 Sequence
1133	236.5	6.0	2752	10	MMU300738	AJ300738 Mus muscu	1206	232.5	5.9	5145	6	BD165892	BD165892 Human hea
1134	236.5	6.0	266868	2	AC096906	AC096906 Rattus no	1207	232.5	5.9	5145	6	E30055	E30055 Human heart
1135	236	6.0	881	6	BC054136	BC054136 Danio rer	1208	232.5	5.9	5145	6	AR204076	AR204076 Sequence
1136	236	6.0	1068	6	A27439	A27439 DNA sequenc	1209	232.5	5.9	6690	9	HSM804919	AL833606 Homo sapi
1137	236	6.0	1068	6	AR059991	AR059991 Sequence	1210	232	5.9	1068	6	A07690	A07690 Synthetic D
1138	236	6.0	1068	6	E01939	E01939 Synthetic D	1211	232	5.9	1677	6	AX814626	AX814626 Sequence
1139	236	6.0	1164	6	E01118	E01118 cDNA encodi	1212	232	5.9	2246	6	CO715376	CO715376 Sequence
1140	236	6.0	1170	6	A27729	A27729 DNA sequenc	1213	232	5.9	2446	10	RATKALP	M30282 Rat plasma
1141	236	6.0	1170	6	E01946	E01946 Synthetic D	1214	232	5.9	2456	10	RATRPK	M58590 Rat plasma
1142	236	6.0	2402	10	AK098094	AK098094 Mus muscu	1215	232	5.9	2583	6	AX401888	AX401888 Sequence
1143	236	6.0	2443	10	MUSCCBFA	M57890 Mouse facto	1216	232	5.9	2609	6	AX477377	AX477377 Sequence
1144	235.5	6.0	978	6	AX365498	AX365498 Sequence	1217	232	5.9	3366	6	CO587289	CO587289 Sequence
1145	235.5	6.0	1068	6	E05897	E05897 DNA sequenc	1218	232	5.9	3374	3	DRDVP	M76976 D.melanogas
1146	235.5	6.0	1103	10	RNU67909	U67909 Rattus norv	1219	232	5.9	3427	3	BT010008	BT010008 Drosophi
1147	235.5	6.0	1445	6	I01255	I01255 Sequence 1	1220	232	5.9	12811	6	CO576228	CO576228 Sequence
1148	235.5	6.0	1595	10	BC079254	BC079254 Rattus no	1221	231.5	5.9	848	5	GMU57055	U57055 Gadus morhu
1149	235.5	6.0	2730	6	AR400897	AR400897 Sequence	1222	231.5	5.9	917	4	BTPELAS	X97635 B.taurus mR
1150	235.5	6.0	2730	6	BD073481	BD073481 Semaphori	1223	231.5	5.9	955	6	CO729939	CO729939 Sequence
1151	235.5	6.0	2730	9	AF022859	AF022859 Homo sapi	1224	231.5	5.9	1170	6	AR059997	AR059997 Sequence
1152	235.5	6.0	2745	4	EEU33171	U33171 Erinaceus e	1225	231.5	5.9	1701	12	SYNCHPL	M69273 Cloning vec
1153	235.5	6.0	2781	6	CO714485	CO714485 Sequence	1226	231.5	5.9	2163	10	AF537099	AF537099 Rattus no
1154	235.5	6.0	2781	6	AR400898	AR400898 Sequence	1227	231.5	5.9	2175	6	AX833435	AX833435 Sequence
1155	235.5	6.0	2781	6	AX743086	AX743086 Sequence	1228	231.5	5.9	2175	9	AK095160	AK095160 Homo sapi
1156	235.5	6.0	2781	6	BD073482	BD073482 Semaphori	1229	231.5	5.9	2265	9	AB028140	AB028140 Homo sapi
1157	235.5	6.0	2781	9	AF022860	AF022860 Homo sapi	1230	231	5.9	723	5	E13204	E13204 Human cDNA
1158	235.5	6.0	2796	9	AF016098	AF016098 Homo sapi	1231	231	5.9	907	5	AF012463	AF012463 Pleuronec
1159	235.5	6.0	3357	9	AF280544	AF280544 Homo sapi	1232	231	5.9	1098	6	A42131	A42131 Sequence 21
1160	235.5	6.0	3372	9	AF280545	AF280545 Homo sapi	1233	231	5.9	1167	6	A42127	A42127 Sequence 17
1161	235.5	6.0	3404	6	BD139219	BD139219 Soluble i	1234	231	5.9	1176	6	A42135	A42135 Sequence 25
1162	235.5	6.0	3404	6	AR409883	AR409883 Sequence	1235	231	5.9	1176	6	A42139	A42139 Sequence 29
1163	235	6.0	1193	10	BC011328	BC011328 Mus muscu	1236	231	5.9	1182	6	A42111	A42111 Sequence 1
1164	235	6.0	1219	6	AR080457	AR080457 Sequence	1237	231	5.9	1182	6	A42113	A42113 Sequence 3
1165	235	6.0	1219	10	MUIMCT	D31789 Mongolian g	1238	231	5.9	1182	6	A42115	A42115 Sequence 5
1166	235	6.0	1521	6	AX814636	AX814636 Sequence	1239	231	5.9	1182	6	A42117	A42117 Sequence 7
1167	235	6.0	1709	5	BC055596	BC055596 Danio rer	1240	231	5.9	1182	6	A42119	A42119 Sequence 9
1168	235	6.0	1992	6	BD130508	BD130508 Secretary	1241	231	5.9	1182	6	A42123	A42123 Sequence 13
1169	235	6.0	6004	6	AX537467	AX537467 Sequence	1242	231	5.9	1182	6	A42125	A42125 Sequence 15
1170	235	6.0	6402	11	BV177788	BV177788 sqnm96732	1243	231	5.9	1182	6	A42153	A42153 Sequence 43
1171	235	6.0	6402	11	BV177912	BV177912 sqnm97463	1244	231	5.9	1182	6	A42155	A42155 Sequence 45
1172	235	6.0	6670	9	HSM805725	BS537423 Homo sapi	1245	231	5.9	1182	6	A42157	A42157 Sequence 47

1246	231	5.9	1185	6	A42133	A42133 Sequence 23	1319	229	5.8	804	3	AF312826	AF312826
1247	231	5.9	1185	6	A42143	A42143 Sequence 33	1320	229	5.8	825	10	AF184895	AF184895
1248	231	5.9	1185	6	A42145	A42145 Sequence 35	1321	229	5.8	1187	6	AX338503	AX338503 Sequence
1249	231	5.9	1185	6	A42147	A42147 Sequence 37	1322	229	5.8	1200	6	AR125379	AR125379 Sequence
1250	231	5.9	1185	6	A42149	A42149 Sequence 39	cl323	229	5.8	1200	6	AR125380	AR125380 Sequence
1251	231	5.9	1185	6	A42151	A42151 Sequence 41	1324	229	5.8	1200	6	AR144651	AR144651 Sequence
1252	231	5.9	1191	6	A42151	A42151 Sequence 11	cl325	229	5.8	1200	6	AR144652	AR144652 Sequence
1253	231	5.9	1191	6	A42121	A42121 Sequence 19	1326	229	5.8	1200	6	AR214385	AR214385 Sequence
1254	231	5.9	1191	6	A42129	A42129 Sequence 27	cl327	229	5.8	1200	6	AR214386	AR214386 Sequence
1255	231	5.9	1194	6	A42137	A42137 Sequence 31	1328	229	5.8	1200	6	BD022582	BD022582 Flea prot
1256	231	5.9	1197	6	A42141	E00853 Hybrid gene	cl329	229	5.8	1200	6	BD022583	BD022583 Flea prot
1257	231	5.9	1479	6	E00853	Q086992 Sequence	1330	229	5.8	1736	3	PLR7668	AJ007668 Pacifasta
1258	231	5.9	2590	6	Q086992	Q086992 Sequence	1331	229	5.8	1887	10	AY234104	AY234104 Mus muscu
1259	231	5.9	2627	6	Q0869994	Q0869994 Sequence	1331	229	5.8	1892	10	BC061800	BC061800 Rattus no
1260	231	5.9	3027	5	GGA012462	AJ012462 Gallus ga	1332	229	5.8	1894	6	AR125377	AR125377 Sequence
1261	231	5.9	4661	6	BD225402	BD225402 Mammalian	1333	229	5.8	1894	6	AR125378	AR125378 Sequence
1262	231	5.9	4661	6	AR343521	AR343521 Sequence	cl334	229	5.8	1894	6	AR142763	AR142763 Sequence
1263	231	5.9	4661	10	AF073526	AF073526 Mus muscu	1335	229	5.8	1894	6	AR144649	AR144649 Sequence
1264	230.5	5.8	780	6	AR487614	AR487614 Sequence	1335	229	5.8	1894	6	AR144650	AR144650 Sequence
1265	230.5	5.8	780	9	AY344794	AY344794 Homo sapi	1337	229	5.8	1894	6	AR214284	AR214284 Sequence
1266	230.5	5.8	873	6	AX577741	AX577741 Sequence	cl337	229	5.8	1894	6	BD022580	BD022580 Flea prot
1267	230.5	5.8	888	6	AR487613	AR487613 Sequence	1338	229	5.8	1894	6	BD022581	BD022581 Flea prot
1268	230.5	5.8	888	9	AY344793	AY344793 Homo sapi	cl339	229	5.8	1894	6	BD022581	BD022581 Flea prot
1269	230.5	5.8	967	6	BD243371	BD243371 Treatment	1340	229	5.8	1894	6	BD022581	BD022581 Flea prot
1270	230.5	5.8	967	6	BD003281	BD003281 Enzyme an	cl341	229	5.8	1894	6	BD022581	BD022581 Flea prot
1271	230.5	5.8	1509	3	AK115721	AK115721 Ciona inc	1342	229	5.8	2202	6	CQ615018	CQ615018 Sequence
1272	230.5	5.8	1916	9	AF045649	AF045649 Homo sapi	1343	229	5.8	4234	12	AB007632	AB007632 Signal se
1273	230.5	5.8	2158	6	AX147449	AX147449 Sequence	1344	228.5	5.8	678	6	CQ716937	CQ716937 Sequence
1274	230.5	5.8	2568	9	HS4488947	AJ488947 Homo sapi	1345	228.5	5.8	891	4	BOVEKCS	LI9663 Bos taurus
1275	230.5	5.8	3180	10	BC061712	BC061712 Rattus no	1346	228.5	5.8	1099	9	AX358867	AX358867 Homo sapi
1276	230.5	5.8	5381	3	DMU34777	DMU34777 Drosophila	1347	228.5	5.8	1113	6	AX392231	AX392231 Sequence
1277	230.5	5.8	5392	3	DMU12634	DMU12634 Drosophila	1348	228.5	5.8	1234	10	S67972	S67972 Mus sp. hap
1278	230	5.8	6669	5	AF229448	AF229448 Danio rer	1349	228.5	5.8	1842	6	BD203763	BD203763 Human nuc
1279	230	5.8	891	6	CQ714155	CQ714155 Sequence	1350	228.5	5.8	1842	6	AX014918	AX014918 Sequence
1280	230	5.8	906	5	AB070720	AB070720 Anguilla	1351	228.5	5.8	3429	3	AF224491	AF224491 Halocynth
1281	230	5.8	1078	6	AX190545	AX190545 Sequence	1352	228.5	5.8	7596	6	AX695382	AX695382 Sequence
1282	230	5.8	1161	6	AR142768	AR142768 Sequence	1353	228.5	5.8	8064	6	AX695381	AX695381 Sequence
1283	230	5.8	1161	6	AR142769	AR142769 Sequence	1354	228.5	5.8	8064	10	MN0TCH	Z11886 M.musculus
1284	230	5.8	1161	6	AR142773	AR142773 Sequence	1355	228.5	5.8	9193	10	AF508809	AF508809 Mus muscu
1285	230	5.8	1161	6	AR142774	AR142774 Sequence	1356	228	5.8	1806	6	AX814638	AX814638 Sequence
1286	230	5.8	1175	6	AR142771	AR142771 Sequence	1357	228	5.8	3690	6	AR096488	AR096488 Sequence
1287	230	5.8	1175	6	AR142772	AR142772 Sequence	1358	228	5.8	3690	6	BD165893	BD165893 Human hea
1288	230	5.8	1314	6	AX190543	AX190543 Sequence	1359	228	5.8	3690	6	E30056	E30056 Human heart
1289	230	5.8	1314	6	AX190546	AX190546 Sequence	1360	228	5.8	3690	6	AR204077	AR204077 Sequence
1290	230	5.8	1373	6	AR142766	AR142766 Sequence	1361	227.5	5.8	827	6	CQ714827	CQ714827 Sequence
1291	230	5.8	1373	6	AR142767	AR142767 Sequence	1362	227.5	5.8	838	9	BC074904	BC074904 Homo sapi
1292	230	5.8	1375	6	Q0729940	Q0729940 Sequence	1363	227.5	5.8	838	9	BC074905	BC074905 Homo sapi
1293	230	5.8	1376	3	AF117749	AF117749 Anopheles	1364	227.5	5.8	862	5	SSTRYP1	X70075 Salmo salar
1294	230	5.8	1614	6	AX360089	AX360089 Sequence	1365	227.5	5.8	888	6	AX360070	AX360070 Sequence
1295	230	5.8	1689	6	AX149579	AX149579 Sequence	1366	227.5	5.8	929	5	GECTHRO	M81392 Gecko gecko
1296	230	5.8	1748	6	AX534544	AX534544 Sequence	1367	227.5	5.8	1018	6	AX370454	AX370454 Sequence
1297	230	5.8	1748	6	AX369323	AX369323 Sequence	1368	227.5	5.8	1460	9	HSHPRGNE	X89214 H.sapiens m
1298	230	5.8	1830	6	AX814630	AX814630 Sequence	1369	227.5	5.8	1494	6	AX814655	AX814655 Sequence
1299	230	5.8	2048	9	AB095845	AB095845 Homo sapi	1370	227.5	5.8	2255	6	AX786894	AX786894 Sequence
1300	230	5.8	2067	6	AX149581	AX149581 Sequence	1371	227	5.8	726	6	AX473052	AX473052 Sequence
1301	230	5.8	2237	9	AY190317	AY190317 Homo sapi	1372	227	5.8	777	5	SSTRYP1B	X70072 Salmo salar
1302	230	5.8	2393	9	AB048796	AB048796 Homo sapi	1373	227	5.8	868	5	SSTRYP1A	X70071 Salmo salar
1303	230	5.8	3005	5	CHKTHROM	M81391 Gallus gall	1374	227	5.8	869	5	AX496969	AX496969 Tautogola
1304	230	5.8	3222	9	BC018715	BC018715 Homo sapi	1375	227	5.8	927	6	AX375719	AX375719 Sequence
1305	230	5.8	3324	9	AB048797	AB048797 Homo sapi	1376	227	5.8	959	6	BD253969	BD253969 Enzyme an
1306	229.5	5.8	1043	6	CQ725563	CQ725563 Sequence	1377	227	5.8	968	6	BD003277	BD003277 Enzyme an
1307	229.5	5.8	1059	6	AX360080	AX360080 Sequence	1378	227	5.8	1030	5	BC054286	BC054286 Xenopus l
1308	229.5	5.8	1494	6	AX814653	AX814653 Sequence	1379	227	5.8	1055	10	AY005145	AY005145 Mus muscu
1309	229.5	5.8	2025	10	AF356627	AF356627 Mus muscu	1380	227	5.8	1055	10	AB059415	AB059415 Mus muscu
1310	229.5	5.8	2559	6	AB078887	AB078887 Lethenter	1381	227	5.8	1084	10	AB033822	AB033822 Mus muscu
1311	229.5	5.8	3469	6	CQ573579	CQ573579 Sequence	1382	227	5.8	1084	10	AF176209	AF176209 Mus muscu
1312	229.5	5.8	4711	3	BT003214	BT003214 Drosophil	1383	227	5.8	1098	4	ECAS15902	AJ515902 Equus cab
1313	229.5	5.8	5366	6	CQ612366	CQ612366 Sequence	1384	227	5.8	1123	10	BC049588	BC049588 Mus muscu
1314	229.5	5.8	5376	3	AY051585	AY051585 Drosophil	1385	227	5.8	1467	3	SMJ11561	AJ011561 Schistoso
1315	229	5.8	726	6	AR125381	AR125381 Sequence	1386	227	5.8	1647	6	AX375310	AX375310 Sequence
1316	229	5.8	726	6	AR144653	AR144653 Sequence	1387	227	5.8	1647	6	AX375718	AX375718 Sequence
1317	229	5.8	726	6	AR214287	AR214287 Sequence	1388	227	5.8	1849	9	AF053915	AF053915 Ctenoceph
1318	229	5.8	726	6	BD022584	BD022584 Flea prot	1389	227	5.8	1895	3	AF053915	AF053915 Ctenoceph
	229	5.8					1390	227	5.8	3896	6	AX149475	AX149475 Sequence
							1391	226.5	5.7	810	5	SSTRYP1II	X70074 Salmo salar

Db	26	ATGGAGCTGGTGTGGAGCAGAGTTGGGGCTCACATTTCTTTCAGCTCCTCTTCATCTCG	85
Qy	21	SerLeuProArgGluTyrThrValIleAenGluUaCysProGlyAlaGluTrpAenIle	40
Db	86	TCCTTGCCAAAGAGTACACAGTCATTAAATGAAGCCTGCGCTGGAGCAGAGTGGAAATATC	145
Qy	41	MetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysProGlyLysArgGlu	60
Db	146	ATGTGTGGAGTGCCTGTGAATATGATCAGATTGAGTGGCTCTGCCCCGGAAGAGGGAA	205
Qy	61	ValValGlyTyrThrIleProCysCysArgAsnGluGluAenGluCysAspSerCysLeu	80
Db	206	GTCTGGGTTATACCAATCCCTTGCTGTCAGGAATGAGGAGNATGAGTGTGACTCTCTGCTG	265
Qy	81	IleHisProGlyCysThrIlePheGluAenCysLysSerCysArgAenGlySerTrpGly	100
Db	266	ATCCACCCAGGTGTACCATCTTTGAAACTGCAAGAGCTGCCGAAATGGCTCATGGGG	325
Qy	101	GlyThrLeuAspPheTyrValIysGlyPheTyrCysAlaGluCysArgAlaGlyTyr	120
Db	326	GSTACCTTGATGACTTCTATGTGAAGGGGTCTACTGTGCAGAGTGCCGAGCAGGCTGG	385
Qy	121	TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu	140
Db	386	TACGAGGAGACTGCAATGCATGTGGCAGGTCTGCGAGCCCCAAAGGGTCAGATTTTG	445
Qy	141	LeuGluSerTyrProLeuAenAlaHisCysGluTyrThrIleHisAlaLysProGlyPhe	160
Db	446	TTGMAAGCTATCCCTTAATGCTCACTGTGAATGGACCAATTCATGCTAAACCTGGGTTT	505
Qy	161	ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp	180
Db	506	GTCAATCAACTAAGATTGTGATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTAGAC	565
Qy	181	TyrValGluValArgAspGlyAspAenArgAspGlyGlnIleIleLysArgValCysGly	200
Db	566	TATGTTGAGTTTGTGATGAGACCAACCGCGATGGCCAGATCATCAAGCGTGTCTGTGGC	625
Qy	201	AsnGluArgProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer	220
Db	626	AACGAGCGGCAGCTCTATCCAGAGCATAGGATCCTCACTCCACGTCCTCTTCCACTCC	685
Qy	221	AspGlySerLysAenPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer	240
Db	686	GATGGCTCCAAAGAAATTTGACGGTTTCCATGCCATTTATGAGGAGATCAGCATGCTCC	745
Qy	241	SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCys	260
Db	746	TCATCCCTTGTTCATGACGGCACGTGGTCTCTTGACAAGGCTGGATCTTACAAGTGT	805
Qy	261	AlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAenLeuLeuGluAluArgAenCys	280
Db	806	GCCTGCTTGGCAGCTATACTGGCAGCGCTGTGAAATCTCCTTGAAGAAAGAAACTGC	865
Qy	281	SerAspProGlyGlyProValAsnGlyTyrGlnLysIleThrGlyGlyProGlyLeuIle	300
Db	866	TCAGACCTCGGGGCCCCAGTCATGGGTACCAAGAAATAACAGGGGCCCTTGGGCTTATC	925
Qy	301	AsnGlyArgHisAlaLysIleGlyThrValValSerPhePheCysAenAenSerTyrVal	320
Db	926	AACGGACCCATGCTAAATTTGGACCGTGGTGTCTTTCTTTGTAACTCCTATGTT	985
Qy	321	LeuSerGlyAenGluLysArgThrCysGlnGlnAenGlyGluTrpSerGlyLysGlnPro	340
Db	986	CTTAGTGGCAATGAGAAAGAACTTGGCAGCAGAAATGGAGAGTGGTCAGGGAAACAGCCC	1045
Qy	341	IleCysIleLysAlaCysArgGluProLysIleSerAspLeuValArgArgValLeu	360
Db	1046	ATCTGCATAAAGCTCCCGGAGAACCAAGATTTTCAGACCTGGTGGAGAGAGATGTTCTT	1105
Qy	361	ProMetGlnValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSer	380
Db	1106	CCGNATGAGGTTTCAGTCAAGGGAGACACCATTTACACGAGCTATACTCAGCGGCTTCAGC	1165
Qy	381	LysGlnLysLeuGlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuPro	400
Db	1166	AAGCAGAAATCTGAGAGTCCCTCTACCAAGAGCCAGCCCTTCCCTTTTGAGATCTGCC	1225
Qy	401	MetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArg	420
Db	1226	ATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCTTCTACCGC	1285
Qy	421	ArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTrpSerGlyArgAlaPro	440
Db	1286	CGCTGGCAGCAGCAGGAGGACATGCTCTGAGGACTGGGAAGTGGAGTGGCGGGACCA	1345
Qy	441	SerCysIleProIleCysGlyLysIleGluAenIleThrAlaProLysThrGlnGlyLeu	460
Db	1346	TCTTGATCCCTATCTGCGGAAATTTGAGAACATCCTCTCTCAAAAGACCCCAAGGGTTG	1405
Qy	461	ArgTrpProTrpGlnAlaAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeu	480
Db	1406	CGCTGGCCGTGGCAGGCAGCCATCTACAGGAGGACCAGCGGGTGCATGACGGCAGCTA	1465
Qy	481	HisLysGlyAlaTrpPheLeuValCysSerGlyAlaLeuValAenGluArgThrValVal	500
Db	1466	CACAGGAGCGTGGTTCCTTAGTCTGACGCGTGCCTGGTGAATGAGCGCATCTGGTG	1525
Qy	501	ValAlaAlaHisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeu	520
Db	1526	GTGGCTGGCCACTGTGTACTGACCTGGGGAAGGTCAACATGATCAAGACAGCAGCTG	1585
Qy	521	LysValValLeuGlyLysPheTyrArgAspAspArgAspGluLysThrIleGlnSer	540
Db	1586	AAAGTTGTTTGGGAAATTTCTACCGGGATGATGACCGGGATGAGAAGACCATCCAGAGC	1645
Qy	541	LeuGlnIleSerAlaIleIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAsp	560
Db	1646	CTACAGATTTCTGCTATCATTTCTGCATCCCACTATGACCCCATCTCTGCTGTGATGCTGAC	1705
Qy	561	IleAlaIleLeuLysLeuLeuAspLysAlaAaGlyIleSerThrArgValGlnProIleCys	580
Db	1706	ATCGCCATCTCTGAAGCTCTTAGCAAGGCCCGGTATCAGCACCCGAGTCCAGCCCATCTGC	1765
Qy	581	LeuAlaAlaSerArgAspLeuSerThrSerPheGlnGluSerHisIleThrValAlaGly	600
Db	1766	CTCGCTGCCAGTCCGGATCTCAGCACTTCTCTCCAGAGTCCCACTCACTGTGGTGGC	1825
Qy	601	TrpAsnValLeuAlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGly	620
Db	1826	TGGAAATGCTCTGGCAGACGTGAGGAGCCCTGGGCTTCAAGAAACGACACACTGCGCTCTGGG	1885
Qy	621	ValValSerValValAspSerLeuCysGluGluGlnHisGluAspHisGlyIlePro	640
Db	1886	GTGGTCAGTGTGTGAGTCCGCTGTGTGTGAGAGCAGCATGAGGACCATGGCATCCCA	1945
Qy	641	ValSerValThrAspAenMetPheCysAlaSerTrpGluProThrAlaProSerAspIle	660
Db	1946	GTGAGTGTCACTGATAACATGTTCTGTGCGAGCTGGGAACCCACTGCCCCCTTGTGATATC	2005
Qy	661	CysThrAlaGluThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGlu	680
Db	2006	TGCACCTGCAGACAGAGGACATCGCGCTGTGTCTTCCCGGACAGCATCTCTCGAG	2065
Qy	681	ProArgTrpHisLeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHisArg	700
Db	2066	CCAGCTGGCATCTGATGGGACTGGTCAGCTGAGGCTATGATATAAACATCGACCCACAGG	2125
Qy	701	LeuSerThrAlaPheThrLysValLeuProPheLysAspTrpIleGluArgAsnMetLys	720
Db	2126	CTCTCCACTGCTTCCCAAGGTGCTGCTTTTAAAGACTGGATTGAAGAAATATGAAA	2185

RESULT 2

AX092306

LOCUS

DEFINITION

Sequence 37 from Patent WO0116318.

2846 bp DNA linear PAT 21-MAR-2001

AX092306
 VERSION AX092306.1 GI:13444467
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Baton, D.L., Filvaroff, E., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and
 Wood, W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0116318-A 37.08-MAR-2001;
 Genentech, Inc. (US)
 FEATURES
 source Location/Qualifiers
 1..2846
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Alignment Scores: Pred. No.: 3,03e-280 Length: 2846
 Score: 3945.00 Matches: 720
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-10-063-692-38 (1-720) x AX092306 (1-2846)
 QY 1 MetGluLeuGlyCysTrpThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuSer 20
 Db 26 ATGGAGCTGGTGTGTGACGAGTGGGCTCACTTTCTTCAGCTCCTTCATCTCG 85
 QY 21 SerLeuProArgGluThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40
 Db 86 TCCTTCCAAAGAGATACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGGAAATATC 145
 QY 41 MetCysArgGluCysGluThrAspGlnIleGluCysValCysProGlyLysArgGlu 60
 Db 146 ATGTGTGGAGTGTGTGTAATATGATCAGATTGAGTGCCTGTGCCCGGAAAGAGGAA 205
 QY 61 ValValGlyThrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
 Db 206 GTCGTGGGTATACCATCCCTCTGTCAGCAATGAGGAGATGAGTGTGACTCTGCTG 265
 QY 81 IleHisProGlyCysThrIlePheGluAsnGlySerCysArgAsnGlySerTrpGly 100
 Db 266 ATCCACCCAGGTGTATACCATCTTTGAAACTGCAAGAGCTGCCGAAATGGCTCATGGGG 325
 QY 101 GlyThrLeuAspAspPheThrValLysGlyPheThrCysAlaGluCysArgAlaGlyTrp 120
 Db 326 GGATCCTTGATGACTTCTATGTGAAGGGTTCTACTGTGACAGTGCCTGAGCAGGCTGG 385
 QY 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu 140
 Db 386 TACGGAGGAGACTGCATGCGATGTGGCCAGTCTTCGAGCCCCCAAGGGTTCAGATTTC 445
 QY 141 LeuGluSerTyrProLeuAsnAlaHisCysGluTrpThrIleHisAlaLysProGlyPhe 160
 Db 446 TTGGAAAGCTATCCCTTAATGTCTACTGTGAATGGACCATTCATGTAACCTGGGTTT 505
 QY 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp 180
 Db 506 GTCATCAACTAAGATTGTGATGTTGAGTCTGGAGTTTACATGATGTCCTGAGTATGAC 565
 QY 181 TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGly 200
 Db 566 TATGTTGAGGTTCTGTGATGAGACACCGCGATGGCCAGATCATCAAGCGTGTCTGGC 625
 QY 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220

Db 626 AACGAGCGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCCACGCTCTTCCATCTCC 685
 QY 221 AspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer 240
 Db 686 GATGGCTCCCAAGAAATTTGACGGTTTCCATGCCATTTATGAGGAGATCAGCATGTCTCC 745
 QY 241 SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCys 260
 Db 746 TCATCCCTCTGTGTTTCCATGACGCGCAGCTGGCTCTTGACCAAGGCTGATCTTACAGTGT 805
 QY 261 AlaCysLeuAlaGlyThrThrGlyGlnArgCysGluAsnLeuGluAlaArgAsnCys 280
 Db 806 GCCTGCTTGGCAGGCTATCTGGCAGCGCTGTGAATAATCTCTTGAAGAAAGAAATGTC 865
 QY 281 SerAspProGlyGlyProValAsnGlyThrGlnLysIleThrGlyGlyProGlyLeuIle 300
 Db 866 TCAGACCTTGGGGGCCCATGTCATGGGTACAGAAATAACAGGGGCCCTGGGCTTATC 925
 QY 301 AsnGlyArgHisAlaLysIleGlyThrValValSerPhePheCysAsnAsnSerTyrVal 320
 Db 926 AACGAGCGCATGCTAAATTTGGCAGCGTGGTCTTTCTTTTGTAAACAATCTCTATGTT 985
 QY 321 LeuSerGlyAsnGluLysArgThrCysGlnAsnGlyGluTrpSerGlyLysGlnPro 340
 Db 986 CTTAGTGGCAATCAGAAAGAACTTGGCAGCAAGATGGAGAGTGGTCAGGAAACAGCCCC 1045
 QY 341 IleCysIleLysAlaCysArgGluProLysIleSerAspLeuValArgArgValLeu 360
 Db 1046 ATCTGCATAAAGCCTGCCGAGAACCAAGATTTTCAGACCTGGTGAGAGGAGATCTTT 1105
 QY 361 ProMetGlnValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSer 380
 Db 1106 CCGATGCGAGTTTCAGTCAAGGAGAGACACCATTAACACAGCTATATCTCAGCGGCTTCAGC 1165
 QY 381 LysGlnLysLeuGlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuPro 400
 Db 1166 AAGCAGAAATCTGAGAGTGCCTTACCAAGAGCCAGCCCTTCCCTTTGGAGATCTCGCC 1225
 QY 401 MetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArg 420
 Db 1226 ATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCTTCTACCGC 1285
 QY 421 ArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTrpSerGlyArgAlaPro 440
 Db 1286 CGCTGGGACGACGAGGAGGACATGTCTGAGGACTGGGAAGTGGAGTGGCGGACCA 1345
 QY 441 SerCysIleProIleCysGlyLysIleGluAsnIleThrAlaProLysThrGlnGlyLeu 460
 Db 1346 TCCTGCATCCCTATCTGCCGGGAAATTTGAGAACATCACTGCTCCAAAGACCCCAAGGGTTG 1405
 QY 461 ArgTrpProTrpGlnAlaAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeu 480
 Db 1406 CGCTGGCCGTGGCAGCAGCGCCATCTACAGGAGACCCAGCGGGTGCATGACGCGAGCTA 1465
 QY 481 HisLysGlyAlaTrpPheLeuValCysSerGlyAlaLeuValAsnGluArgThrValVal 500
 Db 1466 CACAAGGAGCGGTGTTCTTAGTCTGACGCGGTGCCCTGGTGAATGAGCGCACTGTGGTG 1525
 QY 501 ValAlaAlaHisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeu 520
 Db 1526 GTGGCTGCCACCTGTGTTACTGACCTGGGGAAGTCACTATGATCAAGCAGCAGACCTG 1585
 QY 521 LysValValLeuGlyLysPheTyrArgAspAspAspArgAspGluLysThrIleGlnSer 540
 Db 1586 AAGATTGTTTGGGGAATTTCTACCGGGATGATGACCGGGATGAGAGACCATCCAGAGC 1645
 QY 541 LeuGlnIleSerAlaIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAsp 560
 Db 1646 CTACAGATTCTGCTATCTTCTGATCCCACTATGACCCCATCTGCTGTGTTGCTGCTGAC 1705
 QY 561 IleAlaIleLeuLysLeuAspLysAlaArgIleSerThrArgValGlnProIleCys 580

```

Db      1706 ATCGCCATCTGAGCTCTAGACAAGGCCGCTATCAGCACCCGAGTCCAGCCCATCTGC 1765
Qy      581 LeuAlaAserArgAspLeuSerThrSerPheGlnGluSerHisIleThrValAlaGly 600
Db      1766 CTGCGTGCCAGTCGGGATCTCAGCACTTCTCTCCAGAGTCCACATCACTGTGGCTGGC 1825
Qy      601 TrpAsnValLeuAlaAspValArgSerProGlyPheIleAsnAspThrLeuArgSerGly 620
Db      1826 TGGAAATGTCTGGCAGACGTGAGAGCCCTGGCTTCAAGAACACACACTGGCGCTGGG 1885
Qy      621 ValValSerValValAspSerLeuLeuCysGlnGluGlnHisGluAspHisGlyIlePro 640
Db      1886 GTGGTCAGTGTGGTGACTCGCTGCTGTGTGAGAGACGATGAGACCATGGCATCCCA 1945
Qy      641 ValSerValThrAspAsnMetPheCysAlaSerTyrGluProThrAlaProSerAspIle 660
Db      1946 GTGAGTGTCACTGATAACATGTTCTGTGCGAGCTGGGAACCCACTGCCCTCTGATATC 2005
Qy      661 CysThrAlaGluThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGlu 680
Db      2006 TGCACTGCAGAGACAGGAGGCATCGCGCTGTGTCTTCCCGGAGCAGCATCTCTGAG 2065
Qy      681 ProArgTyrHisLeuMetGlyLeuValSerTyrSerTyrAspLysThrCysSerHisArg 700
Db      2066 CCACGCTGGCATCTGATGGACTGGTTCAGCTGGAGCTATGATAAACATGCACCCACAGG 2125
Qy      701 LeuSerThrAlaPheThrIysValLeuProPheLysAspTyrIleGluArgAsnMetLys 720
Db      2126 CTCTCCACTGCTTCACCAAGGTGCTGCTTTTAAAGACTGGATTGAAGAAATATGAAA 2185

RESULT 3
AX376102
LOCUS      2846 bp      DNA      linear      PAT 01-MAR-2002
DEFINITION Sequence 169 from Patent WO0168848.
ACCESSION AX376102
VERSION    AX376102.1 GI:19170443
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
           Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
           Zhang,Z.
TITLE      Secreted and transmembrane polypeptides and nucleic acids encoding
           the same
JOURNAL    Patent: WO 0168848-A 169 20-SEP-2001;
           Genentech, Inc. (US)
FEATURES   source
           Location/Qualifiers
             1..2846
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.:      3,03e-280      Length:      2846
Score:          3945.00      Matches:      720
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              6              Gaps:        0

US-10-063-692-38 (1-720) x AX376102 (1-2846)
Qy      1 MetGluLeuGlyCysTyrThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuSer 20
Db      26 ATGAGCTGGGTGCTGGAGCGAGTGGGGCTCACTTTCTTACGCTCCCTTCATCTCG 85
Qy      21 SerLeuProArgGluTyrThrValIleAsnGluAlaCysProGlyAlaGluTyrAsnIle 40
Db      86 TCCTTGCAGAGAGGTACACAGTCATTATTAAGACCTTGCCTGGAGCAGAGTGGAAATATC 145

```

```

Qy      41 MetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysProGlyLysArgGlu 60
Db      146 ATGTGTCGGAGTGTGTTGAATATGATCATGATGAGTGTGCTGCTGCCCGGAAAGAGGAA 205
Qy      61 ValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
Db      206 GTCTGGGTATACCATCCCTTGTCTGCAGAAATGAGAGATGAGTGTGACTCTCTGCCCTG 265
Qy      81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTyrGly 100
Db      266 ATCCACCCAGGTGTATACCATCTTTGAAAACTGCAGAGCTGCCGAAATGGCTCATGGGG 325
Qy      101 GlyThrLeuAspAspPheTyrValIysGlyPheTyrCysAlaGluCysArgAlaGlyTyr 120
Db      326 GSTTACCTTGGATGACTTCTATGTGAAGGGGTCTCTCTGTGCAGAGTGCAGAGCGCTGG 385
Qy      121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu 140
Db      386 TACGGAGGAGACTGCAATGCGATGTGGCCAGGTCTCGGAGGCCCAAGGGTCAGATTTTG 445
Qy      141 LeuGluSerTyrProLeuAsnAlaHisCysGluTyrThrIleHisAlaLysProGlyPhe 160
Db      446 TTGGAAGCTATCCCTTAAATGCTCACTGTGAATGGACCATTCATGCTAAACCTGGGT 505
Qy      161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp 180
Db      506 GTCATCAACTAAGATTGTTCATGTTGAGTCTGGAGTTTGCATCAATGTGCCAGTATGAC 565
Qy      181 TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGly 200
Db      566 TATGTTGAGGTTGCTGATGGAGACAACCGGATGGCCAGATCATCAAGCGTGTCTGTGGC 625
Qy      201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220
Db      626 AACGAGCGCCAGCTCTCTATCCAGAGCATAGGATCTCTCACTCCACGCTCTTCTTCCACTCC 685
Qy      221 AspGlySerIysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer 240
Db      686 GATGGGTCCAAGAAATTTTGACGGTTCCTATGCGCTTTATGAGGAGATCAGCATGTCTCC 745
Qy      241 SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCys 260
Db      746 TCAATCCCTTGTTCATGACGCGCAGTGGCTCTTGACAAGGCTGATCTTACAAGTGT 805
Qy      261 AlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuGluGluArgAsnCys 280
Db      806 GCCTGTCTGGCAGGCTATATCTGGCGCAGCGCTGTGAAAAATCTCCTTGAGAGAAAGAACTGC 865
Qy      281 SerAspProGlyGlyProValAsnGlyTyrGlnLysIleThrGlyProGlyLeuIle 300
Db      866 TCAGACCTTGGGGGCCCGCAGTCAATGGGTACCAAGAAATTAACAGGGGCCCTGGGCTTATC 925
Qy      301 AsnGlyArgHisAlaLysIleGlyThrValIserPheCysAsnAsnSerTyrVal 320
Db      926 AACGGAGCGCATGCTAAATTTGCACCGTGTGTCTTTCTTTTGTAAACAACCTCTATGTT 985
Qy      321 LeuSerGlyAsnGluLysArgThrCysGlnGlnAsnGlyGluTyrSerGlyLysGlnPro 340
Db      986 CTTAGTGGCAATGAGAAAAAGAACTTGCACAGAAATGAGAGTGGTTCAGGGAAACAGCCCC 1045
Qy      341 IleCysIleLysAlaCysArgGluProLysIleSerAspLeuValArgArgValIleu 360
Db      1046 ATCTGCATAAAGCCTGCCGAGAACCAAGATTTACAGCTGTGTGAGAGAGAGATCTTT 1105
Qy      361 ProMetGlnValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSer 380
Db      1106 CCGATGCGAGTTTCAGTCAAGGAGACACCATTTACCCAGCTATACTCAGCGGCTTCAGC 1165
Qy      381 LysGlnLysLeuGlnSerAlaProThrLysLysProLalalLeuProPheGlyAspLeuPro 400
Db      1166 AAGCAGAAACTGCAGAGTGCCTTACCAAGAGCCAGCCCTTCCCTTTGGAGATCTGCC 1225

```

QY 401 MetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArg 420
Db 1226 ATGGATACCAACATCTGCATACCAGCTCCAGTATGAGTGCATCTCACCTTCTACCGC 1285
QY 421 ArgLeuGlySerSerArgAlaThrCysLeuArgThrGlyLysTyrPheGlyArgAlaPro 440
Db 1286 CGCTGGGAGCAGCAGAGACATCTCTGAGACTGGAGTGGAGTGGCGGGACCA 1345
QY 441 SerCysIleProIleCysGlyLysIleGluAsnIleThrAlaProTyrThrGlnGlyLeu 460
Db 1346 TCCTGCATCCTATCTCGCGAAATTTGAGAACATCATCTGCTCCAAAGACCCAAAGGGTTG 1405
QY 461 ArgTyrProTyrGlnAlaAlaIleTyrArgThrSerGlyValHisAspGlySerLeu 480
Db 1406 CGCTGGCCGTCGGCAGCAGCATCTACAGAGACACCGGGGTGCTATGCGCAGCCTA 1465
QY 481 HisLysGlyAlaTyrPheLeuValCysSerGlyValAlaLeuValAsnGluArgThrValVal 500
Db 1466 CACAGGGAGCGTGTCTTAGTCTGACGGGTGCTGTGTGATGAGCGCATGTGGTG 1525
QY 501 ValAlaAlaHisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeu 520
Db 1526 GTGGCTGCCACCTGTGTACTGACCTGGGGAAGTCAACATGATCAAGACAGCAGACCTG 1585
QY 521 LysValValLeuGlyLysPheTyrArgAspAspArgAspGluLysThrIleGlnSer 540
Db 1586 AAGATTGTGTTTGGGAAATTTCTACCGGGATGATGACCGGGATGAGAAGACCATCCAGAGC 1645
QY 541 LeuGlnIleSerAlaIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAsp 560
Db 1646 CTAAGATTCTGCTATCATCTGCATCCCACTATGACCCCATCTGCTGTGATGCTGAC 1705
QY 561 IleAlaIleLeuLysLeuLeuAspLysAlaArgIleSerThrArgValGlnProIleCys 580
Db 1706 ATGCCATCTGAAGCTCTTAGACAAGGCGGTATCAGCACCCGAGTCCAGCCCATCTGC 1765
QY 581 LeuAlaAlaSerArgAspLeuSerThrPheGlnGluSerHisIleThrValAlaGly 600
Db 1766 CTCGCTGCCAGTCGGGATCTCAGCACTTCCTCCAGAGTCCCACTCATCTGTGGCTGGC 1825
QY 601 TrpAsnValLeuAlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGly 620
Db 1826 TGGAAATGCTGCAGACGTGAGAGCCCTGGCTTCAAGAACACACACTGCGCTCTGGG 1885
QY 621 ValValSerValValAspSerLeuLeuCysGluGluGlnHisGluAspHisGlyIlePro 640
Db 1886 GTGTCAGTGTGTGGACTGCTGCTGTGTGAGGAGCAGCATGAGCACTGCATCCCA 1945
QY 641 ValSerValThrAspAsnMetPheCysAlaSerTyrProThrAlaProSerAspIle 660
Db 1946 GTGAGTGTCACTAATACATGTTCTGTGCCAGCTGGGAACCCACTGCCCTTCTGATATC 2005
QY 661 CysThrAlaGluThrGlyIleAlaAlaValSerPheProGlyArgAlaSerProGlu 680
Db 2006 TGCACTGCAGACAGAGGACATCGCGCTGTGCTCTCCGGGAGAGCATCTCTGAG 2065
QY 681 ProArgTyrHisLeuMetGlyLeuValSerTyrSerTyrAspLysThrCysSerHisArg 700
Db 2066 CCACGCTGGCATCTGATGGACTGTGTGAGTGTGATGATGATGATGATGATGATGATGAT 2125
QY 701 LeuSerThrAlaPheThrLysValLeuProPheLysAspTyrIleGluArgAsnMetLys 720
Db 2126 CTCCTCACTGCCCTTCAACAGGTGCTGCTTTTAAAGACTGGATTGAAAGAAATATGAAA 2185
RESULT 4
AX403343
LOCUS AX403343 2846 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 230 from Patent WO0073454.
ACCESSION AX403343
VERSION AX403343.1 GI:21436887
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
AUTHORS
Aehkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Eaton, D., Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P., Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J., Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z.
TITLE
Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL
Patent: WO 0073454-A 230 07-DEC-2000;
Genentech Inc. (US)
FEATURES
source
1. .2846
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 3.03e-280 Length: 2846
Score: 3945.00 Matches: 720
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-063-692-38 (1-720) x AX403343 (1-2846)
QY 1 MetGluLeuGlyCysThrThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuIleSer 20
Db 26 ATGAGCTGGTGTCTGGACGCGAGTTGGGCTCACTTTCTCAGCTCTCTTCATCTCG 85
QY 21 SerLeuProArgLysThrValIleAsnGluAlaCysProGlyAlaGluTyrAsnIle 40
Db 86 TCTTCCCAAGAGATCACAGTCATTAATGAAGCTGCTCCCTGGAGCAGTGGATATC 145
QY 41 MetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysProGlyLysArgGlu 60
Db 146 ATGTGTGGGAGTGTCTGTAATATGATCAGATTGAGTGTGCTGCCCGGAAAGAGGAA 205
QY 61 ValValGlyTyrThrIleProCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
Db 206 GTGCTGGGTATACCATCTCTGCTCAGAGAAATGAGGAAATGAGTGTGCTCTGCTG 265
QY 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTyrGly 100
Db 266 ATCCACCCAGGTGTACCATCTTTGAAAACTGCAAGAGCTGCCGAAATGGCTCATGGGG 325
QY 101 GlyThrLeuAspAspPheTyrValLysGlyPheTyrCysAlaGluCysArgAlaGlyTyr 120
Db 326 GGTACCTTGGATGACTTCTATGTGAAGGGTCTACTGTGAGAGTCCGAGGAGGCTGG 385
QY 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu 140
Db 386 TACGGAGGAGACTGCTATGCGATGTGGCAGGTCTTCGAGCGCCCAAGGGTCAAGATTTG 445
QY 141 LeuGluSerTyrProLeuAsnAlaHisCysGluTyrThrIleHisLysLysProGlyPhe 160
Db 446 TTGGAAGGTATCTCCCTAAATGCTCACTGTAATGGACCATCATCATCTAAACCTGGGTT 505
QY 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp 180
Db 506 GTATCCCAACTAAGATTCTCATGTGTGAGTCTGGAGTTGACTACATGTGCCAGTATGAC 565
QY 181 TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleLysArgValCysGly 200
Db 566 TATGTTGAGTTCGTGATGGAGACAAACCGCATGGCCAGATCATCAAGCGTGTCTGTGGC 625
QY 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220
Db 626 AACGAGCGGCCAGCTCTCTATCCAGAGCATAGGATCTCTCACTCCACGCTCTCTTCTCCACTCC 685

QY	221	AspGlySerIysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer	240		1766	CTCGCTGCCAGTCGGGATCTCAGCACTTCTTCCAGAGTCCACATCATCTGGGTGGC	1825
Db	686	GATGGCTCCAGAAATTTTGACGGTTTCCATGCGCATTTATGAGAGATCAAGCATGCTCC	745		601	TrpAsnValLeuAlaAspValArgSerProGlyPheIysAsnAspThrLeuArgSerGly	620
QY	241	SerSerProCysPheHisAspGlyThrCysValLeuAspIysAlaGlySerTyrIysCys	260		1826	TGGAATGTCTCGCAGACGTGAGGAGCCCTGGCTTCAAGAAGCACACATGCGCTCTGGG	1885
Db	746	TCATCCCTTGTTTCCATGACGCGCACGTGGTCTTGCACAAAGCTGGATCTTACAAGTGT	805		621	ValValSerValValAspSerLeuLeuCysGluGluGlnHisGluAspHisGlyIlePro	640
QY	261	AlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuLeuGluArgAsnCys	280		1886	GTGGTCAGTGTGGTGACTCGCTGTGTGTGAGGACGATGAGGACCATGSCATCCCA	1945
Db	806	GCCTGTCTGGCAGCTATACTGGGCAGCGCTGTGAATACTCTCTGAAGAAAGAAACTGC	865		641	ValSerValThrAspAsnMetPheCysAlaSerTyrGluProThrAlaProSerAspIle	660
QY	281	SerAspProGlyGlyProValAsnGlyTyrGlnIysIleThrGlyGlyProGlyLeuIle	300		1946	GTGAGTGTCACTGATAACATGTTCTGTGCAGCTGGGAACCCACTGCCCTTCTGATATC	2005
Db	866	TCAGACCTCTGGGGGCCAGTCAATGGGTACAGAAATACAGGGGCCCTTGGGCTTATC	925		661	CysThrAlaGluThrGlyGlyIleAlaAlaValSerPheProGlyValArgAlaSerProGlu	680
QY	301	AsnGlyArgHisAlaIysIleGlyThrValValSerPheCysAsnAsnSerTyrVal	320		2006	TGCACCTGCAGACAGAGGCGCATCGCGGTGTGTCTTCCCGGAGAGCATCTCTTGAG	2065
Db	926	AACGGACGCCATGCTAAATTTGGCACCGTGGTGTCTTTTGTAACTCCTATGTT	985		681	ProArgTyrHisLeuMetGlyLeuValSerTyrAspLysThrCysSerHisArg	700
QY	321	LeuSerGlyAsnGluIysArgThrCysGlnAsnGlyGluTyrPheSerGlyIysGlnPro	340		2066	CCACGTGGCATCTGATGGACTGGTGCAGCTGAGCTATGATAAACATGCACCCACAGG	2125
Db	986	CTTAGTGGCAATCAGAAAAGAACTTGCCACGAGATGGAGAGTGGTCAGGAAACAGCCC	1045		701	LeuSerThrAlaPheThrLysValLeuProPheLysAspTyrIleGluArgAsnMetLys	720
QY	341	IleCysIleIysAlaCysArgGluProLysIleSerAspLeuValArgArgValLeu	360		2126	CTCTCCACTGCCTTCCACAGGTGCTGCTTTTAAAGACTGGATTGAAGAAATATGAAA	2185
Db	1046	ATCTGCATAAAGCTGCCGAGAACCAAGATTTCAGACCTGGTGAAGAGAGATTCTT	1105		RESULT 5		
QY	361	ProMetGlnValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaIaPheSer	380		AY358346		
Db	1106	CCCATCGAGTTTCACTAAGGAGACACCATATACACGCTATACTCAGCGGCTTCAGC	1165		LOCUS	2846 bp mRNA linear PRI 03-OCT-2003	
QY	381	LysGlnLysLeuGlnSerAlaProThrLysIysPheProAlaLeuProPheGlyAspLeuPro	400		DEFINITION	Homo sapiens clone DNA58723 ELGC699 (UNQ699) mRNA, complete cds.	
Db	1166	AAGCAGAAACTGCAGAGTGGCCCTTACCAGAAAGCAGCCCTTCCCTTTGGAGATCTGCC	1225		ACCESSION	AY358346	
QY	401	MetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArg	420		VERSION	AY358346.1 GI:37181816	
Db	1226	ATGGGATACCAATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCTTCTACCCG	1285		KEYWORDS	FLI_CDNA.	
QY	421	ArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTrpSerGlyArgAlaPro	440		SOURCE	Homo sapiens (human)	
Db	1286	CGCTGGCGCAGCAGCAGGAGACATGCTCGAGGACTCGGAAGTGGAGTGGCGGCACCA	1345		ORGANISM	Homo sapiens	
QY	441	SerCysIleProIleCysGlyIysIleGluAsnIleThrAlaProLysThrGlnGlyLeu	460		REFERENCE	1 (bases 1 to 2846)	
Db	1346	TCCTGCATCCCTATCTCGCGGAAATTTGAGACATCACTGCTCAAGAGACCCAAAGGGTGT	1405		AUTHORS	Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wileand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.	
QY	461	ArgTyrProTyrGlnAlaAlaIleTyrArgThrSerGlyValHisAspGlySerLeu	480		TITLE	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment	
Db	1406	CGCTGGCGGTGGCAGGAGCCATCTACGAGGACCGCGGTGCATGACGCGAGCTTA	1465		JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)	
QY	481	HisLysGlyAlaTrpPheLeuValCysSerGlyAlaLeuValAsnGluArgThrValVal	500		PUBMED	12975309	
Db	1466	CACAGGAGCGGTGTTCTTAGTCTGCAGCGGTGCCCTGTGTAATGAGCGACTGTGGTG	1525		REFERENCE	2 (bases 1 to 2846)	
QY	501	ValAlaAlaHisCysValThrAspLeuLysValThrMetIleLysThrAlaAspLeu	520		AUTHORS	Clark,H.F.	
Db	1526	GTGGCTGCCCACTGTGTACTGACCTGGGGAAGGTCCACATGATCAAGACAGCAGACTGT	1585		TITLE	Direct Submission	
QY	521	LysValValLeuGlyIysPheTyrArgAspAspArgAspGluLysThrIleGlnSer	540		JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA	
Db	1586	AAAGTTGTTTGGGGAATTTCTACCGGGATGATGACCGGGATGAGAAGACCATCCAGAGC	1645		FEATURES	Location/Qualifiers	
QY	541	LeuGlnIleSerAlaIleIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAsp	560		source	1. .2846	
Db	1646	CTACAGATTCTGCTATCATCTTCATCCCACTATGACCCCATCTCGCTTGATGCTGAC	1705		gene	/organism="Homo sapiens"	
QY	561	IleAlaIleLeuLysLeuLeuAspIysAlaArgIleSerThrArgValGlnProIleCys	580		CDS	/mol_type="mRNA"	
Db	1706	ATCCCATCTCTGAAGCTCCTAGACAAGCCCGTATCAGACCCCGAGTCCAGCCCATCTGC	1765			/db_xref="taxon:9606"	
QY	581	LeuAlaIaSerArgAspLeuSerThrSerGlnGluSerHisIleThrValAlaGly	600			/clone="DNA58723"	

/translation="MELGWTQLGLTFLQLLLISSLPREYTVINEACPGAEWNIMCRE
 CCEYDLEQVCPGRREVGVITPCCRNEENECDSLIHPGCTTIFENKSCNRNWSGWT
 LDDFYVKGFCACRAGVGDGCMRCQVLRPKQGLVLCESYPLNACEWTHAKGTF
 NIGLRFVMSLEFDVQCYDYVEVRDGDNDGQIIRKVCNERNPAPTISGSLHLVLF
 HSDGSKNPDGPHAIYBEITACSSSPCNDHDTCLVDKAGSVKCAACLAGYTQORCENILLE
 ERNCSDPKPNVGVQKTTGGPGLNGRHKIGTVSPFCNNSVLSSNEKRTCCQNGE
 WSKGQPCICAKREPKLSDVRRVLPQVQSRRETPHLQLYSAAFQKQLQSAFTKFP
 ALSPGLPMQYQHLHTQLQYECISPFYRRIGSSRRCTLRGKWSGRAPSCIPICGKIE
 NITAPKTKGLRWPMQAAIYRRTSGVHDSGLHKGAWFLVCSGALNVERTVVAAHVTD
 LGKVTMIKTADLVKGLFYRDDDEKTKTQSIQISAIILHPNYDPTLLDADTALIKL
 LDKARTISVQPICLAASRDLSFOESHITVAGMNVLDVRSFGFNDTLRSGVSVV
 VDSLLCEEHEDHGIPIVSVTDNMFCASWEPTASDICTAETGGIAAVSPGRASPR
 WHLMGLVSNYSYDKTCSRSLSTAFKVLVLPKDWIERNMK"

ORIGIN

Alignment Scores:

Pred. No.: 3,03e-280 Length: 2846
 Score: 3945.00 Matches: 720
 Percent Similarity: 100.00% Conservativeness: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-063-692-38 (1-720) x AY358346 (1-2846)

Qy 1 MetGluLeuGlyCysTrpThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuLeuSer 20
 Db 26 ATGGAGCTGGTTCGTGGACGAGTGGGGCTCACTTTCTTCAGCTCCTCTCATCTCG 85
 Qy 21 SerLeuProArgGluTyrThrValIleAsnAlaCysProGlyAlaGluTrpAsnIle 40
 Db 86 TCCTTGGCAAGAGAGTACACAGTCATTAAATGAAGCCCTGGCCCTGGAGCAGAGTGGAAATATC 145
 Qy 41 MetCysArgGluCysGluTyrAspGlnIleGluCysValCysProGlyLysArgGlu 60
 Db 146 ATGTGTCGGAGTGTGTGTAATATGATCAGATTGAGTGCCTGTGCCCGGAAAGAGGGA 205
 Qy 61 ValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
 Db 206 GTCGTGGGTATACCATCCCTTGTCTGCAGGAATGAGGAGAAATGAGTGTGACTCCTGCTG 265
 Qy 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100
 Db 266 ATCCACCCAGGTGTACCATCTTTTGAATACTGCAAGAGCTGCCGAAATGGCTCATGGGG 325
 Qy 101 GlyThrLeuAspPheTyrValLysGlyPheTyrCysAlaGluCysArgAlaGlyTrp 120
 Db 326 GGTACCTTGATGACTTCTATGTGAAGGGTCTTACTGTGCAGAGTCCCGAGCAGGCTGG 385
 Qy 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu 140
 Db 386 TACGGAGGAGACTGCATGCGATGGCCAGGTTCTGCGAGCCCAAGGGTCAAGATTTTG 445
 Qy 141 LeuGluSerTyrProLeuAsnAlaHisCysGluTrpThrIleHisAlaLysProGlyPhe 160
 Db 446 TTGGAAGCTATCCCTTAAATGTCTACTGTGAATGGACCAATCATGTAAACCTGGGTTT 505
 Qy 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp 180
 Db 506 GTCATCCAACTAAGATTGTTCATGTGTGAGTCTGGAGTTTGACTACATGTGCCAGTATGAC 565
 Qy 181 TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGly 200
 Db 566 TATGTTGAGTTCGTGATGGAGACAACCGCGATGGCCAGATCATCAAGCGTGTCTGTGGC 625
 Qy 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220
 Db 626 AACGAGCGGCGAGCTCTATCCAGAGCATAGGATCCTCACTCCACGCTCTCTTCCACTCC 685
 Qy 221 AspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer 240
 Db 686 GATGGCTCCAAAGAAATTTTGACGGTTCATGCCATTTATGAGGAGATCAGCATGCTCC 745

Qy 241 SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCys 260
 Db 746 TCATCCCTTTTTCATGACGCGACGTGGTCTCTTGACAGGCTGGATCTTACAGTGT 805
 Qy 261 AlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuLeuGluAlaCysAsnCys 280
 Db 806 GCTTGTGGCAGGCTATCTGGGCGAGCGCTGTGAANAATCTCTTTGAAGAAAGAACTGC 865
 Qy 281 SerAspProGlyGlyProValAsnGlyTyrGlnLysIleThrGlyGlyProGlyLeuIle 300
 Db 866 TCAGACCTTGGGGGCCCCAGTCAATGGGTACCAAGAAAATAACAGGGGGCCCTGGGCTTATC 925
 Qy 301 AsnGlyArgHisAlaLysIleGlyThrValValSerPhePheCysAsnAsnSerTyrVal 320
 Db 926 AACGGACGCCATGCTAAANAATTTGGCACCGTGTCTTTCTTTTGTAACTCTCATGTGT 985
 Qy 321 LeuSerGlyAsnGluLysArgThrCysGlnGlnAsnGlyGluTrpSerGlyLysGlnPro 340
 Db 986 CTTAGTGGCNAATGAGAAAGAACTTGGCAGCAGATGGAGAGTGGTCAGGAAACACAGCCC 1045
 Qy 341 IleCysIleLysAlaCysArgGluProLysIleSerAspLeuValArgArgValLeu 360
 Db 1046 ATCTGCATAAAGCCCTGCCGAGAACCAAGATTTTCAGACCTGGTGTGAGAGAGAGTTCCT 1105
 Qy 361 ProMetGlnValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSer 380
 Db 1106 CCGATGCGAGTTTCAGTCAAGGGAGACACCAATTACACAGCTATATCTCAGCGGCTTCAGC 1165
 Qy 381 LysGlnLysLeuGlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuPro 400
 Db 1166 AAGCAGAAACTGCAGAGTGCCTTACCAAGAACCCAGCCCTTCCCTTTGGAGATCTCGCC 1225
 Qy 401 MetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArg 420
 Db 1226 ATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCTCTTACCGC 1285
 Qy 421 ArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTrpSerGlyArgAlaPro 440
 Db 1286 CGCTGGCGAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTGGAGTGGCGGGGACCA 1345
 Qy 441 SerCysIleProIleCysGlyLysIleGluAsnIleThrAlaProLysThrGlnGlyLeu 460
 Db 1346 TCCTGATCCTCTATCTGCGGGAANAATTTGAGAACATCATCTGCTCCAAAGACCCAGGGTGT 1405
 Qy 461 ArgTrpProTrpGlnAlaAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeu 480
 Db 1406 CGCTGGCCGTGGCAGCAGCCCATCTACAGGAGACCCAGCGGGTGCATGACGCGACCTA 1465
 Qy 481 HisLysGlyAlaTrpPheLeuValCysSerGlyAlaLeuValAsnGluArgThrValVal 500
 Db 1466 CACAGGGAGCGTGTTCCTTAGTCTGACGGTGCCTTGGTGAATGAGCGCACTGTGGTG 1525
 Qy 501 ValAlaAlaHisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeu 520
 Db 1526 GTGGCTGCCACCTGTGTACTGACCTGGGGAAGGTCAACATGATCAAGCAGCAGAGCTGT 1585
 Qy 521 LysValValLeuGlyLysPheTyrArgAspAspAspArgAspGluLysThrIleGlnSer 540
 Db 1586 AAGTTGTTTGGGGAANAATTTACCGGGATGATGACCGGGATGAGAGACCATCCAGAGC 1645
 Qy 541 LeuGlnIleSerAlaIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAsp 560
 Db 1646 CTACAGATTTCTGCTATCATCTTCATCTCCCAACTATGACCCCACTCTGCTTGTATGTGAC 1705
 Qy 561 IleAlaIleLeuLysLeuAspLysAlaAArgIleSerThrArgValGlnProIleCys 580
 Db 1706 ATGCCATCTGAAGCTCTTAGCAAGGCCCGGTATCAGCACCCGAGTCCAGGCCATCTGC 1765
 Qy 581 LeuAlaAlaSerArgAspLeuSerThrSerPheGlnGluSerHisIleThrValAlaGly 600
 Db 1766 CTGCGTCCAGTCCGGGATCTCAGCACTTCTTCCAGGAGTCCCACTCATCTGTGGTGGC 1825
 Qy 601 TrpAsnValLeuAlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGly 620

Db 1826 TGGARATGCTGCGACAGCTGAGAGCCCTGGCTTCAAGAACACACACATGCGCTCTGGG 1885

QY 621 ValValSerValValAaspSerLeuLeuCysGluGluGlnHisGluAaspHisGlyIlePro 640

Db 1886 GTGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGCCATCCCA 1945

QY 641 ValSerValThrAaspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIle 660

Db 1946 GTGAGTGTCTACTGATAACATGTTCTGTGGCAGCTGGGAACCCACTGCCCTTCTGATATC 2005

QY 661 CysThrAlaGluThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGlu 680

Db 2006 TGCACTGCAGACAGAGAGCATCGCGCTGTGTCTTCCGGAGCAGGATCTCTGAG 2065

QY 681 ProArgTrpHisLeuMetGlyLeuValSerTrpSerTrpAaspLysThrCysSerHisArg 700

Db 2066 CCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAATCATGCACCCACAGG 2125

QY 701 LeuSerThrAlaPheThrLysValLeuProPheLysAspTrpIleGluArgAsnMetLys 720

Db 2126 CTCTCCACTGCTCTACCAAGGTGCTGCCTTTTAAAGACTGGATTGAAGAAATATGAAA 2185

RESULT 6

HSR803699 HSM803699 2768 bp mRNA linear PRI 10-JUL-2002

LOCUS Homo sapiens mRNA; cDNA DKFZp667H2312 (from clone DKFZp667H2312).

DEFINITION

AL832391

ACCESSION

AL832391.1

VERSION

GI:21732954

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 2768)

AUTHORS

Koehler, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.

TITLE

Direct Submission

JOURNAL

Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY

COMMENT

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by BWPZ (Biomedical Research Center at the Charite,

Berlin/Germany) within the cDNA sequencing consortium of the German

Genome Project.

This clone (DKFZp667H2312) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further

information about the clone and the sequencing project is available

at <http://mips.gsf.de/proj/cDNA/>.

FEATURES

Location/Qualifiers

1..2768

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="RZPD:DKFZp667H2312"

/db_xref="taxon:9606"

/clone="DKFZp667H2312"

/tissue_type="lymph node"

/clone_lib="667 (synonym: hln02). Vector pSport1; host

DH10B; sites NotI + SalI"

/dev stage="adult"

polyA signal 2672..2677

polyA_site 2698

ORIGIN

Alignment Scores:

Pred. No.: 5,76e-280 Length: 2768

Score: 3941.00 Matches: 719

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.86% Mismatches: 0

Query Match: 99.90% Indels: 0

DB: 9 Gaps: 0

US-10-063-692-38 (1-720) x HSM803699 (1-2768)

QY 1 MetGluLeuGlyCysTrpThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuIleSer 20

Db 13 ATGGAGCTGGTGTGTCGACGAGTTGGGGCTCACATTTTCTTCTCAGCTCCTTCTCATCTCG 72

QY 21 SerLeuProArgGluTrpThrValIleAenGluAlaCysProGlyAlaGluTrpAsnIle 40

Db 73 TCCTTGCCAAAGAGTACACAGTCATTAATGAAGCCCTGCCCTGGAGCAGAGTGGAAATATC 132

QY 41 MetCysArgGluCysCysGluTrpAaspGlnIleGluCysValCysProGlyLysArgGlu 60

Db 133 ATGTGTGGGAGTGTGTGAATATGATCAGATTGAGTGGCTGTGCCCGGAAAGAGGAA 132

QY 61 ValValGlyTrpThrIleProCysCysArgAsnGluGluAsnGluCysAaspSerCysLeu 80

Db 193 GTCTGGGTATTACCATCTCTTGAATACTGAGTGAAGAGTGGCGAAATGGCTCATGGCTG 252

QY 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100

Db 253 ATCCACCCAGGTGTGTACCATCTTGAATACTGAGTGAAGAGTGGCGAAATGGCTCATGGGG 312

QY 101 GlyThrLeuAaspPheTrpValLysGlyPheTrpCysAlaGluCysArgAlaGlyTrp 120

Db 313 GGTACCTTGGATGACTTCTATGTGAAGGGGTCTTACTGTGAGAGTGGCGAGAGGCTGG 372

QY 121 TyrGlyGlyAaspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu 140

Db 373 TAGCGAGGAGACTGCATGCGATGTGGCCAGTTCCTGGAGCCCCAAAGGGTCAGATTTTG 432

QY 141 LeuGluSerTrpProLeuAsnAlaHisCysGluTrpThrIleHisAlaLysProGlyPhe 160

Db 433 TTGGAAGAGTATCCCTTAAATGCTCATGTGTGAATGGACCATTCATGTCAACCTGGGTGT 492

QY 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAaspTrpMetCysGlnTrpAsp 180

Db 493 GTCATCAACTAAGATTGTTCATGTGGCTGGAGTTCAGTACATGTCGCCAGTATGAC 552

QY 181 TyrValGluValArgAaspGlyAaspAsnArgAaspGlyGlnIleLysArgValCysGly 200

Db 553 TATGTTGAGTTCGTGATGGAGACAACCGCGATGGCCAGATCATCAAGCGTCTCTGTGGC 612

QY 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220

Db 613 AACGAGCGGCAGCTCTATCCAGAGCATAGGATCTCTCACTCCACGCTCTTCCACATCC 672

QY 221 AspGlySerLysAsnPheAaspGlyPheHisAlaIleTrpGluGluIleThrAlaCysSer 240

Db 673 GATGGCTCCAAGAAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCATGTCC 732

QY 241 SerSerProCysPheHisAaspGlyThrCysValLeuAaspLysAlaGlySerTrpLysCys 260

Db 733 TCATCCCTTGTTCATGACGGCAGCTGGCTGCTTGACAAGCTGGATCTTACAAGTGT 792

QY 261 AlaCysLeuAlaGlyTrpThrGlyGlnArgCysGluAsnLeuLeuGluArgAsnCys 280

Db 793 GCCTGCTTGGCAGGTATCTACTGGGCGACGCTGTGAAATATCTCTTGAAGAAAGAAATGTC 852

QY 281 SerAaspProGlyGlyProValAsnGlyTrpGlnLysIleThrGlyGlyProGlyLeuIle 300

Db 853 TCAGACCTTGGGGGCCCGCCAGTCATATGGGTACCAAGAAATAACAGGGGGCCCTTGGGCTTATC 912

QY 301 AsnGlyArgHisAlaLysIleGlyThrValValSerPhePheCysAsnAsnSerTrpVal 320

Db 913 AACGGACGCCATGCTAAATTTGGCAGCTGGTGTCTTTCTTTTGTAAACAACATCTATGTT 972

QY 321 LeuSerGlyAsnGluLysArgThrCysGlnGlnAsnGlyGluTrpSerGlyLysGlnPro 340

Db 973 CTTAGTGGCAATCAGAAAAGAACTTGCACAGAAATGAGAGTGGTCAGGGAAACAGCCC 1032

QY 341 IleCysIleLysAlaCysArgGluProLysIleSerAspLeuValArgArgValLeu 360

Db 1033 ATCTGCATAAAGCCTGCCGAGAACCAAGATTTACAGCTTGGTGAGAGGAGATGTTCT 1092

QY 361 ProMetGlnValGlnSerArgGluThrProLeuHisGlnLeuTrpSerAlaAlaPheSer 380


```
QY 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu 140
DB 488 TACGGAGGACATGCAATGCGATGTGGCAGAGTTCTCGAGGCCCCAAAGGGTCAAGATTGG 547
QY 141 LeuGluSerTyrProLeuAenAlaHisCysGluTyrThrIleHisAlaLysProGlyPhe 160
DB 548 TTGGAAAGCTATCCCTCCCTAAATGCTCACTGTGAATGGACCATTCATGCTAAACCTGGGTTT 607
QY 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp 180
DB 608 GTCATCAACTAAGATTGTGATGTTGAGCTTGGAGCTTGACATACATGTGCCAGTATGAC 667
QY 181 TyrValGluValArgAspGlyAspAenArgAspGlyGlnIleIleLysArgValCysGly 200
DB 668 TATGTTGAGGTTCTGATGGAGACAACCGGATGGCCAGATCATCAAGCGTGTCTGTGGC 727
QY 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220
DB 728 AAGAGCGGCCACTCTCTATCCAGAGCATAGGATCCTCACTCCACGTCCTTTCCACTCC 787
QY 221 AspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer 240
DB 788 GATGGCTCCCAAGAAATTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCATGCTCC 847
QY 241 SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCys 260
DB 848 TCATCCCTTGTGTTCCATGACGGCAGCTGGTGGTCTTGACAAGGCTGGATCTTACAAGTGT 907
QY 261 AlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuLeuGluArgAenCys 280
DB 908 GCCTGCTTGGCAGGCTATCTGAGGACGGCTGTGGAAATCTCTTGAAGAAAGAACTGC 967
QY 281 SerAspProGlyGlyProValAenGlyTyrGlnLysIleThrGlyGlyProGlyLeuIle 300
DB 968 TCAGACCTCGGGGCCCGCCAGTCAATGGGTACCAAGAAATAACAGGGGGCCCTGGGCTTATC 1027
QY 301 AsnGlyArgHisAlaLysIleGlyThrValValSerPhePheCysAenAsnSerTyrVal 320
DB 1028 AACGGACGCCATGCTATAAATTTGGACCGTGGTGTCTTTCTTTTGAACAACTCCTATGTT 1087
QY 321 LeuSerGlyAsnGluLysArgThrCysGlnGlnAsnGlyGluTyrPheSerGlyLysGlnPro 340
DB 1088 CTTAGTGGCAATGAGAAAGAACTTGCACAGAAATGGAGAGTGGTCAGGGAAACAGCCC 1147
QY 341 IleCysIleLysAlaCysArgGluProLysIleSerAspLeuValArgArgValLeu 360
DB 1148 ATCTGCATAAAGCTCGCCAGAAACCAAGATTTTCAGACCTGGTGTGAAGGAGAGTCTTT 1207
QY 361 ProMetGlnValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSer 380
DB 1208 CCGATGCGAGTTCAGTCAAGGGAGACACCAATTACACCGCTATCTCAGCGGCTTCAGC 1267
QY 381 LysGlnLysLeuGlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuPro 400
DB 1268 AAGCAGAAACTGCGAGTGCCCTTACCAGAGCCAGCCCTTCCCTTTGGAGATCTGCC 1327
QY 401 MetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArg 420
DB 1328 ATGGGATACCAACATCTGCATACCCAGCTCCAGTATCAGTGCATCTCACCTTCTTACCCG 1387
QY 421 ArgLeuGlySerSerArgThrCysLeuArgThrGlyLysTrpSerGlyArgAlaPro 440
DB 1388 CGCTGGGACGACGACGAGACATGCTGAAGACTGGGAAGTGGAGTGGCGGGGACCA 1447
QY 441 SerCysIleProIleCysGlyLysIleGluAsnIleThrAlaProLysThrGlnGlyLeu 460
DB 1448 TCCTGCATCCTATCTCGGGGAAAATTTGAGACATCATCTGCTCCAAAGACCCCAAGGGTTG 1507
QY 461 ArgTrpProTrpGlnAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeu 480
DB 1508 CGCTGGCGGTGGCAGGCGAGCATCTACAGAGGAGCACCGGGGTGCATGACGGCAGCCTA 1567
QY 481 HisLysGlyAlaTrpPheLeuValCysSerGlyAlaLeuValAenGluArgThrValVal 500
```

```
DB 1568 CACAGGAGACGTGGTTCTTAGTCTGCACGGTGCCTGGTGAATGAGCGCATGTGGTG 1627
QY 501 ValAlaAlaHisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeu 520
DB 1628 GTGGCTGCCACCTGTGTACTGACCTGGGGAAGGTCAACATGATCAAGACAGCAGACCTG 1687
QY 521 LysValValLeuGlyLysPheTyrArgAspAspAspArgAspGluLysThrIleGlnSer 540
DB 1688 AAGTTGTTTGGGGAATTTACCGGATGATGACCGGGATGAGGAAGACCATCCAGAGC 1747
QY 541 LeuGlnIleSerAlaIleIleLeuHisProAenTyrAspProIleLeuLeuAspAlaAsp 560
DB 1748 CTACAGATTTCCTATCATCTTGCATCCCACTATGACCCCATCTCTGTTGATGCTGAC 1807
QY 561 IleAlaIleLeuLysLeuAspLysAlaArgIleSerThrArgValGlnProIleCys 580
DB 1808 ATGCCATCTCTGAAGCTCTAGACAAGGCCCGGTATCAGCACCGGAGTCCAGCCCATCTGC 1867
QY 581 LeuAlaAlaSerArgAspLeuSerThrSerPheGlnGluSerHisIleThrValAlaGly 600
DB 1868 CTGCTGGCAGTCGGGATCTCAGCACTTCTTCCAGAGTCCACATCACTGTGGCTGGC 1927
QY 601 TrpAsnValLeuAlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGly 620
DB 1928 TGGAAATGCTTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGG 1987
QY 621 ValValSerValValAspSerLeuLysGluGlnHisGluAspHisGlyIlePro 640
DB 1988 GTGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGTCATCCCA 2047
QY 641 ValSerValThrAspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIle 660
DB 2048 GTGAGTGTCACTGATAAACATGTTCTGTCCAGCTGGGAACCCACTGCCCCCTTCTGATTC 2107
QY 661 CysThrAlaGluThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGlu 680
DB 2108 TGCACCTGCAGACAGAGGACATCGCGCTGTGTCTTCCGGGACGAGCATCTCCTGAG 2167
QY 681 ProArgTrpHisLeuMetGlyLeuValSerTrpSerTrpSerTrpSerTrpSerHisArg 700
DB 2168 CCACGCTGGCATCTGATGGACTGGTCACTGGAGCTATGATATAAATGATGACCCACAGG 2227
QY 701 LeuSerThrAlaPheThrLysValLeuProPheLysAspTrpIleGluArgAsnMetLys 720
DB 2228 CTCTCCACTGCTTCAACAGGTTGCTGCCTTTTAAAGACTGGATTGAAGAAATATGAAA 2287

RESULT 8
LOCUS AX133839 2306 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 25 from Patent WO0119856.
ACCESSION AX133839
VERSION AX133839.1 GI:14139791
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets,R.A., Fernandes,E., Herrmann,J.L., Liu,X., Yang,M. and Boldog,F.L.
TITLE Secreted human proteins, polynucleotides encoding them and methods of using the same
JOURNAL Patent: WO 0119856-A 25 22-MAR-2001;
FEATURES
source Location/Qualifiers
1..2306
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xrefs="taxon:9606"
128..2290
/notes="unnamed protein product"
/contig_start=1
CDS
```


/protein_id="CAC38970.1"
 /db_xref="GI:14139792"
 /translation="MEIGCWTLQGLTFLQLLLSSLPREYTVINEACPGAEWNIMCRE
 CCYDQIEVCYCPGKREVGYTIPCCRENEECDSLIHPGCTIFENCKSRNGSWGCT
 LDYFVYKGFYCAECRAGWYDQMRGQVLRAPKQGIILLESYPLNAHCEWTIRAKPGF
 VIOLRFVMSLSDPYMCQYDVEVRDGDNRDGOIIRKVCNRPAPIQSGSSHLWLF
 HSDGKNFDPFALYEITACSSPCPHDGTCTVLDKAGSKYKACLAGTQRCENLLE
 ERNCSDPGVPNGTKITGGPLNGRHAKIGTVSPFNNYSVLNGNERKTCQNGE
 WSKQPIICIRACREPKISDLVRRVLPQVQRETPHLQLYSAFASKQLQSAPTKRP
 ALPFGDLPMGYQHLHTLOQYECISPFYRLGSSRKTLCTGKWSGRAPSCIPICGKIE
 NITAPKIQGLRWQMAIYRRRTSGVHDSLHKGAFVLCGALVNERTVVAACHVTD
 LGKVTMIKTADLVKGFVDRDDDEKTIQSLQISAIILHPNVDPTILLDAIILK
 LDKARISTRVQPICLAASRLDSTSPQESHITVAGWNVLDVRSFGKNDILRGVSV
 VDSLLCEQEDHGIPVSDTNMFCASWEPSTAFSDICTAETGGIAAVFPGRASPRR
 WMLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK"

ORIGIN

Alignment Scores:

Align. No.: 6, 42e-280 Length: 2306
 Score: 3939.00 Matches: 718
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 99.72% Mismatches: 0
 Query Match: 99.85% Indels: 0
 DB: 6 Gaps: 0

US-10-063-692-38 (1-720) x AX133839 (1-2306)

Qy	1	MetGluLeuGlyCysTrpThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuLeuSer	20	Db	788	GATGGCTCCAGGAATTTTGTACGGTTCATGCGCCATTTATGAGGAGATCAGACAGTGTCC	847
Db	128	ATGGAGCTGGTGTGTCGAGCGAGTGGGGCTCACTTTCTTCAGCTCTTCACTCG	187	Qy	241	SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCys	260
Qy	21	SerLeuProArgGluThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle	40	Db	848	TCATCCCTTGTTCATGACGCGACGTCCTTGCAAGGCTGGATCTTACAAGTGT	907
Db	188	TCCTTGCCAAAGAGTAGTACAGTCAATTAATGAAGCTGCCCTGAGCAGAGTGGAAATATC	247	Qy	261	AlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuLeuGluGluArgAsnCys	280
Qy	41	MetCysArgGluCysCysGluTrpAspGlnIleGluCysValCysProGlyLysArgGlu	60	Db	908	GCCTGCTTGGCAGCTATCTGCGCAGCGCTGTGAAATCTCTCTTGAAGAAAGAAATCGC	967
Db	248	ATGTGTCGGAGTGTGTGAATATGATCAGATTGAGTGCCTGTCGCCCGGAAAGAGGAA	307	Qy	281	SerAspProGlyGlyProValAsnGlyTyrGlnLysIleThrGlyGlyProGlyLeuIle	300
Qy	61	ValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu	80	Db	968	TCAGACCTGGGGGCCCGCAGTCAATGGGTACAGAAAATAACAGGGGCCCTTGGGCTTATC	1027
Db	308	GTGCTGGTATACCATCCCTTCTGTCAGGAATGAGGAGATGAGTGTGACTCTGCTG	367	Qy	301	AsnGlyArgHisAlaLysIleGlyThrValValSerPhePheCysAsnAsnSerTyrVal	320
Qy	81	IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly	100	Db	1028	AACGGACGCCATGCTAAATTTGGCACCGTGTGTCCTTTTGTAACTCTCTATGTT	1087
Db	368	ATCCACCCAGGTGTGTACCATCTTTGAAACTGCAAGAGCTGCCGAAATGCTCATGGGG	427	Qy	321	LeuSerGlyAsnGluLysArgThrCysGlnGlnAsnGlyGluTrpSerGlyLysGlnPro	340
Qy	101	GlyThrLeuAspAspPheTyrValLysGlyPheTyrCysAlaGluCysArgAlaGlyTrp	120	Db	1088	CTTAGTGGCAATGAGAAAAGAACTTGGCAGCAGAAATGGAGAGTGGTCAGGAAACAGCCC	1147
Db	428	GGTACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTCCCGAGCGCTGG	487	Qy	341	IleCysIleLysAlaCysArgGluProLysIleSerAspLeuValArgArgValLeu	360
Qy	121	TyrGlyCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu	140	Db	1148	ATCTGCATAAAGCTGCCCGAGAACCAAGATTTTCAGACCTGGTGAGAGAGAGTCTT	1207
Db	488	TACGGAGGACATGCATGCATGTGGCCAGGTTCGCGAGCCCCAAAGGTCAGATTTC	547	Qy	361	ProMetGlnValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSer	380
Qy	141	LeuGluSerTyrProLeuAsnAlaHisCysGluTrpThrIleHisAlaLysProGlyPhe	160	Db	1208	CCGATGCGAGTTCAGTCNAGGGAGACACCATTTACACGCTATACTCAGCGGCTTCAGC	1267
Db	548	TTGGAAAGCTATCCCTTAATGTCTCACTGTGAATGGACCATTCATGCTAAACCTGGTTT	607	Qy	381	LysGlnLysLeuGlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuPro	400
Qy	161	ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp	180	Db	1268	AAGCAGAAACTGCAGAGTGCCTTACCAAGAGCCAGCCCTTCCCTTGGAGATCTGCC	1327
Db	608	GTCAATCAACTAAGATTGTGATGTTGAGCTCGAGTTCAGTACATGTGCCAGATGAC	667	Qy	401	MetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArg	420
Qy	181	TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleLysArgValCysGly	200	Db	1328	ATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCCTTCTACCCG	1387
Db	668	TATGTTGAGTTCGTGATGAGAGAACCCCGCATGGCCAGATCAATCAAGCGTGTCTGGC	727	Qy	421	ArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTrpSerGlyArgAlaPro	440
Qy	201	AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer	220	Db	1388	CGCTGGCAGCAGCAGGAGAACATGCTGAAGCTGGGAAGTGGAGTGGCGGGCACCA	1447
Db	728	AACGAGCGGCCAGCTCTATCCAGAGCATAGGATCTCACTCCACGCTCTTCCACTCC	787	Qy	441	SerCysIleProIleCysGlyLysIleGluAsnIleThrAlaProLysThrGlnGlyLeu	460
Qy	221	AspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer	240	Db	1448	TCCTGCTATCCCTATCTGCGGAAAATTTGAGAACATCACTGCTCCAAAGACCCCAAGGTTG	1507
				Qy	461	ArgTrpProTrpGlnAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeu	480
				Db	1508	CGCTGGCGGTGGCAGGAGCCATCTACAGAGGAGCCAGCGGGGTGCATGACGCGAGCCTA	1567
				Qy	481	HisLysGlyAlaTrpPheLeuValCysSerGlyAlaLeuValAsnGluArgThrValVal	500
				Db	1568	CACAAAGGAGCGTGTTCCTAGTCTGACGGTGGCTTGGTGAATGAGCGCATGTGGTG	1627
				Qy	501	ValAlaAlaHisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeu	520
				Db	1628	GTGGCTGCCCATCTGTACTGACCTGGGGAAGTCCCATGATCAAGCAGCAGACCTG	1687
				Qy	521	LysValValLeuGlyLysPheTyrArgAspAspAspArgAspGlyLysThrIleGlnSer	540
				Db	1688	AAAGTTGTTGGGGAATTTCTACCGGGATGATGACCGGGATGAGAGACATCCAGAGC	1747
				Qy	541	LeuGlnIleSerAlaIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAsp	560
				Db	1748	CTACAGATTTCTGCTATCATCTGTCATCCCACTATGACCCCATCTCTGTTGATGTGAC	1807
				Qy	561	IleAlaIleLeuLysLeuLeuAspLysAlaArgIleSerThrArgValGlnProIleCys	580
				Db	1808	ATCGCCATCTCTGAAGCTCTAGACAAGGCCGCTATCAGCACCCGAGTCCAGGCCATCTGC	1867
				Qy	581	LeuAlaAlaSerArgAspLeuSerThrSerPheGlnGluSerHisIleThrValAlaGly	600
				Db	1868	CTGCTGCCAGTGGGATCTCAGCACTTCTTCCAGAGTCCCACTCATCTGTGGTGGC	1927

601 TrpAsnValLeuAlaSerValArgSerProGlyPheLeuAsnAspThrLeuArgSerGly 620
 1928 TGGAAATGCTGGCAGACGTCAGGAGCCCTGGCTTCAAGAACGACACACTGGCGCTCTGGG 1987
 621 ValValSerValValAlaSerLeuLeuCysGluGluHisGluAspHisGlyIlePro 640
 1988 GTGGTCAGTGTGGTGGACGCTGCTGTGTGGAGGAGCAGCATGAGACCATGCACTCCCA 2047
 641 ValSerValThrAspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIle 660
 2048 GTGAGTGTCTACTGATTAACATGTTCTGTGCAGCTGGGACCCACTGCCCTTCTGATATC 2107
 661 CysThrAlaGluThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGlu 680
 2108 TGCACGTGCAGACAGGAGGAGCATCGCGCTGTCTCTCCGGGAGCAGCATCTCCTGAG 2167
 681 ProArgTrpHisLeuMetGlyLeuValSerTrpSerTrpAspIlyThrCysSerHisArg 700
 2168 CCACGCTGGCATCTGATGGAGCTGGTCAGCTGGAGCTATGATAAAACATGCACCCACAGG 2227
 701 LeuSerThrAlaPheThrLysValLeuProPheLysAspTrpIleGluArgAsnMetLys 720
 2228 CTCTCCACTGCCCTTCCACCAAGGTGCTGCTTTTAAAGACTGGATTGAAGAAATATGANA 2287

RESULT 9
 LOCUS BD012236
 DEFINITION A novel gene encoding a serine protease-like protein.
 ACCESSION BD012236
 VERSION BD012236.1 GI:22092425
 KEYWORDS WO 0109349-A/3.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 2289)
 Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K., Otsuki, T., Yano, K., Murakami, K., Kanazaki, K., Inoue, Y., Hashimoto, E. and Kashima, A.
 A novel gene encoding a serine protease-like protein
 Patent: WO 0109349-A 3 08-FEB-2001;
 HELIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, OMOYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI, KAZUHIRO YANO, KOJI MURAKAMI, KOJI KANZAKI, YOSHIHISA INOUE, EMI HASHIMOTO, AKIKO KASHIMA
 PN WO 0109349-A/3
 PD 08-FEB-2001
 PF 28-JUL-2000 WO 2000JP005062
 PR 29-JUL-1999 JP 99P 248036, 27-AUG-1999 JP 99P 300253 PR
 11-JAN-2000 JP 00P 118776, 02-MAY-2000 JP 00P 183767 PR
 18-OCT-1999 US 60/159590, 17-FEB-2000 US 60/183322 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, PI KAORU SAITO, PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI, KAZUHIRO YANO, KOJI MURAKAMI, PI KOJI KANZAKI, PI YOSHIHISA INOUE, EMI HASHIMOTO, AKIKO KASHIMA
 PC C12N15/57, C12N9/64, C12N15/63, C12N5/06, C07K16/40, C12Q1/68, PC
 GOIN3/573,
 CC A61K38/48, A61K31/7052, A61K48/00//C12P21/08, (C12N9/64, C12R1:91)
 PC Description of Artificial Sequence: an artificial sequence FH

Key Location/Qualifiers
 1. 2289
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"

FEATURES
 source
 Location/Qualifiers
 1. 2289
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"

ORIGIN
 Alignment Scores: 1.23e-278 Length: 2289
 Pred. No.: 3921.50 Matches: 719
 Score:

Percent Similarity: 97.56% Conservative: 0
 Best Local Similarity: 97.56% Mismatches: 1
 Query Match: 99.40% Indels: 17
 DB: 6 Gaps: 1

US-10-063-692-38 (1-720) x BD012236 (1-2289)

QY 1 MetGluLeuGlyCysTrpThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuSer 20
 DB 1 ATGGAGCTGGGTGGTGGAGCGAGTTGGGGCTACATTTCTTCAGCTCCTTCTCATCTCG 60
 QY 21 SerLeuProArgGluTrpThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40
 DB 61 TCTTCCCAAGAGAGTACAGCTCATTAATGAAGCTGCCCTGGAGCAGAGTGAATATC 120
 QY 41 MetCysArgGluCysCysGluTrpAspGlnIleGluCysValCysProGlyLysArgGlu 60
 DB 121 ATGTGTGGGAGTGTGTGAATATGATCAGATTAGTGGCTCTGCCCGGAAAGAGGAA 180
 QY 61 ValValGlyTrpThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
 DB 181 GTCGTGGGTATACCATCCTTGTCTCAGGAATGAGGAGAAATGAGTGTGACTCCTGCTG 240
 QY 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100
 DB 241 ATCCACCCAGGTGTACCATCTTTGAAACTGCAAGAGCTGCCGAAATGCTCATGGGG 300
 QY 101 GlyThrLeuAspAspPheTrpValLysGlyPheTrpCysAlaGluCysArgAlaGlyTrp 120
 DB 301 GGTACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTCCGAGCAGGTGG 360
 QY 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu 140
 DB 361 TAGCGAGGAGACTGCAATGCGATGTGGCAGGTTCTGGAGCCCCAAGGGTCAAGATTG 420
 QY 141 LeuGluSerTrpProLeuAsnAlaHisCysGluTrpThrIleHisAlaLysProGlyPhe 160
 DB 421 TTGGAAGCTATCCCTTAATGTCTACTGTGAATGGACCATTCATGCTAAACCTGGT 480
 QY 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTrpMetCysGlnTrpAsp 180
 DB 481 GTCATCAACTAAGATTGTGATGTTGAGCTGGAGTTTGACTACATGTGCCAGTATGAC 540
 QY 181 TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleLysArgValCysGly 200
 DB 541 TATGTTGAGTTCGTGATGGAGACAACCGCGATGGCCAGATCATCAAGCGTGTCTGTGG 600
 QY 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220
 DB 601 AACGAGGGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCCACGTCCTCTTCCACTCC 660
 QY 221 AspGlySerLysAsnPheAspGlyPheHisAlaIleTrpGluGluIleThrAlaCysSer 240
 DB 661 GATGGCTCCCAAGAAATTTGACGGTTTCCATGCTCCATTTATGAGGAGATCACAGCATGCTCC 720
 QY 241 SerSerProCysPheHisAspGlyThrCysValIleAspLysAlaGlySerTrpLysCys 260
 DB 721 TCATCCCTTGTGTTCCATGACGCGATGCTGCTTGACAGGCTGACCTTACAGTGT 780
 QY 261 AlaCysLeuAlaGlyTrpThrGlyGlnArgCysGluAsnLeu----- 274
 DB 781 GCCTGCTGGCAGGCTATATCTGGGCGAGCTGTGAAATCTTCTGGAGGCTGGGAAGTCC 840
 QY 275 -----LeuGluLysArgAsnCysSerAspPro 283
 DB 841 AAGATCAAGGCGTCAGAAAGATTTCATTGTCTGCTTGAAGAAAGAACTGCTCAGACCT 900
 QY 284 GlyGlyProValAsnGlyTrpGlnLysIleThrGlyGlyProGlyLeuIleAsnGlyArg 303
 DB 901 GGGGGCCAGTCAATGGGTACCGAAATTAACAGGGGGCCCTGGGCTTATCAACGCGAGC 960
 QY 304 HisAlaLysIleGlyThrValValSerPhePheCysAsnAsnSerTrpValLeuSerGly 323

Db 961 CATGCTAAATGGCAGCGTGGTCTCTTTCTTTGTAAACACTCCTATGTTCTTAGTGGC 1020
Qy 324 AsnGluLysArgThrCysGlnGlnAsnGlyGluTrpSerGlyLysGlnProIleCysIle 343
Db 1021 AATGAGAAAGAACTTCCAGCAGAAATGGAGAGTGGTCAGGAAACAGCCCATCTGCATA 1080
Qy 344 LysAlaCysArgGluProLysIleSerAspLeuValArgArgValLeuProMetGln 363
Db 1081 AAAGCCCTGCGAGAACCAAGATTTACAGACTGGTGAGAGGAGAGTCTTCGCGATCGAG 1140
Qy 364 ValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSerLysGlnLys 383
Db 1141 GTTCAGTCAGAGGAGACACCATACACAGCTATCTACGGGCTTCAGCAGCAGAAA 1200
Qy 384 LeuGlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuProMetGlyTyr 403
Db 1201 CTGCAGAGTGCCTTACCAAGAGCCAGCCCTTCCCTTTGAGATCTGCCCATCTGGGATAC 1260
Qy 404 GlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArgArgLeuGly 423
Db 1261 CAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCCCTTCTACCCGCCCTGGGC 1320
Qy 424 SerSerArgArgThrCysLeuAlaGlyThrGlyLysTrpSerGlyArgAlaProSerCysIle 443
Db 1321 AGCAGCAGGAGGACATCTCTGAGGACTGGGAGTGGAGTGGGGGACCATCTCTGCATC 1380
Qy 444 ProfileCysGlyLysIleGluAsnIleThrAlaProLysThrGlnGlyLeuAlaGlyTyrPro 463
Db 1381 CCTATCTGCGGGAATTTGAGAACATCACTGCTCCAAAGACCCCAAGGTTGCGCTGGCGC 1440
Qy 464 TrpGlnAlaAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeuHisLysGly 483
Db 1441 TGGCAGCAGCCCATCTACAGGAGGACAGCGGGTGCATGCGGACCCCTACCAAGGGA 1500
Qy 484 AlaTrpPheLeuValCysSerGlyAlaLeuValAsnGluArgThrValValAlaAla 503
Db 1501 GCGTGGTCTTAGTCTGACGGTGGCTCTGGTGAATGAGCGCACTGGTGGTGGTGGC 1560
Qy 504 HisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeuLysValVal 523
Db 1561 CACTGTGTACTGACCTGGGGAAGTCCACATGATCAAGACAGCAGACCTGGAAGTTGTT 1620
Qy 524 LeuGlyLysPheTyrArgAspAspAspArgAspGluLysThrIleGlnSerLeuGlnIle 543
Db 1621 TTGGGGAATTTACCGGGATGATGACCGGGATGAGAAGACCATCCAGAGCCCTACAGATT 1680
Qy 544 SerAlaIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAspIleAlaIle 563
Db 1681 TCTGCTATCATCTGCTATCCCACTATGACCCCATCTGCTTGTATGCTGATCGCCATC 1740
Qy 564 LeuLysLeuLeuAspLysAlaArgIleSerThrArgValGlnProIleCysLeuAlaAla 583
Db 1741 CTGAAGCTCTAGCAAGGCCCGTATCAGCACCGGATCCAGCCCATCTGCTGCTGCC 1800
Qy 584 SerArgAspLeuSerThrSerPheGlnGluSerHisIleThrValAlaGlyTyrAsnVal 603
Db 1801 AGTCGGGATCTCAGCACTTCTTCCAGAGTCCCATCACTCTGGCTGGCTGGATGTC 1860
Qy 604 LeuAlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSer 623
Db 1861 CTGGCAGAGTGAGGAGCCCTGGCTTCAAGAACACACACTGCGCTCTGGGGTGGTCAGT 1920
Qy 624 ValValAspSerLeuLeuCysGluGlnHisGluAspHisGlyIleProValSerVal 643
Db 1921 GTGGTGGACTCGTCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCCGATGAGTGT 1980
Qy 644 ThrAspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAla 663
Db 1981 ACTGATAACATGTTCTGTGCGAGCTGGGAACCCACTGCCCTTCTGATATCTGCATCTG 2040
Qy 664 GluThrGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTrp 683
Db 2041 GAGACAGGAGGCATCGCGGTGTGTCTTCCCGGAGCAGCATCTCTGAGCCACCGCTGG 2100

Qy 684 HisLeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHisArgLeuSerThr 703
Db 2101 CATCTGATGGACTGGTCAGCTGAGCTATGATAAAACATGCAGCCACAGCTCTCCACT 2160
Qy 704 AlaPheThrLysValLeuProPheLysAspTrpIleGluArgAsnMetLys 720
Db 2161 GCCTTACCAGGTGCTGCTTTTAAAGACTGGATTGAAAGAAATATGAAA 2211
RESULT 10
BD157134 2784 bp DNA linear PAT 17-JAN-2003
LOCUS Primer for synthesizing full-length cDNA and use thereof.
DEFINITION BD157134
ACCESSION BD157134
VERSION BD157134.1 GI:27862892
KEYWORDS JP 2002191363-A/11977.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ota, T., Isogai, T., Nishikawa, T., Havaashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 11977 09-JUL-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/11977
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/21, C12N1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof PH Key
Location/Qualifiers
FT CDS (47). (2257).
FEATURES Location/Qualifiers
source 1. .2784
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1.58e-278 Length: 2784
Score: 3921.50 Matches: 719
Percent Similarity: 97.56% Conservatives: 0
Best Local Similarity: 97.56% Mismatches: 1
Query Match: 99.40% Indels: 17
DB: Gaps: 1
US-10-063-692-38 (1-720) x BD157134 (1-2784)
Qy 1 MetGluLeuGlyCysTrpThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuSer 20
Db 47 ATGAGCTGGTGGTGGAGCGCAGTTGGGGCTCACATTTCTCAGCTCTCTTCATCTCG 106
Qy 21 SerLeuProArgGluTyrThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40
Db 107 TCCTTCCAGAGAGGTACACAGTCATTAATGAAGCTTGCCTGGAGCAGAGTGGATATC 166
Qy 41 MetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysProGlyLysArgGlu 60
Db 167 ATGTGTGGGAGTGTGTGAATATGATCAGATTGAGTGGCTCTGCCCGGAAAGAGGAA 226
Qy 61 ValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
Db 227 GTCGTGGGTATACCATCCCTTGTCTGCTCAGGAATGAGGAGATGAGTGTGACTCTCTGCTG 286

QY	81	IleHisProGlyCysThrIlePheGluAenCysLysSerCysArgLanGlySerTrpGly	100
Db	287	ATCCACCCAGGTTGTACCATCTTTGAAAACTGCAAGAGCTGCCGAAATGGCTCATGGGG	346
QY	101	GlyThrLeuAspPhePheValLysGlyPheTyrCysAlaGluCysArgAlaGlyTrp	120
Db	347	GGTACCTTGATGACTTCTATGTGAAGGGGTTCTACTGTGACAGTGCCGAGCAGCTGG	406
QY	121	TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu	140
Db	407	TACGGAGGACATGCATCGCATGCGCATGTGCGCAGGTTCTGCGAGCCCCAAAAGGGTCAGATTTG	466
QY	141	LeuGluSerTyrProLeuAenAlaHisCysGluTrpThrIleHisAlaLysProGlyPhe	160
Db	467	TTGGAAAGCTATCCCTTAATGCTCACTGTGTAATGGACCATTCATGCTAAACCTGGGTTT	526
QY	161	ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp	180
Db	527	GTCAATCAACTAAGATTGTGTCATGTTGAGCTCGAGTTTGACTACATGTGCCAGTATGAC	586
QY	181	TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleLysArgValCysGly	200
Db	587	TATGTTGAGGTTCTGTATGGAGACAACCGCGATGGCCAGATCATCAAGCGTGTCTGTGGC	646
QY	201	AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer	220
Db	647	AACGAGCGGCAGCTCTATCCAGAGCATAGGATCCTCACTCCACGCTCTCTTCCACTCC	706
QY	221	AspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer	240
Db	707	GATGGCTCCAAGAAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGATGCTCC	766
QY	241	SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCys	260
Db	767	TCATCCCTCTGTTCCATGACGACGCTGCTCTTGACAAAGCTGGACCTTACAAAGTG	826
QY	261	AlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAenLeu-----	274
Db	827	GCCTGCTTGGCAGCTATACTGGGCGAGCGCTGTGAAAAATCTTCTGGAGGCTGGGAAGTCC	886
QY	275	-----LeuGluGluArgAenCysSerAspPro	283
Db	887	AAGATCAAGCGGTGAGAAGATTCTGCTGCTTCTGAGAAAGAACTGCTCAGACCT	946
QY	284	GlyGlyProValAsnGlyTyrGlnLysIleThrGlyProGlyLeuIleAsnGlyArg	303
Db	947	GGGGCCCCAGTCAATGGGTACCGAAAAATAACAGGGGGCCCTGGGCTTATCAACGGACGC	1006
QY	304	HisAlaLysIleGlyThrValValSerPhePheCysAsnAsnSerTyrValLeuSerGly	323
Db	1007	CATGCTAAAAATGGCACCGTGTCTCTTTGTTGTAACAACCTCTATGTTCTTAGTGGC	1066
QY	324	AsnGluLysArgThrCysGlnAsnGlyGluTrpSerGlyLysGlnProIleCysIle	343
Db	1067	AATGAGAAAAAGAACTTCCACAGAAATGGAGAGTGGTCAGGAAAAACAGCCCATCTGCATA	1126
QY	344	LysAlaCysArgGluProLysIleSerAspLeuValArgArgValLeuProMetGln	363
Db	1127	AAAGCTGCCGAGAACCAAGATTTTCAGACTGTGTGAGAGGAGAGTTCTTCGATGCAG	1186
QY	364	ValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSerLysGlnLys	383
Db	1187	GTTTCAGTCAAGGGAGACACCATTAACACGAGCTATACTCAGCGGCTTTTCAGCAAGCAGAAA	1246
QY	384	LeuGlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuProMetGlyTyr	403
Db	1247	CTGCAGAGTGCCTTACCAAGAACCCAGCCCTTCCCTTTTGAGATCTGCCCATGGATAC	1306
QY	404	GlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArgLeuGly	423
Db	1307	CAACATCTGCATACCCAGCTCCAGTATGAGTGATCTCACCTTCTACCGCGCGCTGGC	1366
QY	424	SerSerArgArgThrCysLeuArgThrGlyLysTrpSerGlyArgAlaProSerCysIle	443
Db	1367	AGCAGCGAGGAGACATGTTCTGAGGACTGGAAAGTGGAGTGGGGCGGCACCATCTGCATC	1426
QY	444	ProIleCysGlyLysIleGluAenIleThrAlaProLysThrGlnGlyLeuArgTrpPro	463
Db	1427	CCTATCTCGGGAAAAATTGAGAAACATCACTGTCTCCAAAGACCCCAAGGGTTGCGCTGGCCG	1486
QY	464	TrpGlnAlaAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeuHisLysGly	483
Db	1487	TGGCAGCGACCATCTACAGGAGGACAGCGGGGTGCATGACGCGACCTTACACAAGGGA	1546
QY	484	AlaTrpPheLeuValCysSerGlyAlaLeuValAsnGluArgThrValValAlaAlaAla	503
Db	1547	GCCTGGTTCCTAGTCTGACGGGTGCCCTGTGTGAATGAGGCGACTGTGTGGTGGTGCTGCC	1606
QY	504	HisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeuLysValVal	523
Db	1607	CACCTGTGTTACTGACCTGGGGAAGGTCAACCATGATCAAGACAGACAGACCTGAAAGTTGTT	1666
QY	524	LeuGlyLysPheTyrArgAspAspArgAspGluLysThrIleGlnSerLeuGlnIle	543
Db	1667	TTGGGGAATTTCTACCGGATGATGACCGGGATGAGAAAGACCATCCAGACCTTACAGATT	1726
QY	544	SerAlaIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAspIleAlaIle	563
Db	1727	TCGTGCTATCTGCTATCCCACTATGACCCCATCTCTGCTTGATGCTGACATCGGCATC	1786
QY	564	LeuLysLeuLeuAspLysAlaArgIleSerThrArgValGlnProIleCysLeuAlaAla	583
Db	1787	CTGAAGCTCCTAGACAAGCCCGTATCAGCACCGAGTCCAGCCCATCTGCTCGTGCTCC	1846
QY	584	SerArgAspLeuSerThrSerPheGlnGlnLysHisIleThrValAlaGlyTrpAsnVal	603
Db	1847	AGTCGGGATCTCAGCACTTCTTCCAGGAGTCCACATCACTGTGCTGGCTGGAATGTC	1906
QY	604	LeuAlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSer	623
Db	1907	CTGGCAGAGCTGAGGAGCCCTGCTTCCAGAACGACACACTGCGCTCTGGGGTGGTCAGT	1966
QY	624	ValValAspSerLeuLeuCysGluGlnHisGluAspHisGlyIleProValSerVal	643
Db	1967	GTGCTGAGCTCGCTGCTGTGTGAGGAGCAGCATGAGACCATGGCATCCAGTGAGTGTC	2026
QY	644	ThrAspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAla	663
Db	2027	ACTGATAACATGTTCTGTGCCAGCTGGAAACCCACACTGCCCTTCTGATATCTGCACATGCA	2086
QY	664	GluThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTrp	683
Db	2087	GAGACAGGAGGATCGCGCTGTGCTTCCCGGAGCAGCATCTCTGAGCCACGCTGG	2146
QY	684	HisLeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHisArgLeuSerThr	703
Db	2147	CACTCATGGGACTGGTCACTGAGCTATGATAAAACATGACGCCACAGGCTCTCCACT	2206
QY	704	AlaPheThrLysValLeuProPheLysAspTrpIleGluArgAsnMetLys	720
Db	2207	GCCTTCAACAGGTGCTGCCCTTTTAAAGACTGGATTGAAAGAAATATGAAA	2257
RESULT 11			
AX878296			
LOCUS	AX878296	2784 bp	DNA
DEFINITION	Sequence 13201 from Patent EP1074617.		
ACCESSION	AX878296		
VERSION	AX878296.1		
KEYWORDS	GI:40033032		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	PAT 17-DEC-2003		

```

Ihii,S. Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primers for synthesizing full-length cDNA and their use
Patent: EP 1074617-A 13201 07-FEB-2001;
Research Association for Biotechnology (JP)
Location/Qualifiers
1. .2784
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
47. .2260
/notes="unnamed protein product"
/codon_start=1
/protein_id="CA890091.1"
/db_xref="GI:40033033"
/translatation="MELGCTWQLGLTFLLQLLLSSLPREYTVINEACPGAEWNIMCRE
CSDYDITCEYCPGKRGVYGTIPCPCNEENECDSLIHPGCTIPENCKSSRSGWGT
LDYFYVKGFCACRAGYWGDCMRGCVLRAPKGQILLESYPLNAHCWETIAKQGF
VIOLRFVMSLEFDYVMDYDVSVRDGNRDGQILKRVCGNERPAPIQSGSSHLVLF
HSDGKNPFGFHLAYEITACSSSPCFHDGTCVLDKAGPYKCAKAGITGVGCENLLE
AGSKTSLASDSLSULBEENCSDPGPGVYQKITGPGGLINGHAKITGVTSFNN
SYVLSNGEKRTCCQNGEWSGKQPCICAKREPKISDLVRRRVLPVMOVQSRETPHLQY
SAAFSQKQAPATKQKPAIPGDLPMYGQHLHTLOQVECTSPFYRLGSSRRTCLEGT
KWSGAPSCIPICGKIENTAPKTQGLRWPMQAAIYRRTSGVHDGSLHKGAWELVCSG
ALVNERTVVAACHVDLTKVMTIKADLVVLGKGYRDRDRDEKTIQSLQISAILIH
PNYDPIILLDDAIILKLDKARISRVQPICLAASRDLSITSFQESHI TVAGWNVLIAD
RSPGFNDTILRSGVSDVSLICEQEDHGI PVSVTDNNMFCASWEPSTASDICTCTAE
GGTAAVSPFCRASPEPRHMLGMSVSDYKTSCHRLSTAFKTLVPKFDWTERNNK"

```

ORIGIN

Alignment Scores:		
Pred. No.:	1.58e-278	Length: 2784
Score:	3921.50	Matches: 719
Percent Similarity:	97.56%	Conservative: 0
Best Local Similarity:	97.56%	Mismatches: 1
Query Match:	99.40%	Indels: 17
DB:	6	Gaps: 1
US-10-063-693-38 (1-720) x AX878296 (1-2784)		

QY 524 LeuGlyLysPheTyrArgAspAspArgAspGluLysThrIleGlnSerLeuGlnIle 543
 DB 1667 TTGGGGAATTTACCGGATGATGACCGGATGAGAAGACCATCCAGAGCCTACAGATT 1726

QY 544 SerAlaIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAspIleAlaIle 563
 DB 1727 TGTGCTATCATCTGCATCCAACTATGACCCCATCTCTGTTGATGCTGACATCGGCATC 1786

QY 564 LeuLysLeuLeuAspLysAlaArgIleSerThrArgValGlnProIleCysLeuAlaAla 583
 DB 1787 CTGAAGCTCTACAGAGCCCGCTATCAGCACCGAGTCCAGCCCATCTGCTCGCTGCC 1846

QY 584 SerArgAspLeuSerThrSerPheGlnGlnSerHisIleThrValIleGlyTrpAsnVal 603
 DB 1847 AGTCGGGATCTCAGCACTTCTTCCAGGAGTCCACATCACTGTGGCTGGTGGAAATGC 1906

QY 604 LeuAlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSer 623
 DB 1907 CTGGCAGACGTGAGGAGCCCTGCGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTCAGT 1966

QY 624 ValValAspSerLeuLeuCysGluGlnHisGluAspHisGlyIleProValSerVal 643
 DB 1967 GTGGTGGACTCGTCTGTGTGAGGAGCAGCATGGAGCCATGCGATCCCGAGTGTGC 2026

QY 644 ThrAspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAla 663
 DB 2027 ACTGATAACATGTTCTGTGCAGCTGGGAACCCACTGCCCTTCTGATATCTGCACCTGCA 2086

QY 664 GluThrGlyGlyIleAlaAlaValSerPheProGlyValArgAlaSerProGluProAsnGlyTrp 683
 DB 2087 GAGACAGGAGGATCGCGCTGTGCTTCCCGGAGGAGCATCTCTGAGCCACCGCTGG 2146

QY 684 HisLeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHisArgLeuSerThr 703
 DB 2147 CATCTGATGGAGTGGTGCAGTGGAGTATGATAAAACATGCAGCCACAGGCTCTCCACT 2206

QY 704 AlaPheThrLysValLeuProPheLysAspTrpIleGluArgAsnMetLys 720
 DB 2207 GCCTTCAACCAAGGTGCTGCCTTTTAAAGACTGGATTGAAAGAAATATGAAA 2257

RESULT 12
 BD012234
 LOCUS 2784 bp DNA linear PAT 02-AUG-2002
 DEFINITION A novel gene encoding a serine protease-like protein.
 ACCESSION BD012234
 VERSION BD012234.1 GI:22092423
 KEYWORDS WO 0109349-A/1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2784)
 Ota.T., Isogai.T., Nishikawa.T., Hayaashi.K., Saiko.K., Yamamoto.J., Ishii.S., Sugiyama.T., Wakamatsu.A., Nagai.K., Otsuki.T., Yano.K., Murakami.K., Kanzaki.K., Inoue.Y., Hashimoto.E. and Kashima,A.
 A novel gene encoding a serine protease-like protein
 Patent: WO 0109349-A 1 08-FEB-2001;
 HELIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAZUHIRO YANO, JUNICHI YAMAMOTO, SHIZUKO ISHII, OMOYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI, KAZUHIRO YANO, KOJI MURAKAMI, KOJI KANZAKI, YOSHIO INOUE, EMI HASHIMOTO, AKIKO KASHIMA
 OS Homo sapiens (human)
 PN WO 0109349-A/1
 PD 08-FEB-2001
 PF 28-JUL-2000 WO 2000JP005062
 PR 29-JUL-1999 JP 99P 248036, 27-AUG-1999 JP 99P 300253 PR
 11-JAN-2000 JP 00P 118776, 02-MAY-2000 JP 00P 183767 PR
 18-OCT-1999 US 60/159590, 17-FEB-2000 US 60/183322 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, PI KAZUHIRO YANO, PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI, KAZUHIRO YANO, KOJI MURAKAMI, PI

KOJI KANZAKI,
 PI YOSHIO INOUE, EMI HASHIMOTO, AKIKO KASHIMA
 PC C12N15/57, C12N9/64, C12N15/63, C12N5/06, C07K16/40, C12Q1/68, PC
 G01N33/573,
 PC A61K38/48, A61K31/7052, A61K48/00/C12P21/08, C12N9/64, C12R1/91)
 CC
 FH Key Location/Qualifiers
 FT CDS (47). (2257).

FEATURES
 source 1..2784
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 1..58e-278 Length: 2784
 Score: 3921.50 Matches: 719
 Percent Similarity: 97.56% Conservative: 0
 Best Local Similarity: 97.56% Mismatches: 1
 Query Match: 99.40% Indels: 17
 DB: Gaps: 1

US-10-063-692-38 (1-720) x BD012234 (1-2784)

QY 1 MetGluLeuGlyCysTrpThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuIleSer 20
 DB 47 ATGGAGCTGGGTGCTGGAGCGCAGTTGGGGCTCACCTTTCTTCAGCTCCTTCATCTCG 106

QY 21 SerLeuProArgGluTyrThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40
 DB 107 TCCTTCCCAAGAGAGTACACAGTCATTATGAAGCTGCCCTGGAGCAGAGTGGAAATATC 166

QY 41 MetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysProGlyLysArgGlu 60
 DB 167 ATGTGTGGGAGTGTGTGAATATGATCAGATTGAGTGCCTCTGCCCGGAAAGAGGAA 226

QY 61 ValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
 DB 227 GTCGTGGGTATATACCATCCCTTCTGTCAGGAATGAGGAGATGAGTGTGACTCTCTGCTG 286

QY 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100
 DB 287 ATCCACCAGGTGTGACCATCTTTGAAACCTGCAAGAGCTGCCGAAATGCTCATGGGG 346

QY 101 GlyThrLeuAspAspPheTyrValLysGlyPheTyrCysAlaGluCysArgAlaGlyTrp 120
 DB 347 GGTACCTTGCATGACTTCTATGTGAAGGGGTCTTACTGTGCAGAGTCCCGAGCAGGCTGG 406

QY 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu 140
 DB 407 TAGCGAGGAGACTGCGATGCGATGTGGCCAGGTCTTGGAGCCCCCAAGGTCAGATTTC 466

QY 141 LeuGluSerTyrProLeuAsnAlaHisCysGluTrpThrIleHisAlaLysProGlyPhe 160
 DB 467 TTGGAAGCTATCCCTTAATGTCTACTGTGAATGAGACCATTCATGCTAAACCTGGGTTT 526

QY 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp 180
 DB 527 GTCATCCAACTAAGATTGTTCATGTTGAGCCTGGAGTTTGACTACATGTGCCAGTATGAC 586

QY 181 TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGly 200
 DB 587 TATGTTGAGGTTCGTGATGAGAGCAACCGGATGGCCAGATCATCAGCGTGTCTGTGGC 646

QY 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220
 DB 647 AACGAGCGCCAGCTCTCTATCCAGAGCATAGGATCCTCACTCCACGCTCCTTCCACTCC 706

QY 221 AspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer 240
 DB 707 GATGGCTCCAGAAATTTTGCGGTTTCCATGCGCAATTTATGAGGAGATCACAGCATGCTCC 766

QY 241 SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCys 260
DB 767 TCATCCCTCTGTTTCCATGACGGCAGCGTGGCTCTTGCACAGGCTGGACCTTACAGTGT 826
QY 261 AlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeu----- 274
DB 827 GCCTGCTTGGCAGGCTATCTGGGAGCGGCTGTGAAAATCTTCTGGAGGCTGGGAAGTCC 886
QY 275 -----LeuGluGluArgAsnCysSerAspPro 283
DB 887 AAGATCAAGGCGCTCAGAAGATTCAATTGCTCTCTGAAGAAAGAACTGCTCAGACCT 946
QY 284 GlyGlyProValAsnGlyTyrGlnLysIleThrGlyGlyProGlyLeuIleAsnGlyArg 303
DB 947 GGGGGCCAGTCAATGGGTATACAGAAATACAGGGGGCCCTGGGCTTATCAACGGACGC 1006
QY 304 HisAlaLysIleGlyThrValValSerPhePheCysAsnAsnSerTyrValLeuSerGly 323
DB 1007 CATGCTAAATTGGCAGCGTGGTGTCTTCTTTTGTAACTCCTATGTTCTTAGTGGC 1066
QY 324 AsnGluLysArgThrCysGlnGlnAsnGlyLysGlnProIleCysIle 343
DB 1067 AATGAGAAAGAACTTCCAGCAGATGGAGAGTGGTCAGGAAACAGCCCATCTGCATA 1126
QY 344 LysAlaCysArgGluProLysIleSerAspLeuValArgArgValLeuProMetGln 363
DB 1127 AAAGCCCTGCCGAGAACCAAGATTTCAGACCTGGTGAGAGGAGAGTCTTCCGATCGAG 1186
QY 364 ValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSerLysGlnLys 383
DB 1187 GTTCAGTCAAGGAGACACCATACACAGCTATCTACGGGCTTCAGAGGCTTCAGACGAGAA 1246
QY 384 LeuGlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuProMetGlyTyr 403
DB 1247 CTGCAGAGTGCCTTACCAGAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGATAC 1306
QY 404 GlnHisLeuIleThrGlnLeuGlnTyrGluCysIleSerProPheTyrArgArgLeuGly 423
DB 1307 CAACATCTGCATACCCAGCTCCAGTATGAGTGATCTCACCTTCTACCCGCGCTGGC 1366
QY 424 SerSerArgThrCysLeuArgThrGlyLysTyrSerGlyArgAlaProSerCysIle 443
DB 1367 AGCAGCAGGAGGACATGCTGAGGACTGGGAAGTGGAGTGGCGGGCACCATCTTGATC 1426
QY 444 ProIleCysGlyLysIleGluAsnIleThrAlaProLysThrGlnGlyLeuArgTyrPro 463
DB 1427 CCTATCTCGGGAAATTTAGAACATCATCTGCTCCAAAGCCCAAGGGTGGCGTGGCG 1486
QY 464 TrpGlnAlaLysThrArgThrSerGlyValHisAspGlySerLeuHisLysGly 483
DB 1487 TGGCAGGAGCAGCATCTACAGGAGGACCGCGGGTGTGATGACGCGAGCTTACACAGGGA 1546
QY 484 AlaTrpPheLeuValCysSerGlyAlaLeuValAsnGluArgThrValValAlaAla 503
DB 1547 GCGTGGTCTTAGTCTCAGCGGTGCTCGTGAATGAGGCGCATCTGGTGGTGGTGGTGGC 1606
QY 504 HisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeuLysValVal 523
DB 1607 CACTGTGTTACTGACCTGGGAGGTGATCACCATGATCAAGCAGCAGACCTGGAAGTGT 1666
QY 524 LeuGlyLysPheTyrArgAspAspArgAspGluLysThrIleGlnSerLeuGlnIle 543
DB 1667 TTGGGAAATTTACCGGATGATGACCGGATGAGAGGATGAGAGGATGAGAGGATGAGAG 1726
QY 544 SerAlaIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAspIleAlaIle 563
DB 1727 TCTGCTATCATCTGATCCCACTATGACCCCATCTGTTGATGCTGATGATGATGATGAT 1786
QY 564 LeuLysLeuLeuAspLysAlaArgIleSerThrArgValGlnProIleCysLeuAlaAla 583
DB 1787 CTGAGCTCTAGACAGGCGGCTATGAGCAGCCGAGTCCAGCCCATCTGCTGCTGCTGCT 1846
QY 584 SerArgAspLeuSerThrSerPheGlnGluSerHisIleThrValAlaGlyTyrAsnVal 603

DB 1847 AGTCGGGATCTCAGCATTCTCTCCAGAGTCCACATCACTGTGGCTGGCATGTC 1906
QY 604 LeuAlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSer 623
DB 1907 CTGGCAGAGCTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTCA 1966
QY 624 ValValAspSerLeuLeuCysGluGlnHisGluAspHisGlyIleProValSerVal 643
DB 1967 GTGGTGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGATGCCATCCAGTGGTGC 2026
QY 644 ThrAspAsnMetPheCysAlaSerTyrGluProThrAlaProSerAspIleCysThrAla 663
DB 2027 ACTGATAAACATGTTCTGTCCAGCTGGGAACCCCACTGCCCTCTCTGATATCTGCAC 2086
QY 664 GluThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTyr 683
DB 2087 GAGACAGGAGCATCGCGGTGTGTCTTCCGGGAGCAGCATCTCTGAGCCACGGTGG 2146
QY 684 HisLeuMetGlyLeuValSerTyrSerTyrAspLysThrCysSerHisArgLeuSerThr 703
DB 2147 CATCTGATGGACTGGTGCAGCTGAGCTATGATAAAACATGACCCACAGGCTCTCCACT 2206
QY 704 AlaPheThrLysValLeuProPheLysAspTyrIleGluArgAsnMetLys 720
DB 2207 GCCTTCCCAAGGTGCTGCCCTTTTAAAGACTGGATTGAAAGAAATATGAA 2257
RESULT 13
AK027841
LOCUS 2784 bp mRNA linear PRI 30-JAN-2004
DEFINITION Homo sapiens cDNA FLJ14935 fis, clone PLACE100992, weakly similar to LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).
ACCESSION AK027841
VERSION 1 GI:14042813
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Ohyashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuna, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Hara, K., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshihara, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiro, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
Complete sequencing and characterization of 21,243 full-length human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
JOURNAL PUBMED 14702039
TITLE

Qy 404 GlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArgArgLeuGly 423
 Db 1307 CAACATCTGCATACCCAGCTCCAGTAGAGTGCACTTCACCCCTTCTACCGCGCTGGC 1366
 Qy 424 SerSerArgArgThrCysLeuArgThrGlyLysTrpSerGlyArgAlaProSerCysIle 443
 Db 1367 AGCAGCAGGAGGACATGCTGAGAGCTGGGAGTGGAGTGGCGGGCACCACATCTCTGCATC 1426
 Qy 444 ProIleCysGlyLysIleGluAsnIleThrAlaProLysThrGlnGlyLeuArgTrpPro 463
 Db 1427 CCTATCTCGCGGAAATTTGAGAACATCACTGCTCCAAAGACCCCAAGGTTGGCGTGGCG 1486
 Qy 464 TrpGlnAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeuHisLysGly 483
 Db 1487 TGGCAGCAGCAGCACTTACAGAGAGACAGCGGGGTGATGACGCGCAGCTTACACAGGGA 1546
 Qy 484 AlaTrpPheLeuValCysSerGlyAlaLeuValAsnGluArgThrValValAlaAla 503
 Db 1547 GCGTGGTTCCTAGTCTGACGGGTGCCCTGGTGATGAGCGCATGTTGGTGGCTGCC 1606
 Qy 504 HisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeuLysValVal 523
 Db 1607 CACTGTGTACTGACTGGGGAAGTCCCATGATCAAGACAGCAGACCTGAAAGTTGTT 1666
 Qy 524 LeuGlyLysPheTyrArgAspAspArgAspGluLysThrIleGlnSerLeuGlnIle 543
 Db 1667 TTGGGGAATTTCTACCGGGATGATGACCGGATGAGAAGACCATCCAGAGCCTACAGATT 1726
 Qy 544 SerAlaIleIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAspIleAlaIle 563
 Db 1727 TCTGCTATCAATCTGCATCCCACTATGACCCCATCTGCTTGTGATGATGATGCCATC 1786
 Qy 564 LeuLysLeuLeuAspLysAlaArgIleSerThrArgValGlnProIleCysLeuAlaAla 583
 Db 1787 CTGAAGCTCTAGACAAGCGCGTATCAGCACCCGAGTCCAGCCCATCTGCCTCGCTGCC 1846
 Qy 584 SerArgAspLeuSerThrPheGlnGluSerHisIleThrValAlaGlyTrpAsnVal 603
 Db 1847 AGTCGGGATCTCAGCACTTCTTCCAGAGTCCACATCACTGTGGCTGGCTGGAATGTC 1906
 Qy 604 LeuAlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSer 623
 Db 1907 CTGCAGACGTGAGGACCTTGGCTTCAAGAACACACATCGCCCTCTGGGTGGTCACT 1966
 Qy 624 ValValAspSerLeuLeuCysGluGlnHisGluAspHisGlyIleProValSerVal 643
 Db 1967 GTGGTGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGCGCATCCAGTGAGTGC 2026
 Qy 644 ThrAspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAla 663
 Db 2027 ACTGATAACATGTTCTGTGCGAGCTGGGAACCCACTGCGCCCTTCTGATATCTGCACGTCA 2086
 Qy 664 GluThrGlyLysIleAlaAlaValSerPheProGlyValArgAlaSerProGluProArgTrp 683
 Db 2087 GAGACAGAGGATCGCGCTGTGTCTTCCGGGACGAGCATCTCTGAGCCACCGCTGG 2146
 Qy 684 HisLeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHisArgLeuSerThr 703
 Db 2147 CATCTGATGGAGCTGGTCACTGGAGCTGATGATAAATCATGACGCCACAGCTCTCCACT 2206
 Qy 704 AlaPheThrLysValLeuProPheLysAspTrpIleGluArgAsnMetLys 720
 Db 2207 GCCTTCAACCAAGGTGCTGCTTTTAAAGACTGGATTGAAAGAAATATGAAA 2257

RESULT 14

BD012235

LOCUS

BD012235 2244 bp DNA linear PAT 02-AUG-2002

DEFINITION A novel gene encoding a serine protease-like protein.

ACCESSION BD012235

VERSION BD012235.1 GI:22092424

KEYWORDS WO 0109349-A/2.

SOURCE Mus musculus (house mouse)

ORGANISM

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. (bases 1 to 2244)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

PD

PF

PR

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

PI

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 2841)
 Strausberg, R.
 Direct Submission
 Submitted (06-JUN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: gsaops-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegod, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 40 Row: f Column: 22
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis.

FEATURES

source

1. .2841

/organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CZECH II"
 /db_xref="taxon:10090"
 /clone="MGC:30636 IMAGE:3675412"
 /tissue_type="Mammary tumor metastasized to lung. Tumor
 arose spontaneously from a senescent normal mammary
 (clonal) outgrowth infected with the virus MMTV."
 /clone_lib="NCI CGAP_Lu29"
 /lab_host="DH10B"
 /notes="vector: pCMV-SPORT6"

gene

1. .2841

/gene="E430002G05Rik"
 /note="synonyms: 5930437L24, Ramp"
 /db_xref="LocusID:210622"
 /db_xref="MGI:2445082"

CDS

126. .2288

/gene="E430002G05Rik"
 /product="regeneration associated muscle protease"
 /protein_id="AAH31841.1"
 /db_xref="GI:21619442"
 /db_xref="LocusID:210622"
 /db_xref="MGI:2445082"

VDPMLCEBQHEHDHGIPIVSVTDNMFCAKDPSTPDSICTAETGIGIALSPFGRASPEPR
 WHLVGLVSWSYDKTCSNGLSTAFKTLVLPKDWIERNMK"

ORIGIN

Alignment Scores:

Pred. No.: 9,18e-256 Length: 2841
 Score: 3612.00 Matches: 649
 Percent Similarity: 94.72% Conservative: 33
 Best Local Similarity: 90.14% Mismatches: 38
 Query Match: 91.56% Indels: 0
 DB: 10 Gaps: 0

US-10-063-692-38 (1-720) x BC031841 (1-2841)

QY 1 MetGluLeuGlyCysTrpThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuSer 20
 |||||
 Db 126 ATGGAGCTAGACAGATGGCGCAGTTGGGGTGGTCTCTCGAGCTCTCTCACTCA 185
 |||||
 QY 21 SerLeuProArgGluTyrThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40
 |||||
 Db 186 TCGTTGCCAAGAGAGTACACGGTCAATTAATGAAGCCTGTCCCGAGCTGAGTGAACATC 245
 |||||
 QY 41 MetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysPspGlyLysArgGlu 60
 |||||
 Db 246 ATGTGTAGAGAGTGTGTGAATATGATGATGATGATGATGATGATGATGATGATGAT 305
 |||||
 QY 61 ValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
 |||||
 Db 306 GTGGTGGGTTACACCATCCATCCATGATGATGATGATGATGATGATGATGATGATGAT 365
 |||||
 QY 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100
 |||||
 Db 366 ATTCACCCAGGTTGTACCATCTTTGAAATCTGCAAGAGCTGCCGCAATGGCTCTGGGGC 425
 |||||
 QY 101 GlyThrLeuAspAspPheTyrValIleGlyPheTyrCysAlaGluCysArgAlaGlyTrp 120
 |||||
 Db 426 GGAACCTCTGGATGACTTCTACGTGAAGGATTTCTACTGCAAGAGTGCAGGGCAGGTGG 485
 |||||
 QY 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu 140
 |||||
 Db 486 TACGAGGAGAGACTGCATGCATGTCGTCAGGTTCTTCGAGCTTCAAGGGTCAGATCTTG 545
 |||||
 QY 141 LeuGluSerTyrProLeuAsnAlaHisCysGluTrpThrIleHisAlaLysProGlyPhe 160
 |||||
 Db 546 TTGGAGAGCTATCCCTTAAATGCTCACTGTGAATGCAATATTTCATGCCAGACCTGGGTTT 605
 |||||
 QY 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp 180
 |||||
 Db 606 ATCATCCAGTTGAGGTTTGGCATGTTGAGCCTAGAGTTTGACTACATGTGCCAGTATGAC 665
 |||||
 QY 181 TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGly 200
 |||||
 Db 666 TATGTGGAGTCCGCGATGGGGATTAATAGTGCAGCCCTATCATCAAGGTTTCTGTGGC 725
 |||||
 QY 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220
 |||||
 Db 726 AACGAGAGCCAGCTCCCATCAGGACACTGGCTCTTCACTCCATGCTCTTTTCCATCTCT 785
 |||||
 QY 221 AspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer 240
 |||||
 Db 786 GATGGCTCCAGAAGCTTCGATGGCTTCCACGCTGTTTTTGGAGGAGATCAGCGTGTCTCC 845
 |||||
 QY 241 SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCys 260
 |||||
 Db 846 TCATCCCTTGTTCATGATGCGACATGCTCTTGTGACAACTGGGCTTTTCAAGTGT 905
 |||||
 QY 261 AlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuLeuGluArgAsnCys 280
 |||||
 Db 906 GCCTGCTGGCTGGCTACACTGGCGAGCGCTGTGAAAACCTACTTGAAGAAAAGAACTGC 965
 |||||
 QY 281 SerAspProGlyGlyProValAsnGlyTyrGlnLysIleThrGlyGlyProGlyLeuIle 300
 |||||
 Db 966 TCAGACCTTTGGGGGGCCAGTCAATGGGTACAAGAAATCACAGAAGGTCTCTGGACTTCTC 1025
 |||||

```
QY 301 AsnGlyArgHisAlaLysIleGlyThrValValSerPhePheCysAsnAsnSerTyrVal 320
|||
Db 1026 AATGAGCGGCATGTAAAAATGGCAGGTTGTCTCTTTCTTTGTAAACGGCTCATACGTT 1085
|||
QY 321 LeuSerGlyAsnGlyLysArgThrCysGlnGlnAsnGlyGluTrpSerGlyLysGlnPro 340
|||
Db 1086 CTGAGTGGCAATGAGAAACGAATCTGCCAGCAGATGGAGAGTGGTGCAGAAAGCAACCT 1145
|||
QY 341 IleCysIleLysAlaCysArgGluProLysIleSerAspLeuValArgArgValLeu 360
|||
Db 1146 GTCTGCATGAACCTGCCGGAAACCGAAGATCTCAGACCTGGTGAGAGGAGAGTCTT 1205
|||
QY 361 ProMetGlnValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSer 380
|||
Db 1206 TCGATGCAGGTTTCAGTCAAGGGAGACACCATTAATCATCAGCTTTATTTCCACGGCTTT 1265
|||
QY 381 LysGlnLysLeuGlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuPro 400
|||
Db 1266 AAGCAGAAATTTGCAGGATGCCTCTACCAAAAGCCAGCCCTTCCATTTGGAGACCTGCC 1325
|||
QY 401 MetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArg 420
|||
Db 1326 CCTGGATACCAATCTGCACACCCCAAGTCCAGTATGATGATCTCGCCCTTCTACCGC 1385
|||
QY 421 ArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTrpSerGlyArgAlaPro 440
|||
Db 1386 CGCCTGGGAAGCAGCAGGAGGACATCCTGAGAACTGGGAAGTGGAGTGGGGGGCCCCG 1445
|||
QY 441 SerCysIleProIleCysGlyLysIleGluAsnIleThrAlaProLysThrGlnGlyLeu 460
|||
Db 1446 TCCTGTATCCCAATCTGTGGAAAAATCGAGAGCAGCTCTTCTCCAAAGACCCCAAGGCACC 1505
|||
QY 461 ArgTrpProTrpGlnAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeu 480
|||
Db 1506 CGTGGCCCATGGCAGCAGCCATCTACCGAGAGCAGTGTGTACACGATGGTGTCTG 1565
|||
QY 481 HisLysGlyAlaTrpPheLeuValCysSerGlyAlaLeuValAsnGluArgThrValVal 500
|||
Db 1566 CACAAAGGTGCATGGTCTTGGTCTGCAGTGGTGGCCCTGGTGAATGAACCGACTGTAGTT 1625
|||
QY 501 ValAlaAlaHisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeu 520
|||
Db 1626 GTGGCTGCCCATCTGTGTGACTGAGCTGGGAAGCCACCATCATCAAGACGAGACCTC 1685
|||
QY 521 LysValValLeuGlyLysPheTyrArgAspAspArgAspGluLysThrIleGlnSer 540
|||
Db 1686 AAGTTGTCTTGGGAAAAATTTCTACAGGACGATGATCGGATGAGAAGACATCCAGAAT 1745
|||
QY 541 LeuGlnIleSerAlaIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAsp 560
|||
Db 1746 TTACGGGTCTCTGTATCATCTTCGACCCCAACTATGACCTATTCCTGTGACTGCAC 1805
|||
QY 561 IleAlaIleLeuLysLeuLeuAspLysAlaArgIleSerThrArgValGlnProIleCys 580
|||
Db 1806 ATCGCTGTTCTGAGCTCTCTAGACAAAGCTCGCATCATGATCCCGTGTCCAAACCATCTGC 1865
|||
QY 581 LeuAlaAlaSerArgAspLeuSerThrSerPheGlnGluSerHisIleThrValAlaGly 600
|||
Db 1866 CTGGCTACCACTCGGGACCTCAGCACCTCTTTTCAGGAATCCCAACATCATCTGTGGCTGC 1925
|||
QY 601 TrpAsnValLeuAlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGly 620
|||
Db 1926 TGGAAATCTCTGGCAGATGTGAGAGCCCTGGCTTTAAGATGATATACCTTTACATTTGGA 1985
|||
QY 621 ValValSerValValAspSerLeuLeuCysGluGluGlnHisGluAspHisGlyIlePro 640
|||
Db 1986 ATGGTCAGAGTGGTAGACCCCAATGCTTTGTGAGAACACGATGAAGACCATGGCATTTCCA 2045
|||
QY 641 ValSerValThrAspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIle 660
|||
Db 2046 GTTAGTGTCTACTGACACATGTTCTGTGCCCAAGAGATCCCAAGTACCCTTCTGACATC 2105
|||
```

Search completed: May 10, 2005, 03:40:30
Job time : 8462 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2005, 11:21:33 ; Search time 8101 Seconds
(without alignments)
17023.027 Million cell updates/sec

Title: US-10-063-692-37
Perfect score: 2846
Sequence: 1 cgtctggccaccgcgcggc.....aaaaaaaaaaaaaaaaaaaaa 2846

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2846	100.0	2846	6	AR252533 Sequence
2	2846	100.0	2846	6	AX092306 Sequence
3	2846	100.0	2846	6	AX376102 Sequence
4	2846	100.0	2846	6	AX403343 Sequence
5	2846	100.0	2846	9	AY358346
6	2564	90.1	2768	9	HSM803699
7	2043	71.8	2306	6	AX084209
8	1906	67.0	2350	9	BC038457
9	1880	66.1	2144	6	AR339478
10	1827	64.2	2142	6	AR339515
11	1787	62.8	2259	6	AR541687
12	1747	61.4	2784	6	BD157134
13	1747	61.4	2784	6	AX878296
14	1747	61.4	2784	6	BD012234
15	1747	61.4	2784	9	BD012234
16	1747	61.4	2784	9	AX027841
17	1672	58.7	2632	6	AX704692
18	1653	58.1	1669	6	CQ723377 Sequence
19	1633	57.4	1867	6	AX084207 Sequence

20	1340	47.1	2289	6	BD012236
21	1068	37.5	141818	2	AL133389
22	1028	36.1	1088	9	HSM800511
23	1017	35.7	208659	2	AC067845
c 24	948	33.3	142522	9	AC090625
25	522	18.3	705	6	BD150061
26	522	18.3	705	6	AX869999
27	421	14.8	421	6	CQ723379
28	370	13.0	505	6	AR264001
c 29	337	11.8	337	6	AX331347
c 30	329	11.6	337	6	AX331781
31	329	11.6	2886	6	AR263926
32	293	10.3	106657	9	AL354921
33	195	6.9	73880	2	AC090728
34	181	6.4	340	6	BD076812
c 35	181	6.4	208659	2	AC067845
36	137	4.8	1132	10	BC060558
37	137	4.8	1696	5	BC067590
38	137	4.8	2770	9	HSM807752
39	136	4.8	685	10	BC049720
40	136	4.8	2237	10	BC059191
41	136	4.8	2470	10	BC027800
42	136	4.8	3375	9	HSM806652
43	136	4.8	4116	9	HSM807269
44	136	4.8	4362	9	HSM805498
c 45	136	4.8	11394	6	AX323608
46	135	4.7	625	10	BC059134
47	135	4.7	827	10	BC049739
48	135	4.7	1129	10	BC060535
49	135	4.7	1181	10	BC049768
50	135	4.7	1647	9	HSM806080
51	135	4.7	1661	9	BC025755
52	135	4.7	1671	10	BC022180
53	135	4.7	1802	9	AB071113
54	135	4.7	1832	5	BC084269
55	135	4.7	2003	9	BC051760
56	135	4.7	2081	9	HSM806272
57	135	4.7	2302	5	BC079972
58	135	4.7	2674	10	BC083550
59	135	4.7	2684	9	HSM805935
60	135	4.7	2777	5	BC063344
61	135	4.7	3080	9	HSM807488
62	135	4.7	3141	3	AK116783
63	135	4.7	3558	9	HSM803467
64	135	4.7	4316	6	CQ086814
c 65	135	4.7	4316	6	CQ087088
c 66	135	4.7	4316	6	AX795752
c 67	135	4.7	4316	6	AX795868
c 68	135	4.7	4316	6	AX822260
c 69	135	4.7	4316	6	AX822388
c 70	135	4.7	4316	6	AX825900
c 71	135	4.7	4316	6	AX826028
72	135	4.7	4753	10	BC058514
73	135	4.7	4940	9	HSM806769
c 74	135	4.7	5195	6	AX345823
c 75	135	4.7	5306	6	AX345413
c 76	135	4.7	5387	6	AX344633
c 77	135	4.7	5627	9	HSM807499
c 78	135	4.7	6192	6	AX251440
c 79	135	4.7	6944	6	AX347467
c 80	135	4.7	6944	6	AX349188
c 81	135	4.7	6944	6	AX657867
c 82	135	4.7	6944	6	AX659141
c 83	135	4.7	14920	6	AX344738
c 84	135	4.7	73778	6	AX344575
c 85	135	4.7	110000	8	CR382134_12
c 86	135	4.7	113515	2	AX347076
87	135	4.7	153567	2	AC087145
88	135	4.7	191531	2	AC113984
89	135	4.7	256673	2	AC087146
c 90	135	4.7	349980	6	AX344558
91	134	4.7	381	6	CQ526814
92	134	4.7	396	6	CQ525748

C 239	134	4.7	6486	6	AX458534	AX458534 Sequence	312	133	4.7	760	9	BC032326	BC032326 Homo sapi
C 240	134	4.7	6644	6	E23356	E23356 Virus vecto	313	133	4.7	760	9	BC040885	BC040885 Homo sapi
C 241	134	4.7	7369	6	AX598937	AX598937 Sequence	314	133	4.7	781	10	BC049734	BC049734 Mus muscu
C 242	134	4.7	7369	6	AX705387	AX705387 Sequence	315	133	4.7	788	5	BC072244	BC072244 Xenopus l
C 243	134	4.7	7372	6	E23357	E23357 Virus vecto	316	133	4.7	789	9	BC061900	BC061900 Homo sapi
C 244	134	4.7	7609	9	BSM807874	BSM807874 Homo sapi	317	133	4.7	805	10	BC063183	BC063183 Rattus no
C 245	134	4.7	7797	6	E23355	E23355 Virus vecto	318	133	4.7	818	9	BC026261	BC026261 Homo sapi
C 246	134	4.7	7796	6	E23359	E23359 Virus vecto	319	133	4.7	819	9	BSM807474	BSM807474 Homo sapi
C 247	134	4.7	8899	6	AX345739	AX345739 Sequence	320	133	4.7	819	10	BC064002	BC064002 Mus muscu
C 248	134	4.7	8899	6	AX348461	AX348461 Sequence	321	133	4.7	824	9	BC070291	BC070291 Homo sapi
C 249	134	4.7	8946	6	AX345813	AX345813 Sequence	322	133	4.7	828	10	BC049756	BC049756 Mus muscu
C 250	134	4.7	12178	10	AP466694	AP466694 Rattus no	323	133	4.7	828	9	S78214	S78214 APC-tumor s
C 251	134	4.7	15528	6	AP3016	AP3016 Sequence 4	324	133	4.7	837	9	S78214	S78214 APC-tumor s
C 252	134	4.7	15528	12	PEAVGEN	Y07862 Cloning vec	325	133	4.7	845	9	BC044653	BC044653 Homo sapi
C 253	134	4.7	15832	6	AX277943	AX277943 Sequence	326	133	4.7	848	5	BC062495	BC062495 Xenopus t
C 254	134	4.7	15832	6	AX323630	AX323630 Sequence	327	133	4.7	854	5	BC084189	BC084189 Xenopus t
C 255	134	4.7	15832	6	AX346245	AX346245 Sequence	328	133	4.7	860	9	BC039722	BC039722 Homo sapi
C 256	134	4.7	40324	6	AX458633	AX458633 Sequence	329	133	4.7	863	10	BC061014	BC061014 Mus muscu
C 257	134	4.7	349980	6	AX344563	AX344563 Sequence	330	133	4.7	885	10	BC060948	BC060948 Mus muscu
C 258	134	4.7	349980	6	AX344565	AX344565 Sequence	331	133	4.7	879	9	AX780227	AX780227 Sequence
C 259	133	4.7	202	6	BD190570	BD190570 Secretary	332	133	4.7	881	10	BC049733	BC049733 Mus muscu
C 260	133	4.7	202	6	AX099441	AX099441 Sequence	333	133	4.7	887	6	BD260630	BD260630 49 human
C 261	133	4.7	212	6	CO677317	CO677317 Sequence	334	133	4.7	889	10	BC049685	BC049685 Mus muscu
C 262	133	4.7	231	6	CO685486	CO685486 Sequence	335	133	4.7	897	10	BC049625	BC049625 Mus muscu
C 263	133	4.7	240	6	I48979	I48979 Sequence 6	336	133	4.7	909	10	BC035323	BC035323 Mus muscu
C 264	133	4.7	260	6	CO695445	CO695445 Sequence	337	133	4.7	911	10	BC061108	BC061108 Mus muscu
C 265	133	4.7	309	6	CO513146	CO513146 Sequence	338	133	4.7	932	9	BC043537	BC043537 Homo sapi
C 266	133	4.7	351	6	CO410508	CO410508 Sequence	339	133	4.7	935	3	AK174210	AK174210 Ciona int
C 267	133	4.7	368	10	BC049735	BC049735 Mus muscu	340	133	4.7	936	6	BD107846	BD107846 36 human
C 268	133	4.7	375	6	CO513063	CO513063 Sequence	341	133	4.7	942	9	BC043511	BC043511 Homo sapi
C 269	133	4.7	384	3	AF155365	AF155365 Buthus ma	342	133	4.7	970	10	BC049752	BC049752 Mus muscu
C 270	133	4.7	394	6	CO481688	CO481688 Sequence	343	133	4.7	970	10	BC061464	BC061464 Mus muscu
C 271	133	4.7	396	6	AR391230	AR391230 Sequence	344	133	4.7	970	10	BC064826	BC064826 Mus muscu
C 272	133	4.7	396	6	AR392935	AR392935 Sequence	345	133	4.7	971	10	BC030946	BC030946 Mus muscu
C 273	133	4.7	396	6	AR489665	AR489665 Sequence	346	133	4.7	1000	10	BC038055	BC038055 Mus muscu
C 274	133	4.7	396	6	AR493906	AR493906 Sequence	347	133	4.7	1001	10	BC049605	BC049605 Mus muscu
C 275	133	4.7	396	6	AX093235	AX093235 Sequence	348	133	4.7	1004	10	BC025458	BC025458 Mus muscu
C 276	133	4.7	397	3	AF135818	AF135818 Mesobuthu	349	133	4.7	1018	9	BC022044	BC022044 Homo sapi
C 277	133	4.7	406	6	CO397829	CO397829 Sequence	350	133	4.7	1024	9	BC012602	BC012602 Homo sapi
C 278	133	4.7	406	6	CO404124	CO404124 Sequence	351	133	4.7	1030	10	BC049544	BC049544 Mus muscu
C 279	133	4.7	408	6	CO502830	CO502830 Sequence	352	133	4.7	1035	10	BC055104	BC055104 Mus muscu
C 280	133	4.7	408	6	CO511687	CO511687 Sequence	353	133	4.7	1038	9	BC038366	BC038366 Homo sapi
C 281	133	4.7	431	9	BC070144	BC070144 Homo sapi	354	133	4.7	1038	10	BC013496	BC013496 Mus muscu
C 282	133	4.7	437	3	AF155369	AF155369 Buthus ma	355	133	4.7	1044	10	BC049565	BC049565 Mus muscu
C 283	133	4.7	446	3	AF146743	AF146743 Mesobuthu	356	133	4.7	1047	9	BC027974	BC027974 Homo sapi
C 284	133	4.7	480	9	BC055410	BC055410 Homo sapi	357	133	4.7	1048	9	BC063640	BC063640 Homo sapi
C 285	133	4.7	481	6	CO524400	CO524400 Sequence	358	133	4.7	1054	10	BC049758	BC049758 Mus muscu
C 286	133	4.7	481	9	BC070219	BC070219 Homo sapi	359	133	4.7	1085	10	BC049634	BC049634 Mus muscu
C 287	133	4.7	501	6	CO527244	CO527244 Sequence	360	133	4.7	1071	9	AF078844	AF078844 Homo sapi
C 288	133	4.7	508	9	BC017744	BC017744 Homo sapi	361	133	4.7	1071	9	BSM805733	BSM805733 Homo sapi
C 289	133	4.7	525	9	BC034020	BC034020 Homo sapi	362	133	4.7	1080	9	BC022354	BC022354 Homo sapi
C 290	133	4.7	532	10	BC049701	BC049701 Mus muscu	363	133	4.7	1081	10	BC049719	BC049719 Mus muscu
C 291	133	4.7	565	6	CO526051	CO526051 Sequence	364	133	4.7	1084	9	BC026265	BC026265 Homo sapi
C 292	133	4.7	570	6	CO527266	CO527266 Sequence	365	133	4.7	1090	5	BC066372	BC066372 Danio rer
C 293	133	4.7	615	10	BC043668	BC043668 Mus muscu	366	133	4.7	1090	9	BC049543	BC049543 Mus muscu
C 294	133	4.7	658	6	BD275413	BD275413 50 Human	367	133	4.7	1093	9	BC043577	BC043577 Homo sapi
C 295	133	4.7	664	10	BC061046	BC061046 Mus muscu	368	133	4.7	1100	10	BC061092	BC061092 Mus muscu
C 296	133	4.7	675	10	BC059112	BC059112 Rattus no	369	133	4.7	1109	10	BC063150	BC063150 Rattus no
C 297	133	4.7	676	10	BC049769	BC049769 Mus muscu	370	133	4.7	1115	10	BC049678	BC049678 Mus muscu
C 298	133	4.7	679	9	BC052814	BC052814 Homo sapi	371	133	4.7	1119	9	BC070137	BC070137 Homo sapi
C 299	133	4.7	686	10	BC060302	BC060302 Mus muscu	372	133	4.7	1122	10	BC049644	BC049644 Mus muscu
C 300	133	4.7	686	10	BC064030	BC064030 Rattus no	373	133	4.7	1124	9	BC025950	BC025950 Homo sapi
C 301	133	4.7	691	5	BC071138	BC071138 Xenopus l	374	133	4.7	1137	10	BC062232	BC062232 Rattus no
C 302	133	4.7	701	5	BC075162	BC075162 Xenopus l	375	133	4.7	1159	9	BC043507	BC043507 Homo sapi
C 303	133	4.7	720	8	CNS01D7J	ALL1471 Botrytis	376	133	4.7	1172	10	BC061094	BC061094 Mus muscu
C 304	133	4.7	732	5	AY525586	AY525586 Oreochrom	377	133	4.7	1175	5	BC049447	BC049447 Danio rer
C 305	133	4.7	733	9	BC009801	BC009801 Homo sapi	378	133	4.7	1200	5	BC077122	BC077122 Danio rer
C 306	133	4.7	738	9	BSM06309	BSM06309 Homo sapi	379	133	4.7	1201	9	BC050586	BC050586 Homo sapi
C 307	133	4.7	746	10	BC061195	BC061195 Mus muscu	380	133	4.7	1219	10	BC049717	BC049717 Mus muscu
C 308	133	4.7	749	9	BC008417	BC008417 Homo sapi	381	133	4.7	1245	10	BC049747	BC049747 Mus muscu
C 309	133	4.7	757	9	BC051791	BC051791 Homo sapi	382	133	4.7	1248	5	BC071085	BC071085 Xenopus l
C 310	133	4.7	758	9	BC062750	BC062750 Homo sapi	383	133	4.7	1250	9	BC051908	BC051908 Homo sapi
C 311	133	4.7	760	6	CO497632	CO497632 Sequence	384	133	4.7	1251	10	BC038552	BC038552 Mus muscu

385	133	4.7	1269	9	BC072684	BC072684 Homo sapi	458	133	4.7	1941	9	BC051758	BC051758 Homo sapi
386	133	4.7	1271	9	AF090934	AF090934 Homo sapi	459	133	4.7	1944	9	BC028346	BC028346 Homo sapi
387	133	4.7	1273	10	BC049640	BC049640 Mus muscu	460	133	4.7	1954	6	BD270057	BD270057 Secreted
388	133	4.7	1289	10	BC049691	BC049691 Mus muscu	461	133	4.7	1960	10	BC061459	BC061459 Mus muscu
389	133	4.7	1310	9	BSM807559	BSM807559 Mus muscu	462	133	4.7	1985	10	BC049351	BC049351 Mus muscu
390	133	4.7	1333	10	BC010296	BC010296 Mus muscu	463	133	4.7	1986	10	BC050807	BC050807 Mus muscu
391	133	4.7	1337	3	AY118704	AY118704 Drosophil	464	133	4.7	1990	10	BC042668	BC042668 Mus muscu
392	133	4.7	1343	10	BC061103	BC061103 Mus muscu	465	133	4.7	1993	9	BSM803801	BSM803801 Homo sapi
393	133	4.7	1373	10	BC049731	BC049731 Mus muscu	466	133	4.7	2004	9	BC043556	BC043556 Homo sapi
394	133	4.7	1382	10	BC066858	BC066858 Mus muscu	467	133	4.7	2019	10	BC063758	BC063758 Mus muscu
395	133	4.7	1383	9	BC032432	BC032432 Homo sapi	468	133	4.7	2035	9	BSM807574	BSM807574 Homo sapi
396	133	4.7	1384	10	BC052146	BC052146 Mus muscu	469	133	4.7	2040	9	BSM807056	BSM807056 Homo sapi
397	133	4.7	1405	9	BC044934	BC044934 Homo sapi	470	133	4.7	2048	9	BC044243	BC044243 Homo sapi
398	133	4.7	1409	10	BC049776	BC049776 Mus muscu	471	133	4.7	2054	10	BC039272	BC039272 Mus muscu
399	133	4.7	1416	9	AF090943	AF090943 Homo sapi	472	133	4.7	2073	9	BC068024	BC068024 Homo sapi
400	133	4.7	1419	9	BC032340	BC032340 Homo sapi	473	133	4.7	2098	9	BC017717	BC017717 Homo sapi
401	133	4.7	1430	5	BC064202	BC064202 Xenopus t	474	133	4.7	2104	9	BSM806638	BSM806638 Homo sapi
402	133	4.7	1432	10	BC062239	BC062239 Rattus no	475	133	4.7	2132	9	AB072776	AB072776 Macaca fa
403	133	4.7	1472	9	BC017724	BC017724 Homo sapi	476	133	4.7	2158	5	BC082415	BC082415 Xenopus l
404	133	4.7	1493	9	BC042547	BC042547 Homo sapi	477	133	4.7	2164	10	BC005513	BC005513 Mus muscu
405	133	4.7	1501	5	BC080019	BC080019 Xenopus l	478	133	4.7	2190	9	BC048340	BC048340 Homo sapi
406	133	4.7	1528	9	BC043517	BC043517 Homo sapi	479	133	4.7	2233	9	BC040959	BC040959 Homo sapi
407	133	4.7	1545	10	BC062173	BC062173 Mus muscu	480	133	4.7	2237	3	AK112710	AK112710 Ciona int
408	133	4.7	1549	9	BSM808772	BSM808772 Homo sapi	481	133	4.7	2245	9	BC037547	BC037547 Homo sapi
409	133	4.7	1562	5	BC054239	BC054239 Xenopus l	482	133	4.7	2262	6	AR487911	AR487911 Sequence
410	133	4.7	1568	10	BC048399	BC048399 Mus muscu	483	133	4.7	2280	9	BC047310	BC047310 Homo sapi
411	133	4.7	1576	9	BSM806260	BSM806260 Homo sapi	484	133	4.7	2282	9	BC033689	BC033689 Homo sapi
412	133	4.7	1580	5	BC067146	BC067146 Danio rer	485	133	4.7	2284	9	AB055303	AB055303 Macaca fa
413	133	4.7	1589	9	BC043543	BC043543 Homo sapi	486	133	4.7	2312	9	BSM803723	BSM803723 Homo sapi
414	133	4.7	1598	9	BC013323	BC013323 Homo sapi	487	133	4.7	2321	9	BC058898	BC058898 Homo sapi
415	133	4.7	1606	10	BC051176	BC051176 Mus muscu	488	133	4.7	2328	9	BC043587	BC043587 Homo sapi
416	133	4.7	1610	9	BC064141	BC064141 Homo sapi	489	133	4.7	2334	3	AK116665	AK116665 Ciona int
417	133	4.7	1625	9	BSM806623	BSM806623 Homo sapi	490	133	4.7	2350	5	BC078091	BC078091 Xenopus l
418	133	4.7	1626	9	BC050587	BC050587 Homo sapi	491	133	4.7	2356	10	BC061208	BC061208 Mus muscu
419	133	4.7	1684	10	BC064148	BC064148 Homo sapi	492	133	4.7	2387	10	BC048933	BC048933 Mus muscu
420	133	4.7	1684	10	BC055910	BC055910 Mus muscu	493	133	4.7	2390	9	AF090900	AF090900 Homo sapi
421	133	4.7	1694	9	BC012597	BC012597 Homo sapi	494	133	4.7	2393	5	BC070538	BC070538 Xenopus l
422	133	4.7	1696	6	AR256293	AR256293 Sequence	495	133	4.7	2420	5	BC066695	BC066695 Danio rer
423	133	4.7	1719	10	BC045148	BC045148 Mus muscu	496	133	4.7	2435	9	BC050387	BC050387 Homo sapi
424	133	4.7	1725	9	BSM806934	BSM806934 Homo sapi	497	133	4.7	2439	9	BSM807466	BSM807466 Homo sapi
425	133	4.7	1727	5	BC071446	BC071446 Danio rer	498	133	4.7	2441	3	AK174351	AK174351 Ciona int
426	133	4.7	1727	10	BC050800	BC050800 Mus muscu	499	133	4.7	2447	6	AR079032	AR079032 Sequence
427	133	4.7	1730	9	BC033615	BC033615 Homo sapi	500	133	4.7	2447	6	BD190886	BD190886 Secreted
428	133	4.7	1732	9	BSM806991	BSM806991 Homo sapi	501	133	4.7	2464	9	BSM807471	BSM807471 Homo sapi
429	133	4.7	1740	9	BC042437	BC042437 Homo sapi	502	133	4.7	2501	6	AX598878	AX598878 Sequence
430	133	4.7	1743	9	AB070131	AB070131 Macaca fa	503	133	4.7	2501	6	AX599024	AX599024 Sequence
431	133	4.7	1746	9	BC025377	BC025377 Homo sapi	504	133	4.7	2507	10	BC053747	BC053747 Mus muscu
432	133	4.7	1763	10	BC061098	BC061098 Mus muscu	505	133	4.7	2533	9	BC032304	BC032304 Homo sapi
433	133	4.7	1770	9	BC025717	BC025717 Homo sapi	506	133	4.7	2545	9	BC063430	BC063430 Homo sapi
434	133	4.7	1782	10	BC050802	BC050802 Mus muscu	507	133	4.7	2549	10	BC061563	BC061563 Rattus no
435	133	4.7	1786	9	AB070107	AB070107 Macaca fa	508	133	4.7	2556	9	BSM805953	BSM805953 Homo sapi
436	133	4.7	1788	9	BSM806673	BSM806673 Homo sapi	509	133	4.7	2562	9	BSM808661	BSM808661 Homo sapi
437	133	4.7	1793	3	AK112657	AK112657 Ciona int	510	133	4.7	2563	9	AP125949	AP125949 Homo sapi
438	133	4.7	1793	9	BC071757	BC071757 Homo sapi	511	133	4.7	2566	6	CQ834011	CQ834011 Sequence
439	133	4.7	1798	6	AR366535	AR366535 Sequence	512	133	4.7	2585	9	BSM805677	BSM805677 Homo sapi
440	133	4.7	1803	9	BSM807650	BSM807650 Homo sapi	513	133	4.7	2593	9	BSM807470	BSM807470 Homo sapi
441	133	4.7	1808	6	AX535019	AX535019 Sequence	514	133	4.7	2598	5	BC044109	BC044109 Xenopus l
442	133	4.7	1820	8	BT009533	BT009533 Triticum	515	133	4.7	2612	10	BC053749	BC053749 Mus muscu
443	133	4.7	1827	9	AB070106	AB070106 Macaca fa	516	133	4.7	2621	10	MUSBRED	MUSBRED Mus musculu
444	133	4.7	1835	9	BC040063	BC040063 Homo sapi	517	133	4.7	2627	9	BC027919	BC027919 Homo sapi
445	133	4.7	1853	10	BC052346	BC052346 Mus muscu	518	133	4.7	2648	10	BC031180	BC031180 Mus muscu
446	133	4.7	1876	10	BC053422	BC053422 Mus muscu	519	133	4.7	2666	9	BC027972	BC027972 Homo sapi
447	133	4.7	1877	5	BC066464	BC066464 Danio rer	520	133	4.7	2688	9	BC021087	BC021087 Homo sapi
448	133	4.7	1883	10	BC022165	BC022165 Mus muscu	521	133	4.7	2700	9	BC064849	BC064849 Homo sapi
449	133	4.7	1890	9	BSM807434	BSM807434 Homo sapi	522	133	4.7	2722	9	BSM806004	BSM806004 Homo sapi
450	133	4.7	1906	10	BC063161	BC063161 Rattus no	523	133	4.7	2722	10	BC077615	BC077615 Mus muscu
451	133	4.7	1912	10	BC027060	BC027060 Mus muscu	524	133	4.7	2725	5	BSM07764	BSM07764 Sequence
452	133	4.7	1913	9	BC012362	BC012362 Homo sapi	525	133	4.7	2782	9	BSM803706	BSM803706 Homo sapi
453	133	4.7	1931	10	BC036150	BC036150 Mus muscu	526	133	4.7	2846	9	BSM802834	BSM802834 Homo sapi
454	133	4.7	1933	6	BD270058	BD270058 Secreted	527	133	4.7	2869	9	BSM804689	BSM804689 Homo sapi
455	133	4.7	1933	9	BSM806724	BSM806724 Homo sapi	528	133	4.7	2878	9	BSM805674	BSM805674 Homo sapi
456	133	4.7	1935	5	BC065678	BC065678 Danio rer	529	133	4.7	2909	3	AK116710	AK116710 Ciona int
457	133	4.7	1939	5	BC079974	BC079974 Xenopus l	530	133	4.7	2910	9	BC042070	BC042070 Homo sapi

531	133	4.7	2917	9	BC054514	BC054514 Homo sapi	604	133	4.7	5154	9	BSM805947	BSM805947 Homo sapi
532	133	4.7	2922	6	CQ491282	CQ491282 Sequence	605	133	4.7	5155	9	BSM805801	BSM805801 Homo sapi
533	133	4.7	2922	9	BC032692	BC032692 Homo sapi	606	133	4.7	5205	9	BSM805958	BSM805958 Homo sapi
534	133	4.7	2929	10	BC053441	BC053441 Mus muscu	607	133	4.7	5355	9	BSM806819	BSM806819 Homo sapi
535	133	4.7	2936	5	BC077828	BC077828 Xenopus l	608	133	4.7	5365	9	BSM807518	BSM807518 Homo sapi
536	133	4.7	2943	10	BC005526	BC005526 Mus muscu	609	133	4.7	5402	9	BSM804677	BSM804677 Homo sapi
537	133	4.7	2968	10	BC058408	BC058408 Mus muscu	610	133	4.7	5439	9	BSM805827	BSM805827 Homo sapi
538	133	4.7	2972	9	BC023549	BC023549 Homo sapi	c 611	133	4.7	5586	6	AX348391	AX348391 Sequence
539	133	4.7	2975	9	BSM804650	BSM804650 Homo sapi	612	133	4.7	5597	10	BC043113	BC043113 Mus muscu
540	133	4.7	2977	5	BC070986	BC070986 Xenopus l	613	133	4.7	5695	10	BC082548	BC082548 Mus muscu
541	133	4.7	3014	9	BSM803702	BSM803702 Homo sapi	614	133	4.7	5703	10	BC054080	BC054080 Mus muscu
542	133	4.7	3030	3	AX116919	AX116919 Ciona int	615	133	4.7	5763	9	BSM808659	BSM808659 Homo sapi
543	133	4.7	3084	10	BC058950	BC058950 Mus muscu	c 616	133	4.7	6134	6	AX458624	AX458624 Sequence
544	133	4.7	3117	10	BC043717	BC043717 Mus muscu	c 617	133	4.7	6161	6	AX345313	AX345313 Sequence
545	133	4.7	3134	9	BSM805794	BSM805794 Homo sapi	618	133	4.7	7216	9	BSM805762	BSM805762 Homo sapi
546	133	4.7	3149	10	BC040763	BC040763 Mus muscu	c 619	133	4.7	7369	6	AX598791	AX598791 Sequence
547	133	4.7	3159	10	BC030921	BC030921 Mus muscu	c 620	133	4.7	7369	6	AX705365	AX705365 Sequence
548	133	4.7	3178	9	BSM803719	BSM803719 Homo sapi	c 621	133	4.7	8079	6	AX356488	AX356488 Sequence
549	133	4.7	3180	10	BC041774	BC041774 Mus muscu	c 622	133	4.7	9580	14	AF054250	AF054250 Hepatitis
550	133	4.7	3183	9	BC044242	BC044242 Homo sapi	623	133	4.7	9747	9	BSM806689	BSM806689 Homo sapi
551	133	4.7	3189	9	BSM802830	BSM802830 Homo sapi	c 624	133	4.7	10369	6	AX251057	AX251057 Sequence
552	133	4.7	3226	9	AX189289	AX189289 Homo sapi	c 625	133	4.7	10369	6	AX345294	AX345294 Sequence
553	133	4.7	3232	9	AF090901	AF090901 Homo sapi	c 626	133	4.7	11416	6	AX251758	AX251758 Sequence
554	133	4.7	3245	9	BSM805849	BSM805849 Homo sapi	c 627	133	4.7	11416	6	AX345020	AX345020 Sequence
555	133	4.7	3269	5	BC073066	BC073066 Xenopus l	c 628	133	4.7	11416	6	AX348567	AX348567 Sequence
556	133	4.7	3332	10	BC053922	BC053922 Mus muscu	c 629	133	4.7	11729	6	AX345797	AX345797 Sequence
557	133	4.7	3353	9	BSM803622	BSM803622 Homo sapi	c 630	133	4.7	12007	6	AX345619	AX345619 Sequence
558	133	4.7	3380	9	BSM807223	BSM807223 Homo sapi	c 631	133	4.7	14798	6	AX345934	AX345934 Sequence
559	133	4.7	3394	9	BC050550	BC050550 Homo sapi	c 632	133	4.7	16033	6	AX346306	AX346306 Sequence
560	133	4.7	3482	9	BSM800550	BSM800550 Homo sapi	c 633	133	4.7	16633	6	AX344576	AX344576 Sequence
561	133	4.7	3518	9	BSM807510	BSM807510 Homo sapi	c 634	133	4.7	21354	6	AX251544	AX251544 Sequence
562	133	4.7	3525	10	BC034207	BC034207 Mus muscu	c 635	133	4.7	35962	6	AX598758	AX598758 Sequence
563	133	4.7	3530	10	BC053732	BC053732 Mus muscu	c 636	133	4.7	35962	6	AX598904	AX598904 Sequence
564	133	4.7	3532	9	BSM807372	BSM807372 Homo sapi	c 637	133	4.7	70389	2	AX135853	AX135853 Homo sapi
565	133	4.7	3623	10	BC034092	BC034092 Mus muscu	638	133	4.7	193988	2	AC102269	AC102269 Mus muscu
566	133	4.7	3660	10	BC051069	BC051069 Mus muscu	c 639	133	4.7	212273	10	AC104920	AC104920 Mus muscu
567	133	4.7	3681	9	BSM806036	BSM806036 Homo sapi	c 640	133	4.7	349980	6	AX344551	AX344551 Sequence
568	133	4.7	3687	9	BC040431	BC040431 Homo sapi	c 641	133	4.7	349980	6	AX344553	AX344553 Sequence
569	133	4.7	3723	9	BSM808835	BSM808835 Homo sapi	c 642	133	4.7	349980	6	AX344559	AX344559 Sequence
570	133	4.7	3758	9	BSM801755	BSM801755 Homo sapi	c 643	133	4.7	349980	6	AX344566	AX344566 Sequence
571	133	4.7	3796	5	BC066783	BC066783 Xenopus t	c 644	133	4.7	349980	6	AX344572	AX344572 Sequence
572	133	4.7	3883	9	BSM808647	BSM808647 Homo sapi	c 645	132	4.6	549	6	CQ524814	CQ524814 Sequence
c 573	133	4.7	3924	10	MUSBREDA	L31397 Mus musculu	646	132	4.6	711	9	BC051802	BC051802 Homo sapi
574	133	4.7	3973	6	AX345073	AX345073 Sequence	647	132	4.6	774	10	BC013457	BC013457 Mus muscu
c 575	133	4.7	4001	6	AX347363	AX347363 Sequence	648	132	4.6	1000	9	BSM806624	BSM806624 Homo sapi
c 576	133	4.7	4001	6	AX349084	AX349084 Sequence	649	132	4.6	1062	5	BC084361	BC084361 Xenopus l
c 577	133	4.7	4001	6	AX657851	AX657851 Sequence	650	132	4.6	1257	9	BC043535	BC043535 Homo sapi
c 578	133	4.7	4001	6	AX659125	AX659125 Sequence	651	132	4.6	1352	3	AX115954	AX115954 Ciona int
579	133	4.7	4043	10	BC020177	BC020177 Mus muscu	652	132	4.6	1383	5	BC056115	BC056115 Xenopus l
580	133	4.7	4062	5	BC070004	BC070004 Dario rer	653	132	4.6	1457	9	BSM806863	BSM806863 Homo sapi
581	133	4.7	4081	9	BSM807531	BSM807531 Homo sapi	654	132	4.6	1648	9	BSM808551	BSM808551 Homo sapi
582	133	4.7	4086	9	BSM803439	BSM803439 Homo sapi	655	132	4.6	1816	9	BC050396	BC050396 Homo sapi
583	133	4.7	4155	5	BC074405	BC074405 Xenopus l	656	132	4.6	1953	9	AB056420	AB056420 Macaca fa
584	133	4.7	4185	9	BC050532	BC050532 Homo sapi	657	132	4.6	1968	10	BC006016	BC006016 Mus muscu
585	133	4.7	4237	6	BS057918	BS057918 Secreted	658	132	4.6	1983	10	BC005510	BC005510 Mus muscu
586	133	4.7	4286	9	BSM807052	BSM807052 Homo sapi	659	132	4.6	1999	9	BSA242859	BSA242859 Homo sapi
587	133	4.7	4358	10	BC060187	BC060187 Mus muscu	660	132	4.6	2009	3	AX116580	AX116580 Ciona int
588	133	4.7	4389	10	BC058345	BC058345 Mus muscu	661	132	4.6	2027	9	BC063512	BC063512 Homo sapi
589	133	4.7	4413	10	BC053035	BC053035 Mus muscu	662	132	4.6	2394	6	AR374733	AR374733 Sequence
590	133	4.7	4421	10	BC042512	BC042512 Mus muscu	663	132	4.6	2514	9	BC044863	BC044863 Homo sapi
591	133	4.7	4436	10	BC058961	BC058961 Mus muscu	664	132	4.6	2752	9	BSM806735	BSM806735 Homo sapi
592	133	4.7	4457	10	BC070435	BC070435 Mus muscu	665	132	4.6	2943	9	BSM803526	BSM803526 Homo sapi
593	133	4.7	4494	10	BC063058	BC063058 Mus muscu	666	132	4.6	3006	9	BC039068	BC039068 Homo sapi
594	133	4.7	4562	9	BSM805779	BSM805779 Homo sapi	667	132	4.6	4942	9	BSM808887	BSM808887 Homo sapi
595	133	4.7	4574	9	BSM803437	BSM803437 Homo sapi	668	132	4.6	6719	9	BSM803507	BSM803507 Homo sapi
596	133	4.7	4619	9	BSM806714	BSM806714 Homo sapi	c 669	132	4.6	6775	6	AX458643	AX458643 Sequence
597	133	4.7	4636	10	BC057352	BC057352 Mus muscu	c 670	132	4.6	8900	6	CQ806977	CQ806977 Sequence
598	133	4.7	4661	5	BC068849	BC068849 Xenopus l	c 671	132	4.6	8900	6	CQ807251	CQ807251 Sequence
599	133	4.7	4725	9	BC040525	BC040525 Homo sapi	c 672	132	4.6	13054	2	AX149986	AX149986 Strongylo
600	133	4.7	4726	9	BSM808819	BSM808819 Homo sapi	673	131	4.6	358	6	CQ671266	CQ671266 Sequence
601	133	4.7	4828	9	BSM808886	BSM808886 Homo sapi	c 674	131	4.6	1083	9	BSM800561	BSM800561 Homo sapi
602	133	4.7	4838	10	BC082542	BC082542 Mus muscu	675	131	4.6	1094	9	BC039173	BC039173 Homo sapi
603	133	4.7	4946	9	BSM805863	BSM805863 Homo sapi	676	131	4.6	1138	10	BC062234	BC062234 Rattus no

677	131	4.6	1150	5	BC066608	BC066608 Danilo rer	750	128	4.5	1433	3	AK174181	AK174181 Ciona int
678	131	4.6	1372	9	BC024221	BC024221 Homo sapi	751	128	4.5	1456	5	BC077897	BC077897 Xenopus l
679	131	4.6	1414	10	BC049767	BC049767 Mus muscu	752	128	4.5	1560	9	BC032420	BC032420 Homo sapi
680	131	4.6	1788	9	BC044944	BC044944 Homo sapi	753	128	4.5	1715	5	BC067176	BC067176 Danilo rer
681	131	4.6	1941	5	BC053250	BC053250 Danilo rer	754	128	4.5	1728	9	AB070110	AB070110 Macaca fa
682	131	4.6	1985	3	AY118692	AY118692 Drosophil	755	128	4.5	1773	9	BC073559	BC073559 Homo sapi
683	131	4.6	2116	9	BC034379	BC034379 Homo sapi	756	128	4.5	1812	10	BC055113	BC055113 Mus muscu
684	131	4.6	2207	10	BC066857	BC066857 Mus muscu	757	128	4.5	1838	10	BC083573	BC083573 Rattus no
685	131	4.6	2313	10	BC021410	BC021410 Mus muscu	758	128	4.5	1889	9	BC073841	BC073841 Homo sapi
686	131	4.6	2395	9	AF090903	AF090903 Homo sapi	759	128	4.5	1905	9	BC032703	BC032703 Homo sapi
687	131	4.6	2827	6	CQ491125	CQ491125 Sequence	760	128	4.5	1913	3	AY069281	AY069281 Drosophil
688	131	4.6	2827	6	CQ496990	CQ496990 Sequence	761	128	4.5	1985	6	BD172402	BD172402 Secreted
689	131	4.6	3255	9	HSM803224	AL831898 Homo sapi	762	128	4.5	1985	6	BD172721	BD172721 Secreted
690	131	4.6	3383	9	HSM8031701	AL832393 Homo sapi	763	128	4.5	1985	6	BD173040	BD173040 Secreted
691	131	4.6	3916	10	BC018439	BC018439 Mus muscu	764	128	4.5	1985	6	BD173359	BD173359 Secreted
692	131	4.6	4670	9	AF104032	AF104032 Homo sapi	765	128	4.5	1985	6	BD175393	BD175393 Secretory
693	131	4.6	4744	5	BC066770	BC066770 Xenopus l	766	128	4.5	1985	6	BD275145	BD275145 48 Human
694	131	4.6	8712	6	AX344694	AX344694 Sequence	767	128	4.5	1985	6	CQ881212	CQ881212 Sequence
695	131	4.6	31656	2	AC149363	AC149363 Phakopsor	768	128	4.5	1985	6	AR410771	AR410771 Sequence
696	130	4.6	547	9	BC070202	BC070202 Homo sapi	769	128	4.5	1985	6	AR439135	AR439135 Sequence
697	130	4.6	687	10	BC049765	BC049765 Mus muscu	770	128	4.5	1985	6	AR473155	AR473155 Sequence
698	130	4.6	967	9	HSM802777	AL390167 Homo sapi	771	128	4.5	1985	6	AR527141	AR527141 Sequence
699	130	4.6	1078	9	BC035314	BC035314 Homo sapi	772	128	4.5	1985	6	AR566174	AR566174 Sequence
700	130	4.6	1166	9	BC043545	BC043545 Homo sapi	773	128	4.5	1985	6	AX375960	AX375960 Sequence
701	130	4.6	1408	10	BC048693	BC048693 Mus muscu	774	128	4.5	1985	6	AX697621	AX697621 Sequence
702	130	4.6	1447	6	AR237880	AR237880 Sequence	775	128	4.5	1985	6	BD075542	BD075542 Secretory
703	130	4.6	1468	10	BC068202	BC068202 Rattus no	776	128	4.5	1985	9	AV358500	AV358500 Homo sapi
704	130	4.6	1489	9	AB048953	AB048953 Macaca fa	777	128	4.5	2030	9	BC083602	BC083602 Homo sapi
705	130	4.6	1738	6	AR560934	AR560934 Sequence	778	128	4.5	2178	6	AX099370	AX099370 Sequence
706	130	4.6	1738	8	BT009079	BT009079 Triticum	779	128	4.5	2245	9	HSM803715	HSM803715 Sequence
707	130	4.6	1770	9	BC063419	BC063419 Homo sapi	780	128	4.5	2265	10	BC051639	BC051639 Mus muscu
708	130	4.6	1872	9	BC038952	BC038952 Homo sapi	781	128	4.5	2287	9	BC044220	BC044220 Homo sapi
709	130	4.6	1946	5	BC077411	BC077411 Xenopus l	782	128	4.5	2500	10	BC058946	BC058946 Mus muscu
710	130	4.6	2316	10	BC064469	BC064469 Mus muscu	783	128	4.5	2508	10	BC079036	BC079036 Rattus no
711	130	4.6	2905	3	AK174395	AK174395 Ciona int	784	128	4.5	2607	5	BC054610	BC054610 Danilo rer
712	130	4.6	3399	9	BC063840	BC063840 Homo sapi	785	128	4.5	2674	6	AR183261	AR183261 Sequence
713	130	4.6	3582	10	BC053927	BC053927 Mus muscu	786	128	4.5	2674	6	AR456323	AR456323 Sequence
c 714	130	4.6	349980	6	AX344570	AX344570 Sequence	787	128	4.5	3300	9	BC011656	BC011656 Homo sapi
c 715	130	4.6	349980	6	AX344571	AX344571 Sequence	788	128	4.5	3375	9	BC038406	BC038406 Homo sapi
716	129	4.5	502	6	CQ525917	CQ525917 Sequence	789	128	4.5	3454	9	HSM802993	HSM802993 Sequence
717	129	4.5	661	10	BC051629	BC051629 Mus muscu	c 790	128	4.5	61940	2	AC109312	AC109312 Homo sapi
718	129	4.5	681	5	BC055187	BC055187 Danilo rer	791	127	4.5	127	6	BD021987	BD021987 Secreted
719	129	4.5	972	10	BC049738	BC049738 Mus muscu	792	127	4.5	474	6	CQ523390	CQ523390 Sequence
720	129	4.5	1051	6	AR164814	AR164814 Sequence	793	127	4.5	490	6	CQ523744	CQ523744 Sequence
721	129	4.5	1051	6	AR490614	AR490614 Sequence	794	127	4.5	569	6	BD223440	BD223440 94 human
722	129	4.5	1051	6	AR532388	AR532388 Sequence	795	127	4.5	569	6	AR243074	AR243074 Sequence
723	129	4.5	1339	9	BC016710	BC016710 Homo sapi	796	127	4.5	569	6	AR404255	AR404255 Sequence
724	129	4.5	1615	9	AF218014	AF218014 Homo sapi	797	127	4.5	580	10	BC006049	BC006049 Mus muscu
725	129	4.5	1711	9	BC032509	BC032509 Homo sapi	798	127	4.5	607	5	BC049055	BC049055 Danilo rer
726	129	4.5	1994	3	AK116078	AK116078 Ciona int	799	127	4.5	977	9	BC051846	BC051846 Homo sapi
727	129	4.5	2090	9	BC049196	BC049196 Homo sapi	800	127	4.5	981	9	BC041179	BC041179 Homo sapi
728	129	4.5	2548	9	BC040371	BC040371 Homo sapi	801	127	4.5	1012	10	BC049579	BC049579 Mus muscu
729	129	4.5	2604	8	BT009473	BT009473 Triticum	802	127	4.5	1128	9	BC071732	BC071732 Homo sapi
730	129	4.5	2610	9	BC038448	BC038448 Homo sapi	803	127	4.5	1156	5	BC049488	BC049488 Danilo rer
731	129	4.5	2612	9	BC063856	BC063856 Homo sapi	804	127	4.5	1175	9	BC049386	BC049386 Homo sapi
732	129	4.5	2915	10	BC061479	BC061479 Mus muscu	805	127	4.5	1265	9	BC033301	BC033301 Homo sapi
733	129	4.5	4606	10	BC058089	BC058089 Mus muscu	806	127	4.5	1280	9	BC047365	BC047365 Homo sapi
c 734	129	4.5	6484	6	AX344730	AX344730 Sequence	807	127	4.5	1445	9	BC063545	BC063545 Homo sapi
c 735	129	4.5	6577	6	AX251920	AX251920 Sequence	808	127	4.5	1462	10	BC006018	BC006018 Mus muscu
c 736	129	4.5	6577	6	AX346258	AX346258 Sequence	809	127	4.5	1743	10	BC051150	BC051150 Mus muscu
c 737	129	4.5	6577	6	AX348993	AX348993 Sequence	810	127	4.5	1756	9	BC069223	BC069223 Homo sapi
738	128	4.5	510	9	BC070217	BC070217 Homo sapi	811	127	4.5	1793	10	BC062171	BC062171 Mus muscu
739	128	4.5	579	6	CQ526842	CQ526842 Sequence	812	127	4.5	1850	9	BC040123	BC040123 Homo sapi
740	128	4.5	612	10	BC061085	BC061085 Mus muscu	813	127	4.5	1882	5	BC068036	BC068036 Xenopus t
741	128	4.5	705	9	HSM800237	AL049452 Homo sapi	814	127	4.5	1978	10	BC012750	BC012750 Homo sapi
742	128	4.5	720	10	BC061086	BC061086 Mus muscu	815	127	4.5	2029	10	BC050265	BC050265 Mus muscu
743	128	4.5	763	9	BC040916	BC040916 Homo sapi	816	127	4.5	2035	9	BC063696	BC063696 Homo sapi
744	128	4.5	878	6	AX482482	AX482482 Sequence	817	127	4.5	2039	10	BC050804	BC050804 Mus muscu
745	128	4.5	1119	9	BC071717	BC071717 Homo sapi	818	127	4.5	2139	5	BC054626	BC054626 Danilo rer
c 746	128	4.5	1328	8	AL840631	AL840631 Arabidops	819	127	4.5	2247	9	BC009648	BC009648 Homo sapi
747	128	4.5	1329	9	AF544398	AF544398 Homo sapi	820	127	4.5	2337	9	HSM800876	HSM800876 Sequence
748	128	4.5	1402	9	BC040630	BC040630 Homo sapi	821	127	4.5	2530	9	BC036868	BC036868 Homo sapi
749	128	4.5	1429	10	BC022900	BC022900 Mus muscu	822	127	4.5	2690	5	BC077100	BC077100 Danilo rer

823	127	4.5	2728	5	BC081323	BC081323 Xenopus t	896	125	4.4	2633	9	HSM804701	AL833388 Homo sapi
824	127	4.5	2840	5	BC056558	BC056558 Danio rer	897	125	4.4	2641	9	BC020219	BC020219 Homo sapi
825	127	4.5	3341	9	BC032308	BC032308 Homo sapi	898	125	4.4	2661	10	BC026137	BC026137 Mus muscu
826	127	4.5	3446	9	HSM802955	AL713742 Homo sapi	899	125	4.4	2709	10	BC054846	BC054846 Mus muscu
827	127	4.5	4180	10	BC042645	BC042645 Mus muscu	900	125	4.4	2750	10	BC084264	BC084264 Xenopus l
828	127	4.5	4438	10	BC067016	BC067016 Mus muscu	901	125	4.4	2924	6	AX683129	AX683129 Sequence
829	127	4.5	4459	9	HSM804634	AL833321 Homo sapi	902	125	4.4	2924	10	S68736	S68736 Rattus sp.
830	127	4.5	4818	9	HSM807492	AX647348 Homo sapi	903	125	4.4	3626	6	BC012147	BC012147 Homo sapi
831	127	4.5	5251	10	BC065072	BC065072 Mus muscu	904	125	4.4	4124	3	AK112284	AK112284 Ciona int
832	127	4.5	6976	9	HSM808639	AX648491 Homo sapi	905	125	4.4	4169	10	BC053919	BC053919 Mus muscu
833	126	4.4	299	6	C0669036	C0669036 Sequence	c 906	125	4.4	6112	6	AX345565	AX345565 Sequence
834	126	4.4	407	6	C0522526	C0522526 Sequence	c 907	124	4.4	237	6	AX284920	AX284920 Sequence
835	126	4.4	439	6	C0518358	C0518358 Sequence	908	124	4.4	332	6	C0523998	C0523998 Sequence
836	126	4.4	602	9	BC008488	BC008488 Homo sapi	909	124	4.4	603	6	C0526797	C0526797 Sequence
837	126	4.4	674	6	AR283453	AR283453 Sequence	910	124	4.4	745	10	BC049606	BC049606 Mus muscu
838	126	4.4	674	6	AR344221	AR344221 Sequence	911	124	4.4	870	6	BD231669	BD231669 31 human
839	126	4.4	674	6	AR351422	AR351422 Sequence	912	124	4.4	1073	5	BC084065	BC084065 Xenopus l
840	126	4.4	674	6	AR454002	AR454002 Sequence	913	124	4.4	1092	10	BC005748	BC005748 Mus muscu
841	126	4.4	674	6	AR561590	AR561590 Sequence	914	124	4.4	1164	8	BT009497	BT009497 Tricicum
842	126	4.4	674	6	AX282972	AX282972 Sequence	915	124	4.4	1205	9	BC039058	BC039058 Homo sapi
843	126	4.4	674	6	AX303145	AX303145 Sequence	916	124	4.4	1287	3	BT009948	BT009948 Drosophi
844	126	4.4	720	10	BC083088	BC083088 Mus muscu	917	124	4.4	1331	10	BC030915	BC030915 Mus muscu
845	126	4.4	935	10	BC061157	BC061157 Mus muscu	918	124	4.4	1347	10	BC008980	BC008980 Mus muscu
846	126	4.4	1004	9	BC043536	BC043536 Homo sapi	919	124	4.4	1426	5	BC054250	BC054250 Xenopus l
847	126	4.4	1073	9	BC032697	BC032697 Homo sapi	920	124	4.4	1627	9	BC039584	BC039584 Homo sapi
848	126	4.4	1232	10	BC060554	BC060554 Rattus no	921	124	4.4	1665	9	BC041446	BC041446 Homo sapi
849	126	4.4	1350	10	BC072695	BC072695 Rattus no	922	124	4.4	1976	9	BC040113	BC040113 Homo sapi
850	126	4.4	1414	10	BC005487	BC005487 Mus muscu	923	124	4.4	2082	6	AR059958	AR059958 Sequence
851	126	4.4	1457	6	BD231695	BD231695 31 human	924	124	4.4	2085	5	BC077186	BC077186 Xenopus l
852	126	4.4	1487	6	AY423736	AY423736 Tachyglos	925	124	4.4	2150	9	BC025715	BC025715 Homo sapi
853	126	4.4	1527	5	BC064182	BC064182 Xenopus t	926	124	4.4	2212	10	BC046775	BC046775 Mus muscu
854	126	4.4	1588	9	BC070183	BC070183 Homo sapi	927	124	4.4	2320	10	BC046962	BC046962 Mus muscu
855	126	4.4	1608	9	AY358187	AY358187 Homo sapi	928	124	4.4	2465	9	BC013348	BC013348 Homo sapi
856	126	4.4	1706	5	BC082351	BC082351 Xenopus l	929	124	4.4	2754	10	BC066817	BC066817 Mus muscu
857	126	4.4	1775	5	BC053257	BC053257 Danio rer	930	124	4.4	2759	10	BC055046	BC055046 Mus muscu
858	126	4.4	1781	5	BC064253	BC064253 Xenopus t	931	124	4.4	3082	10	BC046972	BC046972 Mus muscu
859	126	4.4	1817	10	BC083562	BC083562 Rattus no	932	124	4.4	3110	10	BC057617	BC057617 Mus muscu
860	126	4.4	2150	6	C0882012	C0882012 Sequence	933	124	4.4	3251	5	BC074658	BC074658 Xenopus t
861	126	4.4	2261	6	C0882010	C0882010 Sequence	934	124	4.4	3307	9	BC025714	BC025714 Homo sapi
862	126	4.4	2270	9	HSM806047	BX537526 Homo sapi	935	124	4.4	3328	10	BC005512	BC005512 Mus muscu
863	126	4.4	2350	9	BC063427	BC063427 Homo sapi	936	124	4.4	3345	9	BC041132	BC041132 Homo sapi
864	126	4.4	2377	8	AY080711	AY080711 Arabidops	937	124	4.4	3499	10	BC007476	BC007476 Mus muscu
865	126	4.4	2578	9	AB049758	AB049758 Homo sapi	938	124	4.4	3686	10	BC043709	BC043709 Mus muscu
866	126	4.4	2790	9	BC048292	BC048292 Homo sapi	939	124	4.4	6251	10	BC050823	BC050823 Mus muscu
867	126	4.4	2841	10	BC045601	BC045601 Mus muscu	940	123	4.3	300	6	BD213699	BD213699 Novel hum
868	126	4.4	2945	5	BC076976	BC076976 Xenopus t	941	123	4.3	500	9	BC070218	BC070218 Homo sapi
869	126	4.4	3050	5	BC066571	BC066571 Danio rer	942	123	4.3	515	6	C0522671	C0522671 Sequence
870	126	4.4	3326	9	HSM808512	BX648364 Homo sapi	943	123	4.3	516	6	C0524041	C0524041 Sequence
871	126	4.4	4651	9	BC042656	BC042656 Homo sapi	944	123	4.3	585	6	C0526237	C0526237 Sequence
872	126	4.4	5277	9	HSM808645	BX648497 Homo sapi	945	123	4.3	586	6	C0524455	C0524455 Sequence
873	125	4.4	458	10	BC061002	BC061002 Mus muscu	946	123	4.3	1076	10	BC062802	BC062802 Rattus no
874	125	4.4	547	6	C0526009	C0526009 Sequence	947	123	4.3	1108	9	BC063631	BC063631 Homo sapi
875	125	4.4	580	6	C0526169	C0526169 Sequence	948	123	4.3	1348	9	BC070154	BC070154 Homo sapi
876	125	4.4	633	5	BC057512	BC057512 Danio rer	949	123	4.3	1501	10	BC039998	BC039998 Mus muscu
877	125	4.4	1065	10	BC049675	BC049675 Mus muscu	950	123	4.3	1690	9	BC049211	BC049211 Homo sapi
878	125	4.4	1130	10	BC043698	BC043698 Mus muscu	951	123	4.3	1722	5	BC063371	BC063371 Xenopus t
879	125	4.4	1359	5	BC053194	BC053194 Danio rer	952	123	4.3	1959	9	BC043548	BC043548 Homo sapi
880	125	4.4	1397	6	C0491382	BC0491382 Sequence	953	123	4.3	2000	9	BC063423	BC063423 Homo sapi
881	125	4.4	1470	9	BC072387	BC072387 Homo sapi	954	123	4.3	2106	5	BC075571	BC075571 Xenopus t
882	125	4.4	1499	9	BC042195	BC042195 Homo sapi	955	123	4.3	2557	9	BC042875	BC042875 Homo sapi
883	125	4.4	1517	9	BC016152	BC016152 Homo sapi	956	123	4.3	2611	9	BC041438	BC041438 Homo sapi
884	125	4.4	1651	10	BC024872	BC024872 Mus muscu	957	123	4.3	2679	10	BC006021	BC006021 Mus muscu
885	125	4.4	1760	9	BC051807	BC051807 Homo sapi	958	123	4.3	2920	3	AK174466	AK174466 Ciona int
886	125	4.4	1765	9	BC063438	BC063438 Homo sapi	959	123	4.3	2922	3	AF479582	AF479582 Boophilus
887	125	4.4	1805	9	AB070053	AB070053 Macaca fa	960	123	4.3	3038	9	HSM806221	BX538051 Homo sapi
888	125	4.4	1880	6	C0769491	C0769491 Sequence	961	123	4.3	4064	10	BC072632	BC072632 Mus muscu
889	125	4.4	1985	5	BC053414	BC053414 Danio rer	962	122	4.3	45685	2	AC087168	AC087168 Homo sapi
890	125	4.4	2005	9	BC013372	BC013372 Homo sapi	963	122	4.3	144	6	BD138840	BD138840 Secreted
891	125	4.4	2012	9	AY125488	AY125488 Homo sapi	964	122	4.3	144	6	BD005387	BD005387 Secreted
892	125	4.4	2161	6	C0414527	C0414527 Sequence	965	122	4.3	144	6	BD005387	BD005387 Secreted
893	125	4.4	2165	5	BC054602	BC054602 Danio rer	966	122	4.3	263	6	CQ663258	CQ663258 Sequence
894	125	4.4	2178	9	BC046358	BC046358 Homo sapi	967	122	4.3	317	6	C0526915	C0526915 Sequence
895	125	4.4	2314	5	BC068218	BC068218 Xenopus t	968	122	4.3	323	6	C0524910	C0524910 Sequence

969	122	4.3	472	6	CQ525172 Sequence	1042	121	4.3	3487	10	BC016095	BC016095 Mus muscu
970	122	4.3	487	10	BC069220 Mus muscu	1043	121	4.3	3491	5	BC059285	BC059285 Xenopus l
971	122	4.3	539	6	CQ523463 Sequence	1044	121	4.3	3498	5	BC065688	BC065688 Danio rer
972	122	4.3	543	6	CQ524637 Sequence	1045	121	4.3	3983	9	BSM803572	AL833265 Homo sapi
973	122	4.3	847	9	BC053571 Homo sapi	1046	121	4.3	4498	10	BC075723	BC075723 Mus muscu
974	122	4.3	894	9	BC044257 Homo sapi	1047	121	4.3	4679	9	BSM808418	BC044257 Homo sapi
975	122	4.3	942	5	BC049498 Homo sapi	1048	121	4.3	4829	10	BC060175	BC060175 Mus muscu
976	122	4.3	1027	9	BC041442 Homo sapi	1049	121	4.3	4969	9	BSM806817	BC041442 Homo sapi
977	122	4.3	1034	9	AK026865 Homo sapi	1050	120	4.2	319	6	CQ670102	BC0670102 Sequence
978	122	4.3	1132	6	BD131068 Secreted	1051	120	4.2	412	6	CQ522434	CQ522434 Sequence
979	122	4.3	1319	9	BC003683 Homo sapi	1052	120	4.2	543	10	BC055944	BC055944 Mus muscu
980	122	4.3	1319	9	BC015490 Homo sapi	1053	120	4.2	608	5	BC075124	BC075124 Xenopus l
981	122	4.3	1331	6	CQ776637 Sequence	1054	120	4.2	791	5	BC077926	BC077926 Xenopus l
982	122	4.3	1461	9	AB048964 Macaca fa	1055	120	4.2	997	9	BC047943	BC047943 Homo sapi
983	122	4.3	1556	9	BC042072 Homo sapi	1056	120	4.2	1155	9	BC036792	BC036792 Homo sapi
984	122	4.3	1630	9	BC039130 Homo sapi	1057	120	4.2	1233	10	BC058696	BC058696 Mus muscu
985	122	4.3	1661	9	BC025753 Homo sapi	1058	120	4.2	1257	10	BC071264	BC071264 Mus muscu
986	122	4.3	1690	9	BC011595 Homo sapi	1059	120	4.2	1286	10	BC062175	BC062175 Mus muscu
987	122	4.3	1789	9	BC070134 Homo sapi	1060	120	4.2	1637	6	AX460089	AX460089 Sequence
988	122	4.3	1846	9	BC038379 Homo sapi	1061	120	4.2	1660	9	BC032309	BC032309 Homo sapi
989	122	4.3	1930	5	BC066725 Danio rer	1062	120	4.2	1691	3	AF044679	AF044679 Leishmani
990	122	4.3	2080	10	BC013564 Mus muscu	1063	120	4.2	1692	8	BT009528	BT009528 Triticum
991	122	4.3	2094	9	BC044310 Homo sapi	1064	120	4.2	1719	3	AK116650	AK116650 Ciona int
992	122	4.3	2173	5	BC068406 Danio rer	1065	120	4.2	1762	9	AF258575	AF258575 Homo sapi
993	122	4.3	2246	9	BC051820 Homo sapi	1066	120	4.2	1810	9	BSM805776	BSM805776 Homo sapi
994	122	4.3	2421	10	BC061106 Mus muscu	1067	120	4.2	1876	9	BC071731	BC071731 Homo sapi
995	122	4.3	2734	5	BC076749 Homo sapi	1068	120	4.2	1923	9	AB093671	AB093671 Macaca fa
996	122	4.3	2788	9	AF111847 Homo sapi	1069	120	4.2	1940	9	BSM807445	BSM807445 Homo sapi
997	122	4.3	2840	10	BC052769 Mus muscu	1070	120	4.2	1946	9	BSM808123	BSM808123 Homo sapi
998	122	4.3	2986	5	BC084243 Xenopus l	1071	120	4.2	1958	10	BC023841	BC023841 Mus muscu
999	122	4.3	3045	9	BSM808843	1072	120	4.2	2064	10	BC053424	BC053424 Mus muscu
1000	122	4.3	3353	6	AX086952 Sequence	1073	120	4.2	2084	9	AB072761	AB072761 Macaca fa
1001	122	4.3	3640	9	BSM806825	1074	120	4.2	2196	9	BSM805743	BSM805743 Homo sapi
1002	122	4.3	3850	10	BC063749 Mus muscu	1075	120	4.2	2216	5	BC054636	BC054636 Danio rer
c1003	122	4.3	5216	6	AX281348 Sequence	1076	120	4.2	2265	9	BC063477	BC063477 Homo sapi
c1004	122	4.3	5216	6	AX345249 Sequence	1077	120	4.2	2367	9	BSM801757	BSM801757 Homo sapi
1005	122	4.3	5325	9	BSM806205	1078	120	4.2	2415	9	BC028002	BC028002 Homo sapi
c1006	122	4.3	6794	6	AX251872 Sequence	1079	120	4.2	2630	9	BC038222	BC038222 Homo sapi
c1007	122	4.3	6794	6	AX344260 Sequence	1080	120	4.2	2683	10	BC052924	BC052924 Mus muscu
c1008	122	4.3	6794	6	AX348651 Sequence	1081	120	4.2	2780	10	BC021914	BC021914 Mus muscu
c1009	122	4.3	349980	6	AX344554 Sequence	1082	120	4.2	3401	9	BC040376	BC040376 Homo sapi
c1010	122	4.3	349980	6	AX344555 Sequence	1083	120	4.2	3686	10	BC023773	BC023773 Mus muscu
1011	121	4.3	125	6	CQ677274 Sequence	1084	120	4.2	3856	9	AX0805531	AL834437 Homo sapi
1012	121	4.3	267	6	CQ525163 Sequence	1085	120	4.2	3997	6	AX086658	AX086658 Sequence
1013	121	4.3	544	6	CQ524776 Sequence	1086	120	4.2	4670	9	BC027849	BC027849 Homo sapi
1014	121	4.3	671	5	BC082915 Xenopus l	1087	120	4.2	5599	10	BC049182	BC049182 Mus muscu
1015	121	4.3	743	10	BC034898 Mus muscu	1088	120	4.2	7240	9	BSM808174	BSM808174 Homo sapi
1016	121	4.3	766	8	AF531371 Gossypium	1089	119	4.2	119	6	AX099495	AX099495 Sequence
1017	121	4.3	793	9	BC018189 Homo sapi	1090	119	4.2	119	6	BD063978	BD063978 Secreted
1018	121	4.3	861	10	BC049709 Mus muscu	1091	119	4.2	452	6	CQ527434	CQ527434 Sequence
1019	121	4.3	872	6	AX068322 Sequence	1092	119	4.2	484	6	CQ526160	CQ526160 Sequence
1020	121	4.3	1117	8	AF243375 Glycine m	1093	119	4.2	528	6	CQ526616	CQ526616 Sequence
1021	121	4.3	1400	9	BC063708 Homo sapi	1094	119	4.2	533	6	CQ527387	CQ527387 Sequence
1022	121	4.3	1591	9	BC050659 Homo sapi	1095	119	4.2	539	10	BC031454	BC031454 Mus muscu
1023	121	4.3	1591	10	AB041801 Mus muscl	1096	119	4.2	549	10	BC048536	BC048536 Mus muscu
1024	121	4.3	1601	9	BC050451 Homo sapi	1097	119	4.2	633	10	BC059147	BC059147 Rattus no
1025	121	4.3	1653	8	BT009403 Triticum	1098	119	4.2	653	10	BC039566	BC039566 Mus muscu
1026	121	4.3	1725	9	BC028081 Homo sapi	1099	119	4.2	706	10	BC055114	BC055114 Mus muscu
1027	121	4.3	1913	9	BC030546 Homo sapi	1100	119	4.2	772	6	BD191024	BD191024 Secreted
1028	121	4.3	1933	9	BSM806048	1101	119	4.2	899	5	BC060392	BC060392 Xenopus l
1029	121	4.3	1944	9	BC025786 Homo sapi	1102	119	4.2	939	10	BC049689	BC049689 Mus muscu
1030	121	4.3	2006	10	BC083579 Rattus no	1103	119	4.2	1010	10	BC061971	BC061971 Rattus no
1031	121	4.3	2053	9	BC030196 Homo sapi	1104	119	4.2	1191	9	BC014547	BC014547 Homo sapi
1032	121	4.3	2072	9	BC044245 Homo sapi	c1105	119	4.2	1197	8	AJ840663	AJ840663 Arabidops
1033	121	4.3	2190	9	BC063454 Homo sapi	1106	119	4.2	1487	10	BC026303	BC026303 Homo sapi
1034	121	4.3	2325	10	BC051401 Mus muscu	1107	119	4.2	1562	10	BC063181	BC063181 Rattus no
1035	121	4.3	2385	6	BD186882 Nucleic a	1108	119	4.2	1568	5	BC050177	BC050177 Danio rer
1036	121	4.3	2445	9	BC019562 Homo sapi	1109	119	4.2	1632	9	BC040434	BC040434 Homo sapi
1037	121	4.3	2500	9	BC065207 Homo sapi	1110	119	4.2	1650	9	BC036926	BC036926 Homo sapi
1038	121	4.3	2607	9	BC053734 Homo sapi	1111	119	4.2	1650	9	BC063391	BC063391 Homo sapi
1039	121	4.3	2692	3	AK173351 Ciona int	1112	119	4.2	1667	10	BC019215	BC019215 Mus muscu
1040	121	4.3	2747	9	BC025706 Homo sapi	1113	119	4.2	1673	6	BD138829	BD138829 Secreted
1041	121	4.3	2820	10	BC062390 Rattus no	1114	119	4.2	1680	10	AF528194	AF528194 Mus muscu

1115	119	4.2	1842	9	BC024042	BC024042 Homo sapi	1188	118	4.1	4057	10	BC067005	BC067005 Mus muscu
1116	119	4.2	2013	9	AB070201	AB070201 Macaca fa	1189	118	4.1	4298	10	BSM804564	AL833251 Homo sapi
1117	119	4.2	2112	5	BC076765	BC076765 Xenopus l	1190	118	4.1	4306	10	BC059824	BC059824 Mus muscu
1118	119	4.2	2134	5	XLCTG	X84990 X.laavis Cc	cl191	118	4.1	4990	6	CQ493127	CQ493127 Sequence
1119	119	4.2	2223	5	BC067619	BC067619 Danio rer	cl192	118	4.1	4990	6	CQ493522	CQ493522 Sequence
1120	119	4.2	2355	9	BSM801346	AL133075 Homo sapi	1193	118	4.1	6003	10	AX426535	AX426535 Mus muscu
1121	119	4.2	2360	9	BC063595	BC063595 Homo sapi	1193	118	4.1	6003	10	AX426535	AX426535 Mus muscu
1122	119	4.2	2447	9	BC027927	BC027927 Homo sapi	cl194	118	4.1	13606	6	AX251315	AX251315 Sequence
1123	119	4.2	2610	10	BC063267	BC063267 Mus muscu	cl195	118	4.1	13606	6	AX278002	AX278002 Sequence
1124	119	4.2	2686	5	AJ719361	AJ719361 Gallus ga	cl196	118	4.1	13606	6	AX323699	AX323699 Sequence
1125	119	4.2	2740	9	BC053595	BC053595 Homo sapi	cl197	118	4.1	13606	6	AX346712	AX346712 Sequence
1126	119	4.2	2747	9	BSM803601	BC053595 Homo sapi	cl198	118	4.1	17934	6	AX346621	AX346621 Sequence
1127	119	4.2	2989	9	BSM807541	AL833294 Homo sapi	cl199	117	4.1	117	6	I89931	I89931 Sequence 3
1128	119	4.2	3010	6	AX358754	AX358754 Sequence	1200	117	4.1	117	6	BD005371	BD005371 Secreted
1129	119	4.2	3010	6	AX362247	AX362247 Sequence	1201	117	4.1	270	6	CQ655781	CQ655781 Sequence
1130	119	4.2	3010	9	AF058753	AF058753 Homo sapi	1202	117	4.1	401	3	AF543047	AF543047 Mesobuthu
1131	119	4.2	3036	9	AF090896	AF090896 Homo sapi	1203	117	4.1	409	9	BC060322	BC060322 Homo sapi
1132	119	4.2	3315	9	AB056768	AB056768 Macaca fa	1204	117	4.1	421	6	CQ526039	CQ526039 Sequence
1133	119	4.2	3547	5	BC084146	BC084146 Xenopus t	1205	117	4.1	527	9	BC032225	BC032225 Homo sapi
1134	119	4.2	3676	10	BC062923	BC062923 Mus muscu	1206	117	4.1	527	9	BC032225	BC032225 Homo sapi
1135	119	4.2	3894	10	BC053925	BC053925 Mus muscu	1207	117	4.1	539	10	BC061539	BC061539 Rattus no
1136	119	4.2	4851	10	BC062121	BC062121 Mus muscu	1208	117	4.1	575	6	CQ526566	CQ526566 Sequence
1137	119	4.2	5249	9	BSM803431	AL8332124 Homo sapi	1209	117	4.1	911	10	BC061126	BC061126 Mus muscu
1138	119	4.2	18682	2	AC107855	AL8332124 Homo sapi	1210	117	4.1	959	9	BC031674	BC031674 Homo sapi
1139	118	4.1	138	6	CQ0705290	CQ0705290 Sequence	1211	117	4.1	1019	10	BC043927	BC043927 Mus muscu
1140	118	4.1	360	6	CQ524586	CQ524586 Sequence	1212	117	4.1	1243	9	BSM802621	AL162083 Homo sapi
cl141	118	4.1	396	6	AR391210	AR391210 Sequence	1213	117	4.1	1287	10	BC061031	BC061031 Mus muscu
cl142	118	4.1	396	6	AR392915	AR392915 Sequence	1214	117	4.1	1376	6	BD194853	BD194853 86 human
cl143	118	4.1	396	6	AR489645	AR392915 Sequence	1215	117	4.1	1376	6	CQ855181	CQ855181 Sequence
cl144	118	4.1	396	6	AR493886	AR493886 Sequence	1216	117	4.1	1526	9	BC041705	BC041705 Homo sapi
cl145	118	4.1	396	6	AR493886	AR493886 Sequence	1217	117	4.1	1555	9	AB063070	AB063070 Macaca fa
1146	118	4.1	410	6	CQ522484	AX093215 Sequence	1218	117	4.1	1656	5	BC064161	BC064161 Xenopus t
1147	118	4.1	514	10	BC061178	BC061178 Mus muscu	1219	117	4.1	1733	6	BD062047	BD062047 Novel tum
1148	118	4.1	614	8	AF165421	AF165421 Mesembrya	1220	117	4.1	1739	9	AK026045	AK026045 Homo sapi
1149	118	4.1	667	6	BD249950	BD249950 50 human	1221	117	4.1	1869	5	BC076804	BC076804 Xenopus l
1150	118	4.1	681	5	BC071507	BC071507 Danio rer	1222	117	4.1	1894	9	AB063046	AB063046 Macaca fa
1151	118	4.1	723	9	BSM808728	BC071507 Homo sapi	1223	117	4.1	2009	5	BC074651	BC074651 Xenopus t
cl152	118	4.1	756	6	CQ399155	CQ399155 Sequence	1224	117	4.1	2108	9	AB047801	AB047801 Homo sapi
cl153	118	4.1	762	6	CQ405433	CQ405433 Sequence	1225	117	4.1	2321	9	BC017105	BC017105 Homo sapi
1154	118	4.1	762	9	BC070287	BC070287 Homo sapi	1226	117	4.1	2371	9	BSM805927	BSM805927 Homo sapi
1155	118	4.1	919	5	BC079985	BC079985 Xenopus l	1227	117	4.1	2403	9	BSM808752	BSM808752 Homo sapi
1156	118	4.1	1108	10	BC032259	BC032259 Mus muscu	1228	117	4.1	2511	6	AX768355	AX768355 Sequence
1157	118	4.1	1113	9	BC030277	BC030277 Homo sapi	1229	117	4.1	2773	6	AR252502	AR252502 Sequence
1158	118	4.1	1116	9	BC032317	BC032317 Homo sapi	1230	117	4.1	2773	6	AX092302	AX092302 Sequence
1159	118	4.1	1171	9	BC056889	BC056889 Homo sapi	1231	117	4.1	2773	6	AX376082	AX376082 Sequence
1160	118	4.1	1237	5	BC075738	BC075738 Danio rer	1232	117	4.1	2773	6	AX403291	AX403291 Sequence
1161	118	4.1	1284	3	AK113775	AK113775 Ciona int	1233	117	4.1	2773	6	AX403291	AX403291 Sequence
1162	118	4.1	1448	10	BC052344	BC052344 Mus muscu	1234	117	4.1	2968	9	BC060758	BC060758 Homo sapi
1163	118	4.1	1498	5	BC077743	BC077743 Xenopus l	1235	117	4.1	3307	10	BC018613	BC018613 Mus muscu
1164	118	4.1	1561	9	BC040443	BC040443 Homo sapi	1236	117	4.1	3310	10	BC061486	BC061486 Mus muscu
1165	118	4.1	1612	9	BC044235	BC044235 Homo sapi	1237	117	4.1	3328	10	BC052770	BC052770 Mus muscu
1166	118	4.1	1650	9	AB047615	AB047615 Macaca fa	1238	117	4.1	3747	10	BC064447	BC064447 Mus muscu
1167	118	4.1	1718	9	AK025339	AK025339 Homo sapi	1239	117	4.1	3937	5	BC068837	BC068837 Xenopus l
1168	118	4.1	1738	3	AK112524	AK112524 Ciona int	1240	117	4.1	4339	9	AF106862	AF106862 Homo sapi
1169	118	4.1	1924	9	BC042674	BC042674 Homo sapi	cl241	117	4.1	5339	3	AY119181	AY119181 Drosophil
1170	118	4.1	1924	9	AK026741	AK026741 Homo sapi	cl242	117	4.1	5845	6	AX346564	AX346564 Sequence
1171	118	4.1	1959	9	BC040005	BC040005 Homo sapi	cl243	117	4.1	17137	6	AX345092	AX345092 Sequence
1172	118	4.1	1975	10	BC052682	BC052682 Mus muscu	1244	116	4.1	235	6	CQ677257	CQ677257 Sequence
1173	118	4.1	2002	9	BC068030	BC068030 Homo sapi	1245	116	4.1	268	6	CQ526263	CQ526263 Sequence
1174	118	4.1	2012	6	AX664375	AX664375 Sequence	1246	116	4.1	381	3	AF159974	AF159974 Butch ma
1175	118	4.1	2012	10	AF362952	AF362952 Mus muscu	1247	116	4.1	472	6	CQ518059	CQ518059 Sequence
1176	118	4.1	2096	10	BC034131	BC034131 Mus muscu	1248	116	4.1	489	6	CQ545523	CQ545523 Sequence
1177	118	4.1	2138	9	BC067301	BC067301 Homo sapi	1249	116	4.1	504	6	CQ526778	CQ526778 Sequence
1178	118	4.1	2261	10	BC072562	BC072562 Mus muscu	1250	116	4.1	515	6	CQ526571	CQ526571 Sequence
1179	118	4.1	2379	9	AB060887	AB060887 Macaca fa	1251	116	4.1	562	10	BC049688	BC049688 Mus muscu
1180	118	4.1	2462	9	BSM800419	AL050116 Homo sapi	1252	116	4.1	572	9	BC032439	BC032439 Homo sapi
1181	118	4.1	2735	9	BC046366	BC046366 Homo sapi	1253	116	4.1	579	6	CQ526139	CQ526139 Sequence
1182	118	4.1	2891	9	BSM804499	AL833188 Homo sapi	1254	116	4.1	898	10	BC026633	BC026633 Mus muscu
1183	118	4.1	3232	10	BC082299	BC082299 Mus muscu	1255	116	4.1	910	10	BC069266	BC069266 Mus muscu
1184	118	4.1	3274	9	BSM807371	BSM807371 Homo sapi	1256	116	4.1	1081	9	BC043527	BC043527 Homo sapi
1185	118	4.1	3294	10	BC053924	BC053924 Mus muscu	1257	116	4.1	1107	3	AK173973	AK173973 Ciona int
1186	118	4.1	3420	10	BC074017	BC074017 Rattus no	1258	116	4.1	1311	5	BC075786	BC075786 Danio rer
1187	118	4.1	3914	9	BSM803724	AL832416 Homo sapi	1259	116	4.1	1573	9	BSM801268	AL122050 Homo sapi
							1260	116	4.1	1590	9	BSM803698	AL832390 Homo sapi

1361	116	4.1	1604	9	BC044260	Homo sapi	1334	115	4.0	2477	9	BC034692	BC034692 Homo sapi
1362	116	4.1	1668	10	BC008187	Mus muscu	1335	115	4.0	2485	10	BC064470	BC064470 Mus muscu
1363	116	4.1	1732	10	BC033364	Mus muscu	1336	115	4.0	2487	6	BD074862	BD074862 Secreted
1364	116	4.1	1741	9	AB063008	Macaca fa	1337	115	4.0	2496	6	BD191411	BD191411 Secreted
1365	116	4.1	1755	9	BC031825	Homo sapi	1338	115	4.0	2765	3	AK115430	AK115430 Ciona int
1366	116	4.1	1813	6	AR164089	Sequence	1339	115	4.0	2800	9	BC053596	BC053596 Homo sapi
1367	116	4.1	1886	9	AK025084	Homo sapi	1340	115	4.0	2820	9	BC065198	BC065198 Homo sapi
1368	116	4.1	1889	9	BC050462	Homo sapi	1341	115	4.0	3002	6	AX354181	AX354181 Sequence
1369	116	4.1	1925	5	BC066381	Danio rer	1342	115	4.0	3117	9	BC043528	BC043528 Homo sapi
1370	116	4.1	1973	3	BC022780	Homo sapi	1343	115	4.0	3597	10	BC036180	BC036180 Mus muscu
1371	116	4.1	2001	3	AK112791	Ciona int	1344	115	4.0	4066	10	BC048824	BC048824 Mus muscu
1372	116	4.1	2026	10	BC030861	Mus muscu	c1345	115	4.0	4255	6	AX346935	AX346935 Sequence
1373	116	4.1	2026	9	BC022399	Homo sapi	1346	115	4.0	4675	9	BSM803445	AL832138 Homo sapi
1374	116	4.1	2081	10	BC043712	Mus muscu	1347	115	4.0	5123	10	BC064466	BC064466 Mus muscu
1375	116	4.1	2095	5	BC067676	Danio rer	1348	115	4.0	5405	10	BC038061	BC038061 Mus muscu
1376	116	4.1	2130	10	BC062005	Rattus no	1349	115	4.0	5567	10	BC052164	BC052164 Mus muscu
1377	116	4.1	2230	5	BC078288	Danio rer	1350	115	4.0	6153	6	BD160662	BD160662 Primer fo
1378	116	4.1	2238	5	BC063964	Danio rer	1351	115	4.0	6153	6	AX884010	AX884010 Sequence
1379	116	4.1	2511	3	AK174016	Ciona int	1352	115	4.0	6153	9	AK027868	AK027868 Homo sapi
1380	116	4.1	2677	9	BC050385	Homo sapi	1353	115	4.0	7165	9	BSM803503	AL832196 Homo sapi
1381	116	4.1	2846	10	BC017647	Mus muscu	c1354	115	4.0	24259	6	AX251447	AX251447 Sequence
1382	116	4.1	2866	9	BSM807768	Sequence	1355	115	4.0	173854	2	AC073047	AC073047 Homo sapi
1383	116	4.1	3000	9	BC036812	Homo sapi	1356	114	4.0	221	6	CQ685593	CQ685593 Sequence
1384	116	4.1	3002	6	AX571883	Sequence	c1357	114	4.0	349	6	CQ410968	CQ410968 Sequence
1385	116	4.1	3059	10	BC051082	Mus muscu	c1358	114	4.0	385	6	CQ398297	CQ398297 Sequence
1386	116	4.1	3221	9	BC015893	Homo sapi	c1359	114	4.0	385	6	CQ404584	CQ404584 Sequence
1387	116	4.1	3475	9	BSM808741	Homo sapi	c1360	114	4.0	436	6	CQ397977	CQ397977 Sequence
1388	116	4.1	3492	5	BC078645	Danio rer	c1361	114	4.0	436	6	CQ404269	CQ404269 Sequence
1389	116	4.1	3605	9	BSM808524	Sequence	1362	114	4.0	439	6	CQ525664	CQ525664 Sequence
1390	116	4.1	3747	9	HSU42766	Human neuro	1363	114	4.0	462	6	CQ523723	CQ523723 Sequence
1391	116	4.1	3884	9	BSM806337	Sequence	c1364	114	4.0	495	6	CQ398141	CQ398141 Sequence
1392	116	4.1	3930	9	BC027963	Homo sapi	c1365	114	4.0	495	6	CQ404428	CQ404428 Sequence
c1393	116	4.1	6668	6	AX346598	Sequence	1366	114	4.0	519	6	CQ522478	CQ522478 Sequence
1394	115	4.0	236	6	CQ664217	Sequence	c1367	114	4.0	544	6	CQ410812	CQ410812 Sequence
1395	115	4.0	240	6	CQ663206	Sequence	1368	114	4.0	659	9	BC022405	BC022405 Homo sapi
1396	115	4.0	247	6	CQ524931	Sequence	1369	114	4.0	806	5	CR405924	CR405924 Gallus ga
1397	115	4.0	297	6	CQ667350	Sequence	c1370	114	4.0	822	9	BC006807	BC006807 Homo sapi
1398	115	4.0	466	11	BV090989	Sequence	c1371	114	4.0	831	6	CQ423554	CQ423554 Sequence
1399	115	4.0	466	11	BV090989	Sequence	c1372	114	4.0	956	5	BC071149	BC071149 Xenopus l
1400	115	4.0	497	6	CQ526425	Sequence	1373	114	4.0	1265	10	BC026436	BC026436 Mus muscu
c1401	115	4.0	501	6	CQ411817	Sequence	1374	114	4.0	1286	9	BC044234	BC044234 Homo sapi
1402	115	4.0	556	9	AB055361	Macaca fa	1375	114	4.0	1306	10	BC070474	BC070474 Mus muscu
1403	115	4.0	782	5	BC051617	Danio rer	1376	114	4.0	1319	9	BC068029	BC068029 Homo sapi
1404	115	4.0	782	9	BC040860	Homo sapi	1377	114	4.0	1355	9	BC063463	BC063463 Homo sapi
c1405	115	4.0	805	6	CQ395292	Sequence	1378	114	4.0	1495	5	BC074583	BC074583 Xenopus t
1406	115	4.0	805	6	CQ401630	Sequence	1379	114	4.0	1498	10	BC083575	BC083575 Rattus no
c1407	115	4.0	917	5	BC084108	Xenopus l	1380	114	4.0	1502	9	BC009739	BC009739 Homo sapi
1408	115	4.0	1044	9	AB019565	Homo sapi	1381	114	4.0	1529	9	BC063597	BC063597 Homo sapi
1409	115	4.0	1053	10	BC049595	Mus muscu	1382	114	4.0	1619	10	BC058767	BC058767 Mus muscu
1410	115	4.0	1087	5	BC083541	Danio rer	1383	114	4.0	1646	9	BC051812	BC051812 Homo sapi
1411	115	4.0	1309	5	BC067650	Danio rer	1384	114	4.0	1680	9	BC053634	BC053634 Homo sapi
1412	115	4.0	1387	9	BC032568	Homo sapi	1385	114	4.0	1734	6	AX092320	AX092320 Sequence
1413	115	4.0	1410	5	BC049418	Danio rer	1386	114	4.0	1734	6	AX358902	AX358902 Sequence
1414	115	4.0	1425	9	BC036851	Homo sapi	1387	114	4.0	1734	6	AX362395	AX362395 Sequence
1415	115	4.0	1458	10	BC061969	Rattus no	1388	114	4.0	1734	6	AX376134	AX376134 Sequence
1416	115	4.0	1549	10	BC005509	Mus muscu	1389	114	4.0	1734	6	AX403750	AX403750 Sequence
1417	115	4.0	1619	9	BC043510	Homo sapi	1390	114	4.0	1734	6	AX454564	AX454564 Sequence
1418	115	4.0	1632	5	BC069370	Danio rer	1391	114	4.0	1734	6	AX491042	AX491042 Sequence
1419	115	4.0	1641	9	BC043576	Homo sapi	1392	114	4.0	1734	6	AX696983	AX696983 Sequence
1420	115	4.0	1756	9	BC029848	Homo sapi	1393	114	4.0	1767	9	AY358412	AY358412 Homo sapi
1421	115	4.0	1904	6	AR528502	Sequence	1394	114	4.0	1831	6	BSM800099	AL049314 Homo sapi
1422	115	4.0	1904	6	AX463966	Sequence	1395	114	4.0	1844	6	CQ498497	CQ498497 Sequence
1423	115	4.0	1904	6	AY358614	Homo sapi	1396	114	4.0	1870	9	AK025958	AK025958 Homo sapi
1424	115	4.0	1929	10	BC058811	Mus muscu	1397	114	4.0	1887	10	BC050801	BC050801 Mus muscu
1425	115	4.0	2205	3	AK115544	Ciona int	1398	114	4.0	1936	10	BC031408	BC031408 Mus muscu
1426	115	4.0	2210	9	AB066547	Macaca fa	1399	114	4.0	2000	9	BC039729	BC039729 Homo sapi
1427	115	4.0	2259	9	BC051847	Homo sapi	1400	114	4.0	2010	10	BC046588	BC046588 Mus muscu
1428	115	4.0	2286	9	BC020211	Homo sapi	1401	114	4.0	2038	9	BC043591	BC043591 Homo sapi
1429	115	4.0	2344	9	BC050578	Homo sapi	1402	114	4.0	2104	9	BC032371	BC032371 Homo sapi
1430	115	4.0	2400	5	BC056284	Danio rer	1403	114	4.0	2108	5	BC084490	BC084490 Xenopus t
1431	115	4.0	2417	9	BSM800967	Sequence	1404	114	4.0	2135	10	BC017640	BC017640 Mus muscu
1432	115	4.0	2419	9	BC043583	Homo sapi	1405	114	4.0	2269	6	BD136822	BD136822 Podocalyx
1433	115	4.0	2429	10	BC049167	Mus muscu	1406	114	4.0				

```
1407 114 4.0 2269 6 AR372112 Sequence
1408 114 4.0 2267 3 AF219137 Homo sapi
1409 114 4.0 2279 3 AK116699 Ciona int
1410 114 4.0 2406 9 BC042542 Homo sapi
1411 114 4.0 2406 9 BC017107 Homo sapi
1412 114 4.0 2475 3 AV296116 Homo sapi
1413 114 4.0 2500 9 BC050384 Homo sapi
1414 114 4.0 2601 5 BC072034 Homo sapi
1415 114 4.0 2628 9 BC021085 Homo sapi
1416 114 4.0 2654 3 AK174482 Ciona int
1417 114 4.0 2868 10 BC006583 Mus muscu
1418 114 4.0 3288 10 BC021457 Mus muscu
1419 114 4.0 3501 6 AR528471 Sequence
1420 114 4.0 3501 6 AR463904 Sequence
1421 114 4.0 3502 9 BX647580 Homo sapi
1422 114 4.0 3669 10 BC038376 Mus muscu
1423 114 4.0 4004 9 BC041086 Homo sapi
1424 114 4.0 4064 6 AR526951 Sequence
1425 114 4.0 4064 10 AF438405 Mus muscu
1426 114 4.0 4812 5 BC068296 Xenopus t
1427 114 4.0 8059 5 BC076779 Xenopus l
1428 114 4.0 15954 6 AK344491 Sequence
1429 114 4.0 15954 6 AK348900 Sequence
1430 113 4.0 277 6 C0671217 Sequence
1431 113 4.0 396 6 AR391193 Sequence
1432 113 4.0 396 6 AR392898 Sequence
1433 113 4.0 396 6 AR489628 Sequence
1434 113 4.0 396 6 AR493869 Sequence
1435 113 4.0 396 6 AX093198 Sequence
1436 113 4.0 432 6 C0526159 Sequence
1437 113 4.0 510 6 C0526266 Sequence
1438 113 4.0 579 6 C0525663 Sequence
1439 113 4.0 606 6 C0524188 Sequence
1440 113 4.0 705 10 BC049708 Mus muscu
1441 113 4.0 727 9 BC024701 Homo sapi
1442 113 4.0 843 10 BC026460 Mus muscu
1443 113 4.0 1003 5 BC067645 Danio rer
1444 113 4.0 1124 10 BC015270 Mus muscu
1445 113 4.0 1164 6 AX098194 Sequence
1446 113 4.0 1240 5 BC055418 Homo sapi
1447 113 4.0 1270 5 BC066442 Homo rer
1448 113 4.0 1345 9 BC073861 Homo sapi
1449 113 4.0 1391 5 BC074604 Xenopus t
1450 113 4.0 1460 9 BC017009 Homo sapi
1451 113 4.0 1560 9 BC073173 Homo sapi
1452 113 4.0 1570 10 BC049624 Mus muscu
1453 113 4.0 1582 10 BC005609 Mus muscu
1454 113 4.0 1614 5 BC071086 Xenopus l
1455 113 4.0 1616 10 BC043714 Mus muscu
1456 113 4.0 1687 9 BC001967 Homo sapi
1457 113 4.0 1690 6 E32442 Mammal-deri
1458 113 4.0 1729 9 BC028039 Homo sapi
1459 113 4.0 1834 9 BC040627 Homo sapi
1460 113 4.0 1889 9 HSM805887 Homo sapi
1461 113 4.0 2085 9 BC029120 Homo sapi
1462 113 4.0 2095 5 BC084410 Xenopus l
1463 113 4.0 2161 9 BC025768 Homo sapi
1464 113 4.0 2196 9 HSM801403 Homo sapi
1465 113 4.0 2208 10 BC052921 Mus muscu
1466 113 4.0 2224 6 B189940 Tumor ant
1467 113 4.0 2224 9 AB062292 Homo sapi
1468 113 4.0 2246 6 AR212256 Sequence
1469 113 4.0 2246 6 AR265251 Sequence
1470 113 4.0 2246 10 AF017152 Mus muscu
1471 113 4.0 2372 9 BC043652 Homo sapi
1472 113 4.0 2435 9 BC028219 Homo sapi
1473 113 4.0 2446 6 C0413150 Sequence
1474 113 4.0 2530 5 BC077396 Xenopus l
1475 113 4.0 2769 10 BC058616 Mus muscu
1476 113 4.0 2789 9 HSM80418 Homo sapi
1477 113 4.0 3236 9 HSM801246 Homo sapi
1478 113 4.0 3448 10 BC034679 Mus muscu
1479 113 4.0 3459 9 BC052964 Homo sapi
```

```
1480 113 4.0 3521 9 BC027712 Homo sapi
1481 113 4.0 3596 9 HSM806341 Homo sapi
1482 113 4.0 4108 9 HSM806223 Homo sapi
1483 113 4.0 4680 9 BC042624 Homo sapi
1484 113 4.0 4864 9 HSM807992 Homo sapi
1485 113 4.0 5219 9 BC057396 Homo sapi
1486 113 4.0 15518 6 AX281513 Sequence
1487 113 4.0 15518 6 AX347074 Sequence
1488 113 4.0 15518 6 AX349039 Sequence
1489 112 3.9 267 6 C0410745 Sequence
1490 112 3.9 372 6 BC071808 Homo sapi
1491 112 3.9 392 6 C0516508 Sequence
1492 112 3.9 420 6 C0526488 Sequence
1493 112 3.9 430 9 BC062435 Homo sapi
1494 112 3.9 442 6 C0526679 Sequence
1495 112 3.9 488 6 C0527061 Sequence
1496 112 3.9 524 11 G53989 SHGC-89277
1497 112 3.9 752 3 AK174753 Ciona int
1498 112 3.9 791 9 BC038970 Homo sapi
1499 112 3.9 814 10 BC025933 Mus muscu
1500 112 3.9 860 9 BC038839 Homo sapi
```

ALIGNMENTS

RESULT 1
LOCUS AR252533 2846 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 230 from patent US 6478825.
ACCESSION AR252533
VERSION AR252533.1 GI:27300441
KEYWORDS SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2846)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the treatment of bone defects
JOURNAL Patent: US 6478825-A 230 12-NOV-2002;
FEATURES Location/Qualifiers
source
1..2846
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 2846; DB 6; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCTCGGGCCACCGCGGCAAGGATGGAGCTGGGTTCGTGGACGCGCAGTTGGGGCTCAC 60
Db 1 CGCTCGGGCCACCGCGGCGGAGAGTGGAGCTGGGTTCGTGGACGCGCAGTTGGGGCTCAC 60

Qy 61 TTTTCTTCAGCTCCTTCTCATCTCGTCTTGCCAAAGAGTACACAGTCATTAATGAAGC 120
Db 61 TTTTCTTCAGCTCCTTCTCATCTCGTCTTGCCAAAGAGTACACAGTCATTAATGAAGC 120

Qy 121 CTGCCCTCGGACGACAGTGGATATCATGTGCGGAGTGTCTGTAATATGATCAGATTGA 180
Db 121 CTGCCCTCGGACGACAGTGGATATCATGTGCGGAGTGTCTGTAATATGATCAGATTGA 180

Qy 181 GTGGCTGTGCCCCGGAAGGGAAGTGTGGGTTCATACCATCCCTTCTGCTCGAGGAATGA 240
Db 181 GTGGCTGTGCCCCGGAAGGGAAGTGTGGGTTCATACCATCCCTTCTGCTCGAGGAATGA 240

Qy 241 GGAGATGAGTGTGACCTCTGCTGATCCATCCAGGTTGTACCACTTTTGAAGAACTGCAA 300
Db 241 GGAGATGAGTGTGACCTCTGCTGATCCATCCAGGTTGTACCACTTTTGAAGAACTGCAA 300

Qy 301 GAGCTGCGGAATGGCTCATGCGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTA 360
Db 301 GAGCTGCGGAATGGCTCATGCGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTA 360

Db 301 GAGCTGCCGAAATGGCTCATGGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTA 360
Qy 361 CTGTGCAAGTGCAGACAGGCTGGTACGGAGGAGACTGCAATGCGATGTGGCCAGGTTCT 420
Db 361 CTGTGCAAGTGCAGACAGGCTGGTACGGAGGAGACTGCAATGCGATGTGGCCAGGTTCT 420
Qy 421 GCGAGCCCAAGGGTCAGATTTTGTGGAAAGCTATCCCTTAATGCTCACTGTGAATG 480
Db 421 GCGAGCCCAAGGGTCAGATTTTGTGGAAAGCTATCCCTTAATGCTCACTGTGAATG 480
Qy 481 GACCATTCATGCTAAACCTGGGTTTGTGCATCCAACTAAGATTTGTCAATGTTGAGTCTGGA 540
Db 481 GACCATTCATGCTAAACCTGGGTTTGTGCATCCAACTAAGATTTGTCAATGTTGAGTCTGGA 540
Qy 541 GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTCTGTATGGAGACACACCGGATGG 600
Db 541 GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTCTGTATGGAGACACACCGGATGG 600
Qy 601 CCAGATCATCAAGGGTGTCTGTGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATC 660
Db 601 CCAGATCATCAAGGGTGTCTGTGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATC 660
Qy 661 CTCACCTCCACTCTTCCACTCCGATGGCTCCAGAAATTTGACGGTTTCCATGCCAT 720
Db 661 CTCACCTCCACTCTTCCACTCCGATGGCTCCAGAAATTTGACGGTTTCCATGCCAT 720
Qy 721 TTATGAGGAGATCACAGATGCTCTCATCCCTTGTTCATGACGGCAGCTGCTCCT 780
Db 721 TTATGAGGAGATCACAGATGCTCTCATCCCTTGTTCATGACGGCAGCTGCTCCT 780
Qy 781 TGACAAGGCTGGATCTTCAAGTGTGCTGTGGCAGGCTATACTGGGAGCGCTGTGA 840
Db 781 TGACAAGGCTGGATCTTCAAGTGTGCTGTGGCAGGCTATACTGGGAGCGCTGTGA 840
Qy 841 AAATCTCTTGAAGAAAGAAACTGCTCAGACCTGGGGGCCAGTCAATGGGTACCAGAA 900
Db 841 AAATCTCTTGAAGAAAGAAACTGCTCAGACCTGGGGGCCAGTCAATGGGTACCAGAA 900
Qy 901 AATAACAGGGGGCCCTGGGCTTATCAACGAGCGCATGCTTAAATTTGGCACCGTGGTGC 960
Db 901 AATAACAGGGGGCCCTGGGCTTATCAACGAGCGCATGCTTAAATTTGGCACCGTGGTGC 960
Qy 961 TTTCTTTTGTAACTCTATGTTCTTAGTGGCAATGAGAAAGAACTTCCAGCAGAGAA 1020
Db 961 TTTCTTTTGTAACTCTATGTTCTTAGTGGCAATGAGAAAGAACTTCCAGCAGAGAA 1020
Qy 1021 TGGAGAGTGTTCAGGGAACAGCCCATCTGCATATAAGCCTGCCAGAAACAAAGATTC 1080
Db 1021 TGGAGAGTGTTCAGGGAACAGCCCATCTGCATATAAGCCTGCCAGAAACAAAGATTC 1080
Qy 1081 AGACTGGTGAAGAGGAGTTCCTCCGATGCAAGTTCAGTTCAGGAGGAGACCATTTACA 1140
Db 1081 AGACTGGTGAAGAGGAGTTCCTCCGATGCAAGTTCAGTTCAGGAGGAGACCATTTACA 1140
Qy 1141 CCAGCTATCTCAGCGGCTTCAGCAAGCAAGAACTGCAGAGTGCCTTACCAAGAAAGCC 1200
Db 1141 CCAGCTATCTCAGCGGCTTCAGCAAGCAAGAACTGCAGAGTGCCTTACCAAGAAAGCC 1200
Qy 1201 AGCCCTTCCCTTTGGAGATCTGCCATGGGATCAACATCTGCATATCCAGTCCAGTA 1260
Db 1201 AGCCCTTCCCTTTGGAGATCTGCCATGGGATCAACATCTGCATATCCAGTCCAGTA 1260
Qy 1261 TGAGTGCATCTACCCCTTCTACCGCGCTGGGAGAGGAGGAGGAGCATGTCTGAGGAC 1320
Db 1261 TGAGTGCATCTACCCCTTCTACCGCGCTGGGAGAGGAGGAGGAGCATGTCTGAGGAC 1320
Qy 1321 TGGGAAGTGGAGTGGGGGGCACCATCTGCATCCCTATCTGCGGGGAAAATTTGAGAAACAT 1380
Db 1321 TGGGAAGTGGAGTGGGGGGCACCATCTGCATCCCTATCTGCGGGGAAAATTTGAGAAACAT 1380
Qy 1381 CACTGCTCCAAAGACCCAGGGGTTGCGCTGGCCGTGGCAGCGACCATCTACAGAGGAC 1440
Db 1381 CACTGCTCCAAAGACCCAGGGGTTGCGCTGGCCGTGGCAGCGACCATCTACAGAGGAC 1440

Qy 1441 CAGCGGGTGCATGACGCGAGCCTTACAAAGGGAGCGTGGTTCTAGTCTCAGCGGTGC 1500
Db 1441 CAGCGGGTGCATGACGCGAGCCTTACAAAGGGAGCGTGGTTCTAGTCTCAGCGGTGC 1500
Qy 1501 CTTGGTGAATGAGCGCACTGTGTGGTGGCTGCCACTGTGTATTACTGACCTGGGGAAAGGT 1560
Db 1501 CTTGGTGAATGAGCGCACTGTGTGGTGGCTGCCACTGTGTATTACTGACCTGGGGAAAGGT 1560
Qy 1561 CACCATGATCAAGACAGACAGACTGAAAAGTTGTTTGGGGAAAATTTCTACCGGGATGATGA 1620
Db 1561 CACCATGATCAAGACAGACAGACTGAAAAGTTGTTTGGGGAAAATTTCTACCGGGATGATGA 1620
Qy 1621 CCGGGATGAGAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCAATCCCACTA 1680
Db 1621 CCGGGATGAGAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCAATCCCACTA 1680
Qy 1681 TGACCCCATCTGCTGATGCTGACATCGCCATCTCTGAAGCTCTAGACAAGGCCCGTAT 1740
Db 1681 TGACCCCATCTGCTGATGCTGACATCGCCATCTCTGAAGCTCTAGACAAGGCCCGTAT 1740
Qy 1741 CAGCACCGAGTCCAGCCCATCTGCTGCTGCCAGTCGGGATCTCAGACATTTCTTTCCA 1800
Db 1741 CAGCACCGAGTCCAGCCCATCTGCTGCTGCCAGTCGGGATCTCAGACATTTCTTTCCA 1800
Qy 1801 GGAGTCCACATCACTGCTGGCTGGTAAATGCTCTGGCAGACGTGAGGAGCCCTGGCTT 1860
Db 1801 GGAGTCCACATCACTGCTGGCTGGTAAATGCTCTGGCAGACGTGAGGAGCCCTGGCTT 1860
Qy 1861 CAAGAACGACACACTGCGCTCTGGGGTGGTCAAGTGTGGTGGACCTCGTGTGTGAGGA 1920
Db 1861 CAAGAACGACACACTGCGCTCTGGGGTGGTCAAGTGTGGTGGACCTCGTGTGTGAGGA 1920
Qy 1921 GCAGCATGAGGAACATGGCATCCAGTGAAGTGTCACTGATAACATGTTCTGTGCCAGCTG 1980
Db 1921 GCAGCATGAGGAACATGGCATCCAGTGAAGTGTCACTGATAACATGTTCTGTGCCAGCTG 1980
Qy 1981 GGAACCCACTGCCCTTCTGATATCTGCATTCAGACAGAGGAGGCATCGCGGTGTGTC 2040
Db 1981 GGAACCCACTGCCCTTCTGATATCTGCATTCAGACAGAGGAGGCATCGCGGTGTGTC 2040
Qy 2041 CTTCCCGGAGCAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGGTCACTGGAG 2100
Db 2041 CTTCCCGGAGCAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGGTCACTGGAG 2100
Qy 2101 CTATGATAAACAATGACAGCCACAGGCTCTCCACTGCTTCCACAGGTCGTCCTTTTAA 2160
Db 2101 CTATGATAAACAATGACAGCCACAGGCTCTCCACTGCTTCCACAGGTCGTCCTTTTAA 2160
Qy 2161 AGACTGATTTGAAAGAAATATGAAATGAACCATGCTCATGCACTCTTGAGAAAGTGTTC 2220
Db 2161 AGACTGATTTGAAAGAAATATGAAATGAACCATGCTCATGCACTCTTGAGAAAGTGTTC 2220
Qy 2221 TGTATATCCGCTGTACGTGTCAATTCGCTGGAAGCAGTGTGGCCTGAAGTGTGATTTG 2280
Db 2221 TGTATATCCGCTGTACGTGTCAATTCGCTGGAAGCAGTGTGGCCTGAAGTGTGATTTG 2280
Qy 2281 GCCTGTGAACCTTGGCTGTGCCAGGCTTCTGACTTCAGGGGCAAAATCTCAGTGAAGGGTG 2340
Db 2281 GCCTGTGAACCTTGGCTGTGCCAGGCTTCTGACTTCAGGGGCAAAATCTCAGTGAAGGGTG 2340
Qy 2341 AGTAGACTCATTTGCTGGTAGGCTGATGCCGCTCCACTACTAGGACAGCAATTTGGAA 2400
Db 2341 AGTAGACTCATTTGCTGGTAGGCTGATGCCGCTCCACTACTAGGACAGCAATTTGGAA 2400
Qy 2401 GATGCCAGGGCTTGCAGAAAGTAAAGTTTCTTCAAAGAGACCATATATACAAACCTCTCCA 2460
Db 2401 GATGCCAGGGCTTGCAGAAAGTAAAGTTTCTTCAAAGAGACCATATATACAAACCTCTCCA 2460
Qy 2461 CTCCACTGACCTGGTGTCTTCCCAACTTTTCAAGTATACGAATGCCATCAGCTTGACCA 2520
Db 2461 CTCCACTGACCTGGTGTCTTCCCAACTTTTCAAGTATACGAATGCCATCAGCTTGACCA 2520


```
Qy 1381 CACTGCTCCAAAGACCCAAAGGTTGCGTGGCCGTTGGCAGCGACCATCTACAGGAGAC 1440
Db 1381 CACTGCTCCAAAGACCCAAAGGTTGCGTGGCCGTTGGCAGCGACCATCTACAGGAGAC 1440
Qy 1441 CAGCGGGTGCATGACGGCAGCCTACACAAGGGAGCGTGTCTCTAGTCTGACAGCGTGC 1500
Db 1441 CAGCGGGTGCATGACGGCAGCCTACACAAGGGAGCGTGTCTCTAGTCTGACAGCGTGC 1500
Qy 1501 CTTGGTGAATGAGGGCACTGTGTGGTGGTGGCTGCCCACTGTGTACTGACCTGGGGAAGGT 1560
Db 1501 CTTGGTGAATGAGGGCACTGTGTGGTGGTGGCTGCCCACTGTGTACTGACCTGGGGAAGGT 1560
Qy 1561 CACCATCATCAAGACACAGACCTGAAAGTTGTTTTCGGGAAATTTCTACCGGGATGATGA 1620
Db 1561 CACCATCATCAAGACACAGACCTGAAAGTTGTTTTCGGGAAATTTCTACCGGGATGATGA 1620
Qy 1621 CCGGGATGAGAAGACCATCCAGAGCCTACAGATTTCTGTATCATTTCTGCATCCCACTA 1680
Db 1621 CCGGGATGAGAAGACCATCCAGAGCCTACAGATTTCTGTATCATTTCTGCATCCCACTA 1680
Qy 1681 TGACCCCATCTGCTTGTGATGTCATCGCATCGCATCTGAAGTCTCTAGACAGGCCCGTAT 1740
Db 1681 TGACCCCATCTGCTTGTGATGTCATCGCATCGCATCTGAAGTCTCTAGACAGGCCCGTAT 1740
Qy 1741 CAGCACCCGAGTCCAGGCCCATCTGCTCGCTCGCTCGAGTCGGATCTCAGCACTTCTCTCCA 1800
Db 1741 CAGCACCCGAGTCCAGGCCCATCTGCTCGCTCGCTCGAGTCGGATCTCAGCACTTCTCTCCA 1800
Qy 1801 GGAGTCCCATCATCTGTGCTGGCTGGAATGTCTCTGGCAGACGTGAGGAGCCCTGGCTT 1860
Db 1801 GGAGTCCCATCATCTGTGCTGGCTGGAATGTCTCTGGCAGACGTGAGGAGCCCTGGCTT 1860
Qy 1861 CAAGAACGACACACTGCGCTCTGGGGTGGTCAGTGTGGTGGACCTCGCTGTGTGAGGA 1920
Db 1861 CAAGAACGACACACTGCGCTCTGGGGTGGTCAGTGTGGTGGACCTCGCTGTGTGAGGA 1920
Qy 1921 GCACATGAGGACCATGGCATCCAGTGAGTGTCACTGATAAATGTTCTGTGCCACTG 1980
Db 1921 GCACATGAGGACCATGGCATCCAGTGAGTGTCACTGATAAATGTTCTGTGCCACTG 1980
Qy 1981 GGAACCCACTGCCCTTCTGATATCTGACATCTGACATGACAGACAGGAGCATCGCGGTGTC 2040
Db 1981 GGAACCCACTGCCCTTCTGATATCTGACATCTGACATGACAGACAGGAGCATCGCGGTGTC 2040
Qy 2041 CTTCCCGGAGCGACATCTCTGAGCCACGCTGCGATCTGATGGGACTGGTCACTGGAG 2100
Db 2041 CTTCCCGGAGCGACATCTCTGAGCCACGCTGCGATCTGATGGGACTGGTCACTGGAG 2100
Qy 2101 CTATGATAAAACATGCAGCCACAGGCTCTCCACTGCTTCAACAAAGTGTGCTGCTTTAA 2160
Db 2101 CTATGATAAAACATGCAGCCACAGGCTCTCCACTGCTTCAACAAAGTGTGCTGCTTTAA 2160
Qy 2161 AGACTGGATTGAAAGAAATATGAATGAACCATGCTCATGCACTCTCTTGAAGAGTGTTC 2220
Db 2161 AGACTGGATTGAAAGAAATATGAATGAACCATGCTCATGCACTCTCTTGAAGAGTGTTC 2220
Qy 2221 TGTATATCCGCTGTAGTGTGTCTATTCGCTGAAGCAGTGTGGCCCTGAAGTGTGATTG 2280
Db 2221 TGTATATCCGCTGTAGTGTGTCTATTCGCTGAAGCAGTGTGGCCCTGAAGTGTGATTG 2280
Qy 2281 GCCTGTGAATCTGGCTGTGCCAGGGCTTCTGACTTTCAGGGACAAATCTCAGTGAAGGGTG 2340
Db 2281 GCCTGTGAATCTGGCTGTGCCAGGGCTTCTGACTTTCAGGGACAAATCTCAGTGAAGGGTG 2340
Qy 2341 AGTAGACCTCATTTGCTGGTAGGCTGATGCGCGCTCCACTACTAGGACAGCCAAATTGGAA 2400
Db 2341 AGTAGACCTCATTTGCTGGTAGGCTGATGCGCGCTCCACTACTAGGACAGCCAAATTGGAA 2400
Qy 2401 GATGCCAGGGCTGCAAGAGTAGTCTTCAAGAGAGCCATATACAAACCTCTCCA 2460
Db 2401 GATGCCAGGGCTGCAAGAGTAGTCTTCAAGAGAGCCATATACAAACCTCTCCA 2460
```

```
Qy 2461 CTCCTACGCTGGTGGTCTTCCCAACTTTCCAGTTATACGAATGCCATCAGCTTGACCA 2520
Db 2461 CTCCTACGCTGGTGGTCTTCCCAACTTTCCAGTTATACGAATGCCATCAGCTTGACCA 2520
Qy 2521 GGAAGATCTGGGCTTCATGAGGCCCTTTTGAGGCTCTCAAGTCTTAGAGAGCTGCTG 2580
Db 2521 GGAAGATCTGGGCTTCATGAGGCCCTTTTGAGGCTCTCAAGTCTTAGAGAGCTGCTG 2580
Qy 2581 TGGGACAGCCCGAGGCGAGAGCTGGGATGTGGTGCATGCCCTTGTGTACATGCCACCA 2640
Db 2581 TGGGACAGCCCGAGGCGAGAGCTGGGATGTGGTGCATGCCCTTGTGTACATGCCACCA 2640
Qy 2641 GTACAGTCTGGTCTTCTTCCCTTCCCATCTCTTGTACACATTTTAAATAAATAGGGTGT 2700
Db 2641 GTACAGTCTGGTCTTCTTCCCTTCCCATCTCTTGTACACATTTTAAATAAATAGGGTGT 2700
Qy 2701 GCTTCTGAATACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2760
Db 2701 GCTTCTGAATACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2760
Qy 2761 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 2820
Db 2761 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 2820
Qy 2821 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 2846
Db 2821 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 2846

RESULT 3
AX376102 2846 bp DNA linear PAT 01-MAR-2002
LOCUS Sequence 169 from Patent WO0168848.
DEFINITION AX376102
ACCESSION AX376102
VERSION AX376102.1 GI:19170443
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 169 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
1..2846
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 2846; DB 6; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGCTCGGGCAACGACCGCGGAGATGGAGCTGGGTGTGTCGACGCGAGTTGGGGCTCAC 60
Db 1 CGCTCGGGCAACGACCGCGGAGATGGAGCTGGGTGTGTCGACGCGAGTTGGGGCTCAC 60
Qy 61 TTTTCTTCAGCTCTTCTCATCTCGCTTGTGCCAAGAGAGTACACAGTCAATTAATGAAGC 120
Db 61 TTTTCTTCAGCTCTTCTCATCTCGCTTGTGCCAAGAGAGTACACAGTCAATTAATGAAGC 120
Qy 121 CTGCCCTGGAGCAGAGTGAATATCATGTGTGCGGAGTGTGCTGTAATATATCATCAGATTGA 180
Db 121 CTGCCCTGGAGCAGAGTGAATATCATGTGTGCGGAGTGTGCTGTAATATATCATCAGATTGA 180
Qy 181 GTGCGTCTGCCCGGAAAGAGGGAAGTCTGGGTATTACCATCCCTTGTCTGCAGGAATGA 240
```

Db 181 GTGGCTGTGCCCCGGAAGAGGGAGTCTGTGGTTATACCATCCCTTCTGCAGGAATGA 240
Qy 241 GGAGAAAGAGTGTGACTCTCTCCCTGATCCACCACCGAGTTGTACCATCTTTGAAAACTGCAA 300
Db 241 GGAGAAAGAGTGTGACTCTCTCCCTGATCCACCACCGAGTTGTACCATCTTTGAAAACTGCAA 300
Qy 301 GAGCTGCCGAATGGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCTA 360
Db 301 GAGCTGCCGAATGGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCTA 360
Qy 361 CTGTGCAGATGCCAGCAGGCTGTACGGAGGAGACTGCATGCGATGTGCCAGGTTCT 420
Db 361 CTGTGCAGATGCCAGCAGGCTGTACGGAGGAGACTGCATGCGATGTGCCAGGTTCT 420
Qy 421 GCGAGCCCAAGGGTCAAGTTTTGTGGAAAGCTATCCCCATAATGCTCACTGTGAATG 480
Db 421 GCGAGCCCAAGGGTCAAGTTTTGTGGAAAGCTATCCCCATAATGCTCACTGTGAATG 480
Qy 481 GACCAATTCATGCTAAACCTGGGTTGTCTATCCAACTAAGATTTGTTCATGTTGAGTCTGGA 540
Db 481 GACCAATTCATGCTAAACCTGGGTTGTCTATCCCAACTAAGATTTGTTCATGTTGAGTCTGGA 540
Qy 541 GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTGCTGATGAGACAACCCGATGG 600
Db 541 GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTGCTGATGAGACAACCCGATGG 600
Qy 601 CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGCCAGCTCCTATCCAGAGCATAGGATC 660
Db 601 CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGCCAGCTCCTATCCAGAGCATAGGATC 660
Qy 661 CTCACCTCACGTCCTCTTCCACTCGGATGGCTCCAGAAATTTTGAACGTTTCCATGCCAT 720
Db 661 CTCACCTCACGTCCTCTTCCACTCGGATGGCTCCAGAAATTTTGAACGTTTCCATGCCAT 720
Qy 721 TTATGAGGAGATCACAGCATGCTCTCATCCCTTTGTTTCCATGACGCGCATGCGTCT 780
Db 721 TTATGAGGAGATCACAGCATGCTCTCATCCCTTTGTTTCCATGACGCGCATGCGTCT 780
Qy 781 TGACAAGGCTGGATCTTACAAGTGTGCTGTGGCAGGCTATATCTGGCAGCGCTGTGA 840
Db 781 TGACAAGGCTGGATCTTACAAGTGTGCTGTGGCAGGCTATATCTGGCAGCGCTGTGA 840
Qy 841 AAATCTCTTGAAGAAAGAACTGTGTCAGACCTTGGGGGCCAGTCAATGGGTACCGAA 900
Db 841 AAATCTCTTGAAGAAAGAACTGTGTCAGACCTTGGGGGCCAGTCAATGGGTACCGAA 900
Qy 901 AATAACAGGGGGCCCTGGGCTTATCAACGAGCGCATGCTAAATTTGCAACCGTGTGTC 960
Db 901 AATAACAGGGGGCCCTGGGCTTATCAACGAGCGCATGCTAAATTTGCAACCGTGTGTC 960
Qy 961 TTTCTTTTGTAACTCCTATGTTCTTGTGGCAATGAGAAAGAACTTGGCAGCAGAA 1020
Db 961 TTTCTTTTGTAACTCCTATGTTCTTGTGGCAATGAGAAAGAACTTGGCAGCAGAA 1020
Qy 1021 TGGAGATGTGTGAGGAAACAGCCCATCTGCATAAAGCCTGCCAGAACCAAGATTTTC 1080
Db 1021 TGGAGATGTGTGAGGAAACAGCCCATCTGCATAAAGCCTGCCAGAACCAAGATTTTC 1080
Qy 1081 AGACTGTGTGAGAGGAGTTCTTCCGATCGAGTTTCAGTCAAGGGAGACCACTTACA 1140
Db 1081 AGACTGTGTGAGAGGAGTTCTTCCGATCGAGTTTCAGTCAAGGGAGACCACTTACA 1140
Qy 1141 CCAGCTATCTCAGCGGCTTTCAGCAACGAGAACTGCAGAGTGCCCTACCAAGAGGCC 1200
Db 1141 CCAGCTATCTCAGCGGCTTTCAGCAACGAGAACTGCAGAGTGCCCTACCAAGAGGCC 1200
Qy 1201 AGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGTCCAGTA 1260
Db 1201 AGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGTCCAGTA 1260
Qy 1261 TGAGTGCATCTACCCCTTCTACCGCGCTGGGAGCAGGAGGAGCATGTCTGAGGAC 1320
Db 1261 TGAGTGCATCTACCCCTTCTACCGCGCTGGGAGCAGGAGGAGCATGTCTGAGGAC 1320

Qy 1321 TGGAAAGTGAAGTGGGCGGGCACCATCTCTGATCCCTATCTGCGGGAATAATTGAGAACAT 1380
Db 1321 TGGAAAGTGAAGTGGGCGGGCACCATCTCTGATCCCTATCTGCGGGAATAATTGAGAACAT 1380
Qy 1381 CACTGCTCCAAAGAACCCAAAGGTTGCGCTGGCGGTGGCAGCGACCATCTACAGGAGAC 1440
Db 1381 CACTGCTCCAAAGAACCCAAAGGTTGCGCTGGCGGTGGCAGCGACCATCTACAGGAGAC 1440
Qy 1441 CAGCGGGGTGCATGACGCGCAGCTTACAAAGGAGCGTGGTTCTTAGTCTGCAGCGGTGC 1500
Db 1441 CAGCGGGGTGCATGACGCGCAGCTTACAAAGGAGCGTGGTTCTTAGTCTGCAGCGGTGC 1500
Qy 1501 CCTGGTGAATGAGCGCATCTGTGTGTGGTGGCCCATCTGTGTATCTGACCTGGGGAAGGT 1560
Db 1501 CCTGGTGAATGAGCGCATCTGTGTGTGGTGGCCCATCTGTGTATCTGACCTGGGGAAGGT 1560
Qy 1561 CACCATCATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAATAATCTACCGGGATGATGA 1620
Db 1561 CACCATCATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAATAATCTACCGGGATGATGA 1620
Qy 1621 CCGGGATGAGAAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCAATCCAACTA 1680
Db 1621 CCGGGATGAGAAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCAATCCAACTA 1680
Qy 1681 TGACCCCATCTGCTGTGATGCTGACATCGCCCATCTGAAAGCTCTAGACAAAGGCCGTAT 1740
Db 1681 TGACCCCATCTGCTGTGATGCTGACATCGCCCATCTGAAAGCTCTAGACAAAGGCCGTAT 1740
Qy 1741 CAGCACCGGAGTCAGGCCCATCTGCTCGCTGCGTCAGGATCTCAGCACTTCTTCCCA 1800
Db 1741 CAGCACCGGAGTCAGGCCCATCTGCTCGCTGCGTCAGGATCTCAGCACTTCTTCCCA 1800
Qy 1801 GGAGTCCCAATCACTGTGCTGGCTGGAATGTCTTGGCAGACGTCGAGAGCCCTGGCTT 1860
Db 1801 GGAGTCCCAATCACTGTGCTGGCTGGAATGTCTTGGCAGACGTCGAGAGCCCTGGCTT 1860
Qy 1861 CAAGAAAGCACAACCTGCGCTCTGGGGTGTGAGTGTGGTGGACTCGCTGCTGTGTGAGGA 1920
Db 1861 CAAGAAAGCACAACCTGCGCTCTGGGGTGTGAGTGTGGTGGACTCGCTGCTGTGTGAGGA 1920
Qy 1921 GCAGCATGAGGACCATGGCATCCAGTGTGTCACCTGATTAACATGTTCTGTGCGCAGCTG 1980
Db 1921 GCAGCATGAGGACCATGGCATCCAGTGTGTCACCTGATTAACATGTTCTGTGCGCAGCTG 1980
Qy 1981 GGAACCCACTGCGCCCTTCTGATATCTGCATCTGCAGACAGGAGGCATCGCGGTGTGTC 2040
Db 1981 GGAACCCACTGCGCCCTTCTGATATCTGCATCTGCAGACAGGAGGCATCGCGGTGTGTC 2040
Qy 2041 CTTCCCGGAGCAGACATCTCTTGAGCCACGCTGCATCTGTATGGGACTGTGTCAGTGGAG 2100
Db 2041 CTTCCCGGAGCAGACATCTCTTGAGCCACGCTGCATCTGTATGGGACTGTGTCAGTGGAG 2100
Qy 2101 CTATGATAAACAATGACAGCCACAGGCTCTCCATGCTTCCAAAGGTGTGCTTCTTTAA 2160
Db 2101 CTATGATAAACAATGACAGCCACAGGCTCTCCATGCTTCCAAAGGTGTGCTTCTTTAA 2160
Qy 2161 AGACTGATTAAGAAAGAAATATGAATGAAACATGCTCATGCACTCTTGAAGAGTGTTC 2220
Db 2161 AGACTGATTAAGAAAGAAATATGAATGAAACATGCTCATGCACTCTTGAAGAGTGTTC 2220
Qy 2221 TGATATCCGCTGTGTACGTGTCTATTGCGTGAAGCAGTGTGGCCCTGAAAGTGTGATTTG 2280
Db 2221 TGATATCCGCTGTGTACGTGTCTATTGCGTGAAGCAGTGTGGCCCTGAAAGTGTGATTTG 2280
Qy 2281 GCCTGTGAATCTGGCTGTGCCAGGCTTCTGACTTTCAGGGACAAACCTCAGTGAAGGCTG 2340
Db 2281 GCCTGTGAATCTGGCTGTGCCAGGCTTCTGACTTTCAGGGACAAACCTCAGTGAAGGCTG 2340
Qy 2341 AGTAGACCTCATTTGCTGGTAGGCTGATGCCGCTCCACTACTAGGACAGCAATTTGAA 2400
Db 2341 AGTAGACCTCATTTGCTGGTAGGCTGATGCCGCTCCACTACTAGGACAGCAATTTGAA 2400

Db 1201 AGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATATCCAGCTCCAGTA 1260
Qy 1261 TGAGTGCATCTCACCTTCTTACCGCCGCTGGGAGAGAGGAGGACATCTCTGAGGAC 1320
Db 1261 TGAGTGCATCTCACCTTCTTACCGCCGCTGGGAGAGAGGAGGACATCTCTGAGGAC 1320
Qy 1321 TGGGAAGTGGAGTGGGGGGGACCATCTGTCATCCCTATCTGCGGGAAAAATTGAGAACAT 1380
Db 1321 TGGGAAGTGGAGTGGGGGGGACCATCTGTCATCCCTATCTGCGGGAAAAATTGAGAACAT 1380
Qy 1381 CACTGCTCCAAAGACCCAAAGGTTGGCGTGGCGGCTGGCAGGAGGACCATCTACAGAGGAC 1440
Db 1381 CACTGCTCCAAAGACCCAAAGGTTGGCGTGGCGGCTGGCAGGAGGACCATCTACAGAGGAC 1440
Qy 1441 CAGCGGGGTGCATGACGGCAGCCTACACAAAGGAGCGTGGTCTCTAGTCTGCAGCGGTGC 1500
Db 1441 CAGCGGGGTGCATGACGGCAGCCTACACAAAGGAGCGTGGTCTCTAGTCTGCAGCGGTGC 1500
Qy 1501 CCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTTACTGACCTGGGGAAAGT 1560
Db 1561 CACTATGATCAAGACAGCAGCCTGAAAGTTGTTTGGGGAAATTTCTACCGGGATGATGA 1620
Qy 1561 CACTATGATCAAGACAGCAGCCTGAAAGTTGTTTGGGGAAATTTCTACCGGGATGATGA 1620
Db 1621 CCGGGATGAGAAAGACCTACAGAGCCTACAGATTTCTGCTATCATTTCTGCATCCCACTA 1680
Qy 1681 TGACCCCATCTGTTGATGCTGACATCGCCATCTGAAAGTCTCTAGCAAGGCCCGTAT 1740
Db 1681 TGACCCCATCTGTTGATGCTGACATCGCCATCTGAAAGTCTCTAGCAAGGCCCGTAT 1740
Qy 1741 CAGCACCGGAGTCAGGCCATCTGCTCGCTGGCAGTGGGATCTCAGCACTTCTTCCA 1800
Db 1741 CAGCACCGGAGTCAGGCCATCTGCTCGCTGGCAGTGGGATCTCAGCACTTCTTCCA 1800
Qy 1801 GGAGTCCACATCACTGTGGTGGCTGGAATGTCTGGCAGACGTGAGGAGCCCTGGCTT 1860
Db 1801 GGAGTCCACATCACTGTGGTGGCTGGAATGTCTGGCAGACGTGAGGAGCCCTGGCTT 1860
Qy 1861 CAAGAAGCACACACTGCGCTCTGGGGTGGTCAAGTGTGGTGGACCTCGCTGTGTGAGGA 1920
Db 1861 CAAGAAGCACACACTGCGCTCTGGGGTGGTCAAGTGTGGTGGACCTCGCTGTGTGAGGA 1920
Qy 1921 GCAGCATGAGACCATGGCATCCAGTGAGTGTCACTGATTAACATGTTCTGTGCCAGCTG 1980
Db 1921 GCAGCATGAGACCATGGCATCCAGTGAGTGTCACTGATTAACATGTTCTGTGCCAGCTG 1980
Qy 1981 GGAACCCACTGCCCTTCTGATATCTGCACATGACAGACAGGAGCATCGCGGTGTGTC 2040
Db 1981 GGAACCCACTGCCCTTCTGATATCTGCATCTGCAGACAGAGGAGCATCGCGGTGTGTC 2040
Qy 2041 CTTCCCGGGAGCAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGTGTGAGTGTGAG 2100
Db 2041 CTTCCCGGGAGCAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGTGTGAGTGTGAG 2100
Qy 2101 CTATGATAAACAATGACAGCAGCTTCCATGCTTCCATGCTTCCAAAGTGTGCTTTTAA 2160
Db 2101 CTATGATAAACAATGACAGCAGCTTCCATGCTTCCATGCTTCCAAAGTGTGCTTTTAA 2160
Qy 2161 AGACTGGATTGAAGAATATGAATGAACCATCTCATGCACTCTTGTGAAAGTGTTC 2220
Db 2161 AGACTGGATTGAAGAATATGAATGAACCATCTCATGCACTCTTGTGAAAGTGTTC 2220
Qy 2221 TGTATATCCGCTCTGATGCTGTGATTCATGCGTGAAGCAGTGTGGCCCTCAAGTGTGATTG 2280
Db 2221 TGTATATCCGCTCTGATGCTGTGATTCATGCGTGAAGCAGTGTGGCCCTCAAGTGTGATTG 2280
Qy 2281 GCCTGTGAATCTGCTGTGCCAGGGCTTCTGACTTTCAGGGGCAAAATCTCAGTGAAGGGTG 2340

Db 2381 GCCTGTGAATCTTGCTGTGCCAGGGCTTCTGACTTTCAGGGGCAAAATCTCAGTGAAGGGTG 2340
Qy 2341 AGTAGACCTCCATCTGCTGGTAGGCTGATGCCGCTCTCACTACTAGGAGCAGCAATTTGAA 2400
Db 2341 AGTAGACCTCCATCTGCTGGTAGGCTGATGCCGCTCTCACTACTAGGAGCAGCAATTTGAA 2400
Qy 2401 GATGCCAGGGCTTGCAGAAAGTAAAGTTTCTTCAAAGAGACCATATACAAACCTCTCCA 2460
Db 2401 GATGCCAGGGCTTGCAGAAAGTAAAGTTTCTTCAAAGAGACCATATACAAACCTCTCCA 2460
Qy 2461 CTCCACTGACTGCTGGTCTTCCCAACTTTTCAGTTATACGAATGCCATCAGCTTGACCA 2520
Db 2461 CTCCACTGACTGCTGGTCTTCCCAACTTTTCAGTTATACGAATGCCATCAGCTTGACCA 2520
Qy 2521 GGGAAAGATCTGGGCTTCATGAGGCCCTTTTGGAGCTCTCAAGTTCTAGAGAGTGCCTG 2580
Db 2521 GGGAAAGATCTGGGCTTCATGAGGCCCTTTTGGAGCTCTCAAGTTCTAGAGAGTGCCTG 2580
Qy 2581 TGGGACAGCCAGGGCAGCAGAGCTGGGATGTGTGTCATGCTTGTGTATCATGGCCACA 2640
Db 2581 TGGGACAGCCAGGGCAGCAGAGCTGGGATGTGTGTCATGCTTGTGTATCATGGCCACA 2640
Qy 2641 GTACAGTCTGGTCTTCTTCCCTCCCATCTCTTGTACACATTTTAAATAAATAAGGGTTG 2700
Db 2641 GTACAGTCTGGTCTTCTTCCCTCCCATCTCTTGTACACATTTTAAATAAATAAGGGTTG 2700
Qy 2701 GCTTCTGAATACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2760
Db 2701 GCTTCTGAATACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2760
Qy 2761 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 2820
Db 2761 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 2820
Qy 2821 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 2846
Db 2821 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 2846

RESULT 5
AY358346
LOCUS AY358346 2846 bp mRNA linear PRI 03-OCT-2003
DEFINITION Homo sapiens clone DNA58723 ELGc699 (UNQ699) mRNA, complete cds.
ACCESSION AY358346
VERSION AY358346.1 GI:37181816
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2846)
AUTHORS Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Haas, P.E.,
Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,
Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wleand, D., Woods, K.,
Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
Goddard, A., Wood, W.I. and Godowski, P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL PUBMED 12975309
REFERENCE 2 (bases 1 to 2846)
AUTHORS Clark, H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES Location/Qualifiers
source 1.2846
/organism="Homo sapiens"

```
/mol_type="mRNA"
/db_xref="taxon:9606"
/cid="DNA58723"
1..2846
/locus_tag="UNQ699"
26..2188
/locus_tag="UNQ699"
/notes="PRO1344"
/codon_start=1
/product="ELG699"
/protein_id="AAQ88712.1"
/db_xref="GI:37181817"
/translation="MELGCMQLGLTFLQLLISSLPREYTVINEACPGAEWIMICRE
CEEVDQTECVCPKREVGVYTPICRNEEEDSCLIHPGCTIPENCKSRNGSWGTF
LDPEYVGFYCAECRAGWYGDQMRQGVLRAPKGOILLBSYPLNACHCEITHAKPGF
VIQLRFWMLSEFDFYMCQYDYEVDRDGRDQQLIKVCGNERPAPQISGSSLHLVF
HSDGSKNPFDFHAIYEITACSSPFCFHDGTCVLDKAGSKYKACLAGYTGORECNLE
ERNCSDFGPNVNGIKITGGFLINGRHAQIGTVYFPCNNYSVLSENERKTCQOQNE
WSGKQPTICIKACREPKISDLVRRVLPMQVSRRETPLHLYSAFSAFKLQSAPTKPE
ALPFGDLPMLGVLHQLTOYECISPPYRLLSSRRCTCLRTGKWSGRAPSCIPICGKTE
NITAPKTQGLRWPQRAIYRBTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHVVD
LGKTMILKTADLKVLKSFYRDRDDEKTIQSLOISAIILHPNYDPIILLDAITAILKL
LDKARISTRVQPICLAASRDLSFQESHITVAGNVLADVRSPFGKNDITLRSGVSV
VDSLCEQHEHDGIPVSVTDNMFCAWSPEPTAPSDICTABTGGTAAVSFPGRASPEPR
WHLMLGVSWSYDKTCSHRLSTAFTKVLFPKDWIERNMK"
```

Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CGCTCGGSCACAGCCGCGCAAGATGGAGCTGGTGGTGGAGCGAGTGGGGCTCAC	60
Db	1	CGCTCGGSCACAGCCGCGCAAGATGGAGCTGGTGGTGGAGCGAGTGGGGCTCAC	60
Qy	61	TTTTCTTCAGCTCCTCTCATCTCGTCTGCCAAGAGAGTACACAGTCAATTAATGAAGC	120
Db	61	TTTTCTTCAGCTCCTCTCATCTCGTCTGCCAAGAGAGTACACAGTCAATTAATGAAGC	120
Qy	121	CTGCCCTGGAGCAGATGGATATCATGTGTGGGAGTGTGTAATATGATCAGATTGA	180
Db	121	CTGCCCTGGAGCAGATGGATATCATGTGTGGGAGTGTGTAATATGATCAGATTGA	180
Qy	181	GTGGCTGTGCCCCGGAAGAGGAACTCGTGGGTATACCATCCCTGTGCTGCAGGAATGA	240
Db	181	GTGGCTGTGCCCCGGAAGAGGAACTCGTGGGTATACCATCCCTGTGCTGCAGGAATGA	240
Qy	241	GGAGAAATGAGTGTGACTCTCGCTGATCCACCCAGGTTGTACCATCTTTGAAAACTGCAA	300
Db	241	GGAGAAATGAGTGTGACTCTCGCTGATCCACCCAGGTTGTACCATCTTTGAAAACTGCAA	300
Qy	301	GAGCTGCCGAATGGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTA	360
Db	301	GAGCTGCCGAATGGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTA	360
Qy	361	CTGTGCAGATGCGCAGCAGCTGTGTACGAGGAGACTGTGATGCGATGTGCCAGGTTCT	420
Db	361	CTGTGCAGATGCGCAGCAGCTGTGTACGAGGAGACTGTGATGCGATGTGCCAGGTTCT	420
Qy	421	GCGAGCCCCAAGGGTCAGATTTTGTGGAAAGCTATCCCCCTAAATGCTCATCTGGAATG	480
Db	421	GCGAGCCCCAAGGGTCAGATTTTGTGGAAAGCTATCCCCCTAAATGCTCATCTGGAATG	480
Qy	481	GACCATTCATGCTAAACCTGGGTTTGTATCCCACTAAGATTTCATGTTGAGTCTGGA	540
Db	481	GACCATTCATGCTAAACCTGGGTTTGTATCCCACTAAGATTTCATGTTGAGTCTGGA	540
Qy	541	GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTCTGATGGAGACACCCGATGG	600
Db	541	GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTCTGATGGAGACACCCGATGG	600
Qy	601	CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCGAGCTCCTATCCAGACATAGGATC	660
Db	601	CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCGAGCTCCTATCCAGACATAGGATC	660

ORIGIN

Db	601	CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCGAGCTCCTATCCAGACATAGGATC	660
Qy	661	CTCACTCCAGCTCTCTTCCACTCCGATGCTCAAGAAATTTTGCAGGTTTCCATGCCAT	720
Db	661	CTCACTCCAGCTCTCTTCCACTCCGATGCTCAAGAAATTTTGCAGGTTTCCATGCCAT	720
Qy	721	TTATGAGGAGATCACAGCATGCTCTCATCCCTTTGTTTCCATGACGGCAGTGCCTCT	780
Db	721	TTATGAGGAGATCACAGCATGCTCTCATCCCTTTGTTTCCATGACGGCAGTGCCTCT	780
Qy	781	TGACAAGGCTGGATCTTCAAGTGTGCTGCTGGAGGCTATATCTGGGAGCGCTGTGA	840
Db	781	TGACAAGGCTGGATCTTCAAGTGTGCTGCTGGAGGCTATATCTGGGAGCGCTGTGA	840
Qy	841	AAATCTCTTTGAAGAAAGAACTGCTCAGACCCCTGGGGGCCAGTCAATGGGTACCAAG	900
Db	841	AAATCTCTTTGAAGAAAGAACTGCTCAGACCCCTGGGGGCCAGTCAATGGGTACCAAG	900
Qy	901	AATAACAGGGGGCCCTGGGCTTATCAAACGAGCGCATGCTAAATTTGGCACCGTGTCT	960
Db	901	AATAACAGGGGGCCCTGGGCTTATCAAACGAGCGCATGCTAAATTTGGCACCGTGTCT	960
Qy	961	TTTCTTTTGTAAACAACTCTTATGTTCTTAGTGGCAATGAGAAAAGAACTTGGCCAGCA	1020
Db	961	TTTCTTTTGTAAACAACTCTTATGTTCTTAGTGGCAATGAGAAAAGAACTTGGCCAGCA	1020
Qy	1021	TGGAGAGTGTGAGGAAACAGCCCATCTGCATAAAAAGCTGCCGAGAACCAAGATTTTC	1080
Db	1021	TGGAGAGTGTGAGGAAACAGCCCATCTGCATAAAAAGCTGCCGAGAACCAAGATTTTC	1080
Qy	1081	AGACCTGCTGAGAGGAGAGTCTTCCGATGTCAGTTTTCAGTCAAGGGAGACACCATTACA	1140
Db	1081	AGACCTGCTGAGAGGAGAGTCTTCCGATGTCAGTTTTCAGTCAAGGGAGACACCATTACA	1140
Qy	1141	CCAGCTATCTCAGCGGCTTTCAGCAAGCAAGAACTGCAGAGTCCCCCTACCAAGAGCC	1200
Db	1141	CCAGCTATCTCAGCGGCTTTCAGCAAGCAAGAACTGCAGAGTCCCCCTACCAAGAGCC	1200
Qy	1201	AGCCCTTCCCTTTGGAGATCTGCCCATGGGATCAACATCTGCATACCAGCTCCAGTA	1260
Db	1201	AGCCCTTCCCTTTGGAGATCTGCCCATGGGATCAACATCTGCATACCAGCTCCAGTA	1260
Qy	1261	TGAGTGCATCTCACCTTCTACCGCCCTGGGAGCAGCAGGAGGAGCATGTCTGAGGAC	1320
Db	1261	TGAGTGCATCTCACCTTCTACCGCCCTGGGAGCAGCAGGAGGAGCATGTCTGAGGAC	1320
Qy	1321	TGGGAAGTGAAGTGGGCGGCGCACCATCTGATCCCTCTCTCGGGGAAAATTTGAGAACAT	1380
Db	1321	TGGGAAGTGAAGTGGGCGGCGCACCATCTGATCCCTCTCTCGGGGAAAATTTGAGAACAT	1380
Qy	1381	CACCTGCTCCAAAGACCCAAAGGTTGCGCTGGCCGTGGCAGCAGCAGCATCTACAGAGGAC	1440
Db	1381	CACCTGCTCCAAAGACCCAAAGGTTGCGCTGGCCGTGGCAGCAGCAGCATCTACAGAGGAC	1440
Qy	1441	CAGCGGGTGCATGACGGCAGCCTTACAAAGGAGCGTGGTTCCTAGTCTGACGGGTGC	1500
Db	1441	CAGCGGGTGCATGACGGCAGCCTTACAAAGGAGCGTGGTTCCTAGTCTGACGGGTGC	1500
Qy	1501	CTGTGTAATGAGCGCCTGTGTGGTGGTGGCCACTGTGTACTGTACTGCTGGGGAGGT	1560
Db	1501	CTGTGTAATGAGCGCCTGTGTGGTGGTGGCCACTGTGTACTGTACTGCTGGGGAGGT	1560
Qy	1561	CACCATGATCAAGACAGCAGACCTGAAAGTTGTTTTGGGGAATAATTTACCCGGGATGATGA	1620
Db	1561	CACCATGATCAAGACAGCAGACCTGAAAGTTGTTTTGGGGAATAATTTACCCGGGATGATGA	1620
Qy	1621	CCGGGATGAGAAACCATCCAGAGCCTACAGATTTCTGTATCATTTCTGCAATCCCACTA	1680
Db	1621	CCGGGATGAGAAACCATCCAGAGCCTACAGATTTCTGTATCATTTCTGCAATCCCACTA	1680
Qy	1681	TGACCCCATCTGCTTGTATGCTGACATCGGCATCTGAAAGCTCTTAGACAAAGGCCGTTAT	1740
Db	1681	TGACCCCATCTGCTTGTATGCTGACATCGGCATCTGAAAGCTCTTAGACAAAGGCCGTTAT	1740

```
Qy 1741 CAGCACCCGAGTCAGCCCATCTGCTCGTGCAGTCGGATCTCAGCATTCTCTTCCA 1800
Db 1741 CAGCACCCGAGTCAGCCCATCTGCTCGTGCAGTCGGATCTCAGCATTCTCTTCCA 1800

Qy 1801 GGAGTCCCATCATCTGTGCTGGCTGGATGTCCTGGCAGCTGAGGAGCCCTGGCTT 1860
Db 1801 GGAGTCCCATCATCTGTGCTGGCTGGATGTCCTGGCAGCTGAGGAGCCCTGGCTT 1860

Qy 1861 CAAGAAGCACACATCGGCTCTGGGGTGTTCAGTGTGGTGGACTCGCTGCTGTGTAGGA 1920
Db 1861 CAAGAAGCACACATCGGCTCTGGGGTGTTCAGTGTGGTGGACTCGCTGCTGTGTAGGA 1920

Qy 1921 GCAGCATGAGGACCATGGCATCCAGTGTGTCATGATTAACATGTTCTGTGCCAGCTG 1980
Db 1921 GCAGCATGAGGACCATGGCATCCAGTGTGTCATGATTAACATGTTCTGTGCCAGCTG 1980

Qy 1981 GGAACCCACTGCCCCCTTCTGATATCTGCATGCGAGCAGGAGGAGGATCGGGCTGTGC 2040
Db 1981 GGAACCCACTGCCCCCTTCTGATATCTGCATGCGAGCAGGAGGAGGATCGGGCTGTGC 2040

Qy 2041 CTTCCCGGAGCAGCATCTCTGAGCCACGCTGGCATCTCATGGACTGTGTGAGTGGAG 2100
Db 2041 CTTCCCGGAGCAGCATCTCTGAGCCACGCTGGCATCTCATGGACTGTGTGAGTGGAG 2100

Qy 2101 CTATGATTAACATGACAGGCTCTCCACTGCTTCAACCAAGTGTGCTGCTTTTAA 2160
Db 2101 CTATGATTAACATGACAGGCTCTCCACTGCTTCAACCAAGTGTGCTGCTTTTAA 2160

Qy 2161 AGACTGATTAAGAAATATGAATGAACATGCTCATGCTCATGCTTGTGAGAGTGTTC 2220
Db 2161 AGACTGATTAAGAAATATGAATGAACATGCTCATGCTCATGCTTGTGAGAGTGTTC 2220

Qy 2221 TGTATATCCGCTGTGCTGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 2280
Db 2221 TGTATATCCGCTGTGCTGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 2280

Qy 2281 GCCTGTGAATCTGGCTGTGCCAGGCTTCTGACTTTCAGGAGCAAACTCAGTGAAGGGTG 2340
Db 2281 GCCTGTGAATCTGGCTGTGCCAGGCTTCTGACTTTCAGGAGCAAACTCAGTGAAGGGTG 2340

Qy 2341 AGTAGACCTCATGCTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 2400
Db 2341 AGTAGACCTCATGCTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 2400

Qy 2401 GATGCCAGGCTTGCAAGAAGTAACTTCTTCAAGAGAACCATATACAAACCTCTCCA 2460
Db 2401 GATGCCAGGCTTGCAAGAAGTAACTTCTTCAAGAGAACCATATACAAACCTCTCCA 2460

Qy 2461 CTCCACTGACCTGGTGTCTTCCCAACTTTCAGTTATACGAATGCCATCAGCTTGACCA 2520
Db 2461 CTCCACTGACCTGGTGTCTTCCCAACTTTCAGTTATACGAATGCCATCAGCTTGACCA 2520

Qy 2521 GGAAGATCTGGGCTTCATGAGGCCCTTTTGGAGCTCTCAAGTTCTAGAGAGCTGCTG 2580
Db 2521 GGAAGATCTGGGCTTCATGAGGCCCTTTTGGAGCTCTCAAGTTCTAGAGAGCTGCTG 2580

Qy 2581 TGGGACAGCCAGGCGAGCAGCTGGATGTGGTGCATGCTTGTGTACATGGCCACA 2640
Db 2581 TGGGACAGCCAGGCGAGCAGCTGGATGTGGTGCATGCTTGTGTACATGGCCACA 2640

Qy 2641 GTACAGTCTGGTCTTCTTCTTCCCATCTCTGTACACATTTTAAATAAATAAGGGTTG 2700
Db 2641 GTACAGTCTGGTCTTCTTCTTCCCATCTCTGTGTACACATTTTAAATAAATAAGGGTTG 2700

Qy 2701 GCTTCTGAATACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2760
Db 2701 GCTTCTGAATACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2760

Qy 2761 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2820
Db 2761 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2820
```

```
Qy 2821 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2846
Db 2821 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2846

RESULT 6
HSM803699 2768 bp mRNA linear PRI 10-JUL-2002
LOCUS Homo sapiens mRNA; cDNA DKF2p667H2312 (from clone DKF2p667H2312).
DEFINITION AL832391
ACCESSION AL832391.1 GI:21732954
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2768)
AUTHORS Koehler K., Beyer A., Mewes H.W., Weil B. and Wiemann S.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) 1, D-85764 Neuberberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
This clone (DKF2p667H2312) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mlps.gsf.de/proj/cDNA/.
FEATURES
Location/Qualifiers
source 1..2768
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="RZPD:DKF2p667H2312"
/db_xref="taxon:9606"
/clone="DKF2p667H2312"
/tissue_type="lymph node"
/clone_lib="667 (synonym: hln02). Vector pSport1; host
DH10B; sites NotI + SalI"
/dev_stage="adult"
polyA_signal 2672..2677
polyA_site 2698
ORIGIN
Query Match 90.1%; Score 2564; DB 9; Length 2768;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2764; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 14 GCCGCGCGAAGATGGAGCTGGGTTGCTGGACGACGTTGGGGCTCACTTTTCTCAGCTC 73
Db 1 GCCGCGCGAAGATGGAGCTGGGTTGCTGGACGACGTTGGGGCTCACTTTTCTCAGCTC 60

Qy 74 CTTCTCATCTGTCCTTGTCCCAAGAGATACACAGTCAATTAATGAAGCTGCCCTGGAGCA 133
Db 61 CTTCTCATCTGTCCTTGTCCCAAGAGATACACAGTCAATTAATGAAGCTGCCCTGGAGCA 120

Qy 134 GAGTGAATATCATGTGTCGGGAGTCTGTGAATATGATCAGATTGAGTGGCTGCCCC 193
Db 121 GAGTGAATATCATGTGTCGGGAGTCTGTGAATATGATCAGATTGAGTGGCTGCCCC 180

Qy 194 GGAAGAGGGAAGTCTGTCGGGTTATACCATCCCTTGTGTCAGGAATGAGGAGATGAGTGT 253
Db 181 GGAAGAGGGAAGTCTGTCGGGTTATACCATCCCTTGTGTCAGGAATGAGGAGATGAGTGT 240

Qy 254 GACTCTGCTGTATCCACCAGCTGTGTACATCTTTGAAATCTGCAAGAGCTGCCGAAT 313
Db 241 GACTCTGCTGTATCCACCAGCTGTGTACATCTTTGAAATCTGCAAGAGCTGCCGAAT 300

Qy 314 GGCTCATGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCTACTGTGACAGTGC 373
Db 301 GGCTCATGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCTACTGTGACAGTGC 360
```


QY 374 CGACGAGCTGGTACGAGGAGAGACTGCATGCGATGTGGCCAGAGTCTGCGAGCCCCAAAG 433
DB 361 CGACGAGCTGGTACGAGGAGAGACTGCATGCGATGTGGCCAGAGTCTGCGAGCCCCAAAG 420
QY 434 GGTGAGATTTTGTGGAAAGCTATCCCTTAATCTCACTGTGAATGGACCATTCATGCT 493
DB 421 GGTGAGATTTTGTGGAAAGCTATCCCTTAATCTCACTGTGAATGGACCATTCATGCT 480
QY 494 AAACCTGGTGTGTCATCCAACTAAGATTTGTCATGTTGAGTCTGGAGTTTGATCATG 553
DB 481 AAACCTGGTGTGTCATCCAACTAAGATTTGTCATGTTGAGCCTGGAGTTTGATCATG 540
QY 554 TGCCAGTATGACTATGTTGAGTTCGTGATGGAGACAACCGCCGATGGCCAGATCATCAAG 613
DB 541 TGCCAGTATGACTATGTTGAGTTCGTGATGGAGACAACCGCCGATGGCCAGATCATCAAG 600
QY 614 CGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCCAGTC 673
DB 601 CGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCCAGTC 660
QY 674 CTCTTCCACTCCGATGGCTCCAGAAATTTGACGGTTCATGCTCCATTTATGAGGATC 733
DB 661 CTCTTCCACTCCGATGGCTCCAGAAATTTGACGGTTCATGCTCCATTTATGAGGATC 720
QY 734 ACAGCATGCTCCTCATCCCTTGTTCATGACGGCACGTCGCTCCTTGAACAAGCTGGA 793
DB 721 ACAGCATGCTCCTCATCCCTTGTTCATGACGGCACGTCGCTCCTTGAACAAGCTGGA 780
QY 794 TCTTAAAGTGTGCTCTGGCAGGCTATATCTGGCAGCGCTGTGAAATCTCCTTGAA 853
DB 781 TCTTAAAGTGTGCTCTGGCAGGCTATATCTGGCAGCGCTGTGAAATCTCCTTGAA 840
QY 854 GAAAGAACTGCTCAGACCTGGGGGCCAGTCAATGGGTACCAAGAAATAACAGGGGC 913
DB 841 GAAAGAACTGCTCAGACCTGGGGGCCAGTCAATGGGTACCAAGAAATAACAGGGGC 900
QY 914 CCTGGGCTTATCAACGAGCGCATGTCTAAATTTGGCACCGTGTCTCTTCTTTGTAAC 973
DB 901 CCTGGGCTTATCAACGAGCGCATGTCTAAATTTGGCACCGTGTCTCTTCTTTGTAAC 960
QY 974 AACTCTATGTTCTTAGTGGAATAGAGAAAGAACTTGGCCAGCAGAGATGGAGTGTCTCA 1033
DB 961 AACTCTATGTTCTTAGTGGAATAGAGAAAGAACTTGGCCAGCAGAGATGGAGTGTCTCA 1020
QY 1034 GGGAAACAGCCCATCTGCATAAAGCTGCGGAAACCAAGATTTTCAGACCTGGTGAGA 1093
DB 1021 GGGAAACAGCCCATCTGCATAAAGCTGCGGAAACCAAGATTTTCAGACCTGGTGAGA 1080
QY 1094 AGGAGAGTCTTCCGATGCGAGTTCAGTCAAGGGAGACACCATTTACACGACTATCTCA 1153
DB 1081 AGGAGAGTCTTCCGATGCGAGTTCAGTCAAGGGAGACACCATTTACACGACTATCTCA 1140
QY 1154 GCGGCCCTTACAGACGAGAACTGCGAGTGGCCCTTACCAAGAACCGAGCCCTTCCCTTT 1213
DB 1141 GCGGCCCTTACAGACGAGAACTGCGAGTGGCCCTTACCAAGAACCGAGCCCTTCCCTTT 1200
QY 1214 GGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGATGATCTCA 1273
DB 1201 GGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGATGATCTCA 1260
QY 1274 CCTTCTACCGCCCTGGGAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTGGAGT 1333
DB 1261 CCTTCTACCGCCCTGGGAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTGGAGT 1320
QY 1334 GGGCGGCAACATCCTGCATCCCTATCTGCGGGAATAATGAGAACATCATCTGCTCCAAAG 1393
DB 1321 GGGCGGCAACATCCTGCATCCCTATCTGCGGGAATAATGAGAACATCATCTGCTCCAAAG 1380
QY 1394 ACCCAAGGTTGCGCTGGCGTGGCAGCGCATCTACAGGAGCACGCGGGTGCAT 1453
DB 1381 ACCCAAGGTTGCGCTGGCGTGGCAGCGCATCTACAGGAGCACGCGGGTGCAT 1440
QY 1454 GACGGCAGCCTTACAAAGGAGCGTGGTTCCTAGTCTGCGAGCGTGGTGGTGAATGAG 1513

DB 1441 GACGGCAGCCTACACAAGGAGCGTGGTTCCTAGTCTGACGCGTGGTGGTGAATGAG 1500
QY 1514 CGACATGTGTGTGGTGGCTGCCACTGTGTACTGACCTGGGAGAGTTCACCATGATCAAG 1573
DB 1501 CGACATGTGTGTGGTGGCTGCCACTGTGTACTGACCTGGGGAAGTTCACCATGATCAAG 1560
QY 1574 ACAGCAGACCTGAAAGTGTGTTTGGGGAATTTCTACCGGATGATGACCGGGATGAGAAG 1633
DB 1561 ACAGCAGACCTGAAAGTGTGTTTGGGGAATTTCTACCGGATGATGACCGGGATGAGAAG 1620
QY 1634 ACCATCCAGAGCCTTACAGATTTCTGTATCATTTGCAATCCCAACTATGACCCCATCTG 1693
DB 1621 ACCATCCAGAGCCTTACAGATTTCTGTATCATTTCTGATCCCAACTATGACCCCATCTG 1680
QY 1694 CTTGATGCTGACATCGCCATCTGTGAAGCTCTAGACAAGGCCGTATACGACCCCGAGTC 1753
DB 1681 CTTGATGCTGACATCGCCATCTGTGAAGCTCTAGACAAGGCCGTATACGACCCCGAGTC 1740
QY 1754 CAGCCCATCTGCGCTGCGAGTCCGGAATCTCAGCACTTCTTCCAGGAGTCCCAATC 1813
DB 1741 CAGCCCATCTGCGCTGCGAGTCCGGAATCTCAGCACTTCTTCCAGGAGTCCCAATC 1800
QY 1814 ACTGTGCTGGCTGGAAATGCTTGGCAGACGCTGAGGAGCCCTGGCTTCAAGAACGACACA 1873
DB 1801 ACTGTGCTGGCTGGAAATGCTTGGCAGACGCTGAGGAGCCCTGGCTTCAAGAACGACACA 1860
QY 1874 CTGGGCTCTGGGTGGTCACTGTGGTGAATGCTGCTGCTGTGTGAGGAGCAGCATGAGAC 1933
DB 1861 CTGGGCTCTGGGTGGTCACTGTGGTGAATGCTGCTGCTGTGTGAGGAGCAGCATGAGAC 1920
QY 1934 CATGGCATCCAGTGTGCTCACTGATAACATGTTCTGTGCGCAGCTGGGAACCCACTGCCC 1993
DB 1921 CATGGCATCCAGTGTGCTCACTGATAACATGTTCTGTGCGCAGCTGGGAACCCACTGCCC 1980
QY 1994 CCTTCTGATATCTGCATGCGAGACAGGAGGCATCCGCTGTGTCTTCCCGGGACGA 2053
DB 1981 CCTTCTGATATCTGCATGCGAGACAGGAGGCATCCGCTGTGTCTTCCCGGGACGA 2040
QY 2054 GCATCTCTGAGCCACGCTGGCATCTGATGGGACTGCTGCTGAGCTGAGCTATGATAAACA 2113
DB 2041 GCATCTCTGAGCCACGCTGGCATCTGATGGGACTGCTGCTGAGCTGAGCTATGATAAACA 2100
QY 2114 TGACGACCAAGGCTCTCCACTGCTTCAACCAAGTGTGCTTTTAAAGACTGATTTGAA 2173
DB 2101 TGACGACCAAGGCTCTCCACTGCTTCAACCAAGTGTGCTTTTAAAGACTGATTTGAA 2160
QY 2174 AGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAAGTGTCTGTATATCCGTCT 2233
DB 2161 AGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAAGTGTCTGTATATCCGTCT 2220
QY 2234 GTAGCTGTGTCATTTGCGTGAAGCAGTGTGGCCCTGAAAGTGTGATTTGGCCTGTGAACCTG 2293
DB 2221 GTAGCTGTGTCATTTGCGTGAAGCAGTGTGGCCCTGAAAGTGTGATTTGGCCTGTGAACCTG 2280
QY 2294 GCTGTGCGCAGGCTTCTGACTTCAAGGACAAAACCTCAGTGAAGGCTGAGTAGACCTCCAT 2353
DB 2281 GCTGTGCGCAGGCTTCTGACTTCAAGGACAAAACCTCAGTGAAGGCTGAGTAGACCTCCAT 2340
QY 2354 TGCTGTGAGCTGATGCCGCTCCACTACTAGGACAGCCAAATTTGGAAGATGCCAGGGCTT 2413
DB 2341 TGCTGTGAGCTGATGCCGCTCCACTACTAGGACAGCCAAATTTGGAAGATGCCAGGGCTT 2400
QY 2414 GCAAGAAATGATTTCTTCAAGNAGACCATATACAAAACCTCTCCACTCCACTGACCTG 2473
DB 2401 GCAAGAAATGATTTCTTCAAGNAGACCATATACAAAACCTCTCCACTCCACTGACCTG 2460
QY 2474 GTGTCTTCCCAACTTTTCAAGTATACGAATGCCATCAGCTTGACAGGGAAGATCTGGG 2533
DB 2461 GTGTCTTCCCAACTTTTCAAGTATACGAATGCCATCAGCTTGACAGGGAAGATCTGGG 2520
QY 2534 CTTCAATGAGGCCCTTTTGGGCTCTCAAGTCTTAGAGAGCTGCTGTGGGACAGCCGAC 2593

Db 2521 CTTGATGAGGCCCTTTTGGGCTCTCAAGTTCTAGAGAGCTGCTGTGGGACAGCCGAG 2580
Qy 2594 GGCAGCAGAGCTGGAGTGGTGGATGCTTTGTGTATCATGCCACACAGTACAGTCTGGTC 2653
Db 2581 GGCAGCAGAGCTGGAGTGGTGGATGCTTTGTGTATCATGCCACACAGTACAGTCTGGTC 2640
Qy 2654 CTTTCTCTCCCATCTCTGTACACATTTTAAATAAATAGGGTTGGCTTCTGAACATC 2713
Db 2641 CTTTCTCTCCCATCTCTGTACACATTTTAAATAAATAGGGTTGGCTTCTGAACATC 2700
Qy 2714 AA 2773
Db 2701 AA 2760
Qy 2774 AAAAAAAAA 2781
Db 2761 AAAAAAAAA 2768

RESULT 7
AX084209
LOCUS AX084209 2306 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 3 from Patent WO0110902.
ACCESSION AX084209
VERSION AX084209.1 GI:13185712
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Shimkets, R.A. and Fernandes, E.
Nucleic acids and secreted polypeptides encoded thereby
Patent: WO 0110902-A 3 15-FEB-2001;
Curagen Corporation (US)
FEATURES
source
1..2306
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
128..2290
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC33410.1"
/translation="MELGCTQLGLTFLQLLLISSLPREVTVINEACPGAENIMCRE
CCEYDQIECVCPKREVVGVYTI PCRNENEEDCSLIHPGCTIFENCKSCRNCSWGCT
LDDFYVGFYCAECRAGWYGGDCMRQGVLRAPGQILLISYPLNAHCEWTHAKPGF
VIQRFVWLSLEFDYMCQDYVEVRDGDNRDQIIKRVCGNERPAPIQSIGSSLHLVLP
HSDGKRFDFGPHATYEBITACSSPCFHDGTCLVDKAGSYKACLAGYTGQRCENLLE
ERNCSDPGPVNGYKQITGGPGLNGRHAKIGTVVSPFCNNYSVLGNEKRTCOONGE
WSGKQPICIKACREPKISDLVRRRLVPMQVSRPTPLHOLYSAPFSKQKLSAPTKKP
ALPFGDLPMPQWHLHTQLOVEICISPFYRRLGSSRKTCLKTGKWSGRAPSCIPLGKLE
NITAPKQGLRWQAALYRTSGVHDSLHKGANFLVCSGALVNERIVVAAHCVTD
LGKVTIMTKLDKLVKFKYRDLDDDEKTIQSLQISAIILHPNYDPIILLDAILKL
LDKARISTRVQPICLAASRDLSTFQESHITVAGMNVLDVSPFGNDLIRSGVSV
VDSLCEQHDHGIPVSVTDNMFCAWSEPTAPSDICTAETGTGIIAAVSPFGRASPEPR
WHLMLVSWSYDKTCSHRLSTAFKVLFPFKDIERNK"

ORIGIN
Query Match 71.8%; Score 2043; DB 6; Length 2306;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2193; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 9 CACAGCGCGGCAAGGATGAGCTGGGTTCTGCGACCGCAGTTGGGCTGACTTTCTTC 68
Db 111 CACAGCGCGGCAAGGATGAGCTGGGTTCTGCGACCGCAGTTGGGCTGACTTTCTTC 170
Qy 69 AGCTCTCTCATCTCGCTTGGTCAAGAGAGTACACAGTCAATTAAGAGCCCTGCCCTG 128
Db 171 AGCTCTCTCATCTCGCTTGGTCAAGAGAGTACACAGTCAATTAAGAGCCCTGCCCTG 230
Qy 129 GAGCAGAGTGAATATCATGTGCGGAGTGTGTGAATATGATGAGTTCGCTCT 188

Db 231 GAGCAGAGTGAATATCATGTGTCGGAGTGTGTGAATATGATCAGATTGAGTGCCTCT 290
Qy 189 GCCCGCGAAGAGAGGAAGTGTGGTTTATACCATCTCTTGTGCGAGAAATGAGGAGATG 248
Db 291 GCCCGCGAAGAGAGGAAGTGTGGTTTATACCATCTCTTGTGCGAGAAATGAGGAGATG 350
Qy 249 AGTGTGATCTCTGCTGATCCACCCAGGTTGTACATCTTTGAAATCTGCAAGAGCTGCC 308
Db 351 AGTGTGATCTCTGCTGATCCACCCAGGTTGTACATCTTTGAAATCTGCAAGAGCTGCC 410
Qy 309 GAATGTGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCTACTGTGCGAG 368
Db 411 GAATGTGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCTACTGTGCGAG 470
Qy 369 AGTCCCGAGCAGGCTGGTACGGAGGAGACTGCGATGCGATGTGGCCAGGTTCTGGAGGCC 428
Db 471 AGTCCCGAGCAGGCTGGTACGGAGGAGACTGCGATGCGATGTGGCCAGGTTCTGGAGGCC 530
Qy 429 CAAAGGTCAGATTTTGTGGAAAGCTATCCCCCTAAATGCTCACTGTGAATGGACCATTC 488
Db 531 CAAAGGTCAGATTTTGTGGAAAGCTATCCCCCTAAATGCTCACTGTGAATGGACCATTC 590
Qy 489 ATGCTAAACCTGGGTTGTCTCACTCAACTAGATTTGTCTGAGTCTGAGTCTGAGTTGACT 548
Db 591 ATGCTAAACCTGGGTTGTCTCACTCAACTAGATTTGTCTGAGTCTGAGTCTGAGTTGACT 650
Qy 549 ACATGTGCCAGTATGACTATGTTGAGGTTCTGTGATGAGACAAACCGGATGGCCAGATCA 608
Db 651 ACATGTGCCAGTATGACTATGTTGAGGTTCTGTGATGAGACAAACCGGATGGCCAGATCA 710
Qy 609 TCAAGCTGTCTGTGGCAAGCAGCGGCGAGCTCTATCTCCAGAGCATAGGATCTCACTCC 668
Db 711 TCAAGCTGTCTGTGGCAAGCAGCGGCGAGCTCTATCTCCAGAGCATAGGATCTCACTCC 770
Qy 669 ACCTCTCTTCCACTCCGATGGCTCCAGAAATTTTGAAGTTTCCAGCTGCTCCATTTATGAGG 728
Db 771 ACCTCTCTTCCACTCCGATGGCTCCAGAAATTTTGAAGTTTCCAGCTGCTCCATTTATGAGG 830
Qy 729 AGATCACAGATGCTCCTCATCTCCCTTGTTCATGACGCGACGCTGGCTCTTGCACAGG 788
Db 831 AGATCACAGATGCTCCTCATCTCCCTTGTTCATGACGCGACGCTGGCTCTTGCACAGG 890
Qy 789 CTGGATCTTAAAGTGTGCTGTGGCAGGCTATCTGGGACGCTGTGAAATCTCC 848
Db 891 CTGGATCTTAAAGTGTGCTGTGGCAGGCTATCTGGGACGCTGTGAAATCTCC 950
Qy 849 TTGAAGAAAGAACTGCTCAGACCTGGGGGCCCGAGTCATGGGTACCAAGAAATACAG 908
Db 951 TTGAAGAAAGAACTGCTCAGACCTGGGGGCCCGAGTCATGGGTACCAAGAAATACAG 1010
Qy 909 GGGGCCCTGGGCTTATCAACGAGCGCATGCTAAAAATTGGCACCGTGTGTCTTTCTTTT 968
Db 1011 GGGGCCCTGGGCTTATCAACGAGCGCATGCTAAAAATTGGCACCGTGTGTCTTTCTTTT 1070
Qy 969 GTAAACAATCTCTATGTTCTTAGTGGCAATGAGAAAAAGAACTTGCACAGAAATGAGAGT 1028
Db 1071 GTAAACAATCTCTATGTTCTTAGTGGCAATGAGAAAAAGAACTTGCACAGAAATGAGAGT 1130
Qy 1029 GGTGAGGAAACAGCCCATCTGCATAAAGCCTCGCGAGACCAAGAAATTCAGACCTGG 1088
Db 1131 GGTGAGGAAACAGCCCATCTGCATAAAGCCTCGCGAGACCAAGAAATTCAGACCTGG 1190
Qy 1089 TGAGAGGAGAGTCTTTCCGATGAGGTTTCACTCAAGGAGACCACTTACACAGCTAT 1148
Db 1191 TGAGAGGAGAGTCTTTCCGATGAGGTTTCACTCAAGGAGACCACTTACACAGCTAT 1250
Qy 1149 ACTCAGCGGCTTTCAGCAAGCAGAAATCTGAGAGTGTCCCTTCAAGAGCCAGCCCTTC 1208
Db 1251 ACTCAGCGGCTTTCAGCAAGCAGAAATCTGAGAGTGTCCCTTCAAGAGCCAGCCCTTC 1310
Qy 1209 CTTTGGAGATCTGCCCATGGGATACCAACATCTGCTATACCAGCTCCAGTATGAGTGA 1268

Qy	489	ATGCTAAACCTGGGTTTGTCTATCAAACTAAGATTGTTCATGTTGAGTCTCGAGTTTCACT	548
Db	591	ATGCTAAACCTGGGTTTGTCTATCAAACTAAGATTGTTCATGTTGAGCCTCGAGTTTCACT	650
Qy	549	ACATGTCCAGTATGACTATGTTTCAGGTTCTGTGATGGAGACAACCGCGATGGCCAGATCA	608
Db	651	ACATGTCCAGTATGACTATGTTTCAGGTTCTGTGATGGAGACAACCGCGATGGCCAGATCA	710
Qy	609	TCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCC	668
Db	711	TCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCC	770
Qy	669	ACGTCTCTTCCACTCCGATGGCTCCAAAGAAATTTTGACGGTTTCCATGCGCATTTATGAGG	728
Db	771	ACGTCTCTTCCACTCCGATGGCTCCAAAGAAATTTTGACGGTTTCCATGCGCATTTATGAGG	830
Qy	729	AGATCAGAGCATGCTCTCACTCCCTTGTTCATGACGCGACGTGCGTCTCTTGACAAGG	788
Db	831	AGATCAGAGCATGCTCTCACTCCCTTGTTCATGACGCGACGTGCGTCTCTTGACAAGG	890
Qy	789	CTGGATCTTACAAGTGTGCCCTGTTCGACGGCTATATCTGGCGACGCTGTGAAAATCTCC	848
Db	891	CTGGATCTTACAAGTGTGCCCTGTTCGACGGCTATATCTGGCGACGCTGTGAAAATCTCC	950
Qy	849	TTGAAGAAAGAAACTGCTCAGACCTCTGGGGGCCAGTCAATGGGTACAGAAAATAACAG	908
Db	951	TTGAAGAAAGAAACTGCTCAGACCTCTGGGGGCCAGTCAATGGGTACAGAAAATAACAG	1010
Qy	909	GGGGCCCTGGGCTTATCAAGCGGCCATGCTAAAAATTTGGCACGGTGGTCTTCTTTT	968
Db	1011	GGGGCCCTGGGCTTATCAAGCGGCCATGCTAAAAATTTGGCACGGTGGTCTTCTTTT	1070
Qy	969	GTAACAACTCTATGTTCTTAGTGGCAATGAGAAAAGAACTTGCCACAGAAATGGAGGT	1028
Db	1071	GTAACAACTCTATGTTCTTAGTGGCAATGAGAAAAGAACTTGCCACAGAAATGGAGGT	1130
Qy	1029	GGTCAGGGAAACAGCCCATCTGCATAAAAGCTGCCGAGAACCAAGAAATTCAGACTGG	1088
Db	1131	GGTCAGGGAAACAGCCCATCTGCATAAAAGCTGCCGAGAACCAAGAAATTCAGACTGG	1190
Qy	1089	TGAGAAAGGAGTTCTTCGATGAGGTTTCAATCAAGGGAGACACCAATTCACACGCTAT	1148
Db	1191	TGAGAAAGGAGTTCTTCGATGAGGTTTCAATCAAGGGAGACACCAATTCACACGCTAT	1250
Qy	1149	ACTCAGCGGCTTCAGCAAGCAGAAACTGCAGAGTGCCTTACCAAGAACCGACCCCTTC	1208
Db	1251	ACTCAGCGGCTTCAGCAAGCAGAAACTGCAGAGTGCCTTACCAAGAACCGACCCCTTC	1310
Qy	1209	CTTTTGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCA	1268
Db	1311	CTTTTGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCA	1370
Qy	1269	TCTCACCTTCTACCGCGCTTGGGACGACGAGGAGACATGTTCTGAGAGCTGGGAAGT	1328
Db	1371	TCTCACCTTCTACCGCGCTTGGGACGACGAGGAGACATGTTCTGAGAGCTGGGAAGT	1430
Qy	1329	GGAGTGGCGGGACCACTCTGCATCCCTATCTGCGGGAAAATTTGAGAACATCACTGCTC	1388
Db	1431	GGAGTGGCGGGACCACTCTGCATCCCTATCTGCGGGAAAATTTGAGAACATCACTGCTC	1490
Qy	1389	CAAAAGCCCAAGGGTTGCGCTGGCGGTGGCAGGACGCATCTACAGGAGGACAGCGGGG	1448
Db	1491	CAAAAGCCCAAGGGTTGCGCTGGCGGTGGCAGGACGCATCTACAGGAGGACAGCGGGG	1550
Qy	1449	TGCATGACGGCAGCTTACAAAGGGAGGTTGGTTCTTAGTCTGACGCGGTGCCCTGTGTGA	1508
Db	1551	TGCATGACGGCAGCTTACAAAGGGAGGTTGGTTCTTAGTCTGACGCGGTGCCCTGTGTGA	1610
Qy	1509	ATGAGCCCACTGTGGTGGCTGCCCACTGTGTTACTGACCTTGGGGAAGGTCAACCATGA	1568
Db	1611	ATGAGCCCACTGTGGTGGCTGCCCACTGTGTTACTGACCTTGGGGAAGGTCAACCATGA	1670
Qy	1569	TCAAGACAGCAGACCTCAAAAGTTGTTTGTGGGAAAATTTCTACCGGGATGATGACCGGGATG	1628

Db	1671	TCAGACAGCAGACCTGGAAGTGTGTTTGGGGAATTCCTACCGGATGATGATCCGGGATG	1730
Qy	1629	AGAAGACCATCCAGAGCCTACAGATTCTTGCTATCATTTCTGCAATCCCAACTATGACCCCA	1688
Db	1731	AGAAGACCATCCAGAGCCTACAGATTCTGCTATCATTTCTGCAATCCCAACTATGACCCCA	1790
Qy	1689	TCCTGTTGATGTGATCATGCCATCCTGAGACTCTAGACAAGGCCGTATCAGACCC	1748
Db	1791	TCCTGTTGATGTGATCATGCCATCCTGAAGCTCTAGACAAGGCCGTATCAGACCC	1850
Qy	1749	GAGTCCAGGCCATCTGCTCGCTGCCAGTCCGGATCTCAGCACTTCTCTCCAGGAGTCCC	1808
Db	1851	GAGTCCAGGCCATCTGCCCTGCTGCCAGTCCGGATCTCAGCACTTCTCTCCAGGAGTCCC	1910
Qy	1809	ACATCATGTGGCTGGCTGGGAATGTCCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACG	1868
Db	1911	ACATCATGTGGCTGGCTGGGAATGTCCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACG	1970
Qy	1869	ACACACTGCGCTCTGGGTTGGTCAGTGTGTGAGTACTCGCTGCTGTGTGAGGAGCAGCATG	1928
Db	1971	ACACACTGCGCTCTGGGTTGGTCAGTGTGTGAGTACTCGCTGCTGTGTGAGGAGCAGCATG	2030
Qy	1929	AGGACCATGGCATCCCAAGTGAAGTGTCACTGATAAACATGTTCTGTGCAGCTGGGAACCCA	1988
Db	2031	AGGACCATGGCATCCCAAGTGAAGTGTCACTGATAAACATGTTCTGTGCAGCTGGGAACCCA	2090
Qy	1989	CTGCCCCCTCTGATATCTGCACATGCAGACAGAGGAGGCATCGGGCTGTGTCTCTCCCGG	2048
Db	2091	CTGCCCCCTCTGATATCTGCATGACAGACAGGAGGCATCGGGCTGTGTCTCTCCCGG	2150
Qy	2049	GACGAGCATCTCTGAGCCAACGCTGGCATCTGTATGGGACTGTGTCACTGGAGCTATGATA	2108
Db	2151	GACGAGCATCTCTGAGCCAACGCTGGCATCTGTATGGGACTGTGTCACTGGAGCTATGATA	2210
Qy	2109	AAACATGCGCCACAGCCTCTCCACATGCCCTTCAACCAAGGTGCTGCTTTTAAAGACTGGA	2168
Db	2211	AAACATGCGCCACAGCCTCTCCACATGCCCTTCAACCAAGGTGCTGCTTTTAAAGACTGGA	2270
Qy	2169	TTGAAAGAAATATGAAATGAACCATGCTCATGCACT	2204
Db	2271	TTGAAAGAAATATGAAATGAACCATGCTCATGCACT	2306

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 2350)
 Strausberg, R.
 Direct Submission
 Submitted (04-OCT-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakealey, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W.,
 Tourgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, B.D.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 78 Row: b Column: 7.
 Location/Qualifiers
 1..2350
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clones="IMAGE:4526572"
 /tissue type="Bladder, transitional cell papilloma"
 /clone_lib="NIH_MGC_93"
 /lab_host="DH10B"
 /note="vector: pCMV-SPORT6"

Query Match 67.0%; Score 1906; DB 9; Length 2350;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1956, Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 846 TCCTTGAAGAAAGAACTGCTCAGACCCCTGGGGCCAGTCAATGGGTACAGAAATAA 905
 Db 394 TCCTTGAAGAAAGAACTGCTCAGACCCCTGGGGCCAGTCAATGGGTACAGAAATAA 453

Qy 906 CAGGGGGCCCTGGGCTTATCAACGGAGCCATGCTAAATGGACACGTTGTCTTCT 965
 Db 454 CAGGGGGCCCTGGGCTTATCAACGGAGCCATGCTAAATGGACACGTTGTCTTCT 513

Qy 966 TTCTGTAACTCTCTATGTTCTTAGTGCAATGAGAAAGAACTTGGCAGCAATGGAG 1025
 Db 514 TTGTGTAACTCTCTATGTTCTTAGTGCAATGAGAAAGAACTTGGCAGCAATGGAG 573

Qy 1026 AGTGGTCAGGAAACAGCCCATCTGCATAAAGCTCCGAGAACCAAGATTTAGAC 1085
 Db 574 AGTGGTCAGGAAACAGCCCATCTGCATAAAGCTCCGAGAACCAAGATTTAGAC 633

Qy 1086 TGGTGAAGAGAGATTTCTCCGATGCAAGTTTCTAGTCAAGGAGACACCATTAAC 1145
 Db 634 TGGTGAAGAGAGATTTCTCCGATGCAAGTTTCTAGTCAAGGAGACACCATTAAC 693

Qy 1146 TATACTCAGCGGCTTCAGCAAGCAGAAACTGCAGAGTGGCCCTTACCAAGAGCCAGCC 1205

Db 694 TATACTCAGCGGCTTCAGCAAGCAGAAACTGCAGAGTGGCCCTTACCAAGAGCCAGCC 753

Qy 1206 TTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGTCCAGTATGAGT 1265

Db 754 TTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGTCCAGTATGAGT 813

Qy 1266 GCATCTCACCTCTTACCGCGCTGGGAGCAGCAGGAGACATGTCTGAGGACTGGGA 1325

Db 814 GCATCTCACCTCTTACCGCGCTGGGAGCAGCAGGAGACATGTCTGAGGACTGGGA 873

Qy 1326 AGTGGAGTGGCGGGCACCATCTCTGCATCCCTATCTCGGGGAAAATTTGAGAACATCACTG 1385

Db 874 AGTGGAGTGGCGGGCACCATCTCTGCATCCCTATCTCGGGGAAAATTTGAGAACATCACTG 933

Qy 1386 CTCCAAAGACCAAGGGTTGGCGCTGGCGGAGGAGCCATCTACAGGAGGACCGG 1445

Db 934 CTCCAAAGACCAAGGGTTGGCGCTGGCGGAGGAGCCATCTACAGGAGGACCGG 993

Qy 1446 GGGTGCATGACGGCAGCCTACAAAGGAGCGTGGTTCTTAGTCTGCAGCGGTGCCCTGG 1505

Db 994 GGGTGCATGACGGCAGCCTACAAAGGAGCGTGGTTCTTAGTCTGCAGCGGTGCCCTGG 1053

Qy 1506 TGAATGAGCGCACCTGTGTGGTGGCTGCCCACTGTGTACTGACCTCGGGGAAGTCAACA 1565

Db 1054 TGAATGAGCGCACCTGTGTGGTGGCTGCCCACTGTGTACTGACCTCGGGGAAGTCAACA 1113

Qy 1566 TGATCAAGACAGCAGACCTGAAAGTTGTTTTGGGAAAATTTCTACCGGATGATACCGGG 1625

Db 1114 TGATCAAGACAGCAGACCTGAAAGTTGTTTTGGGAAAATTTCTACCGGATGATACCGGG 1173

Qy 1626 ATGAGAAGACCAATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCATCCCACTATGACC 1685

Db 1174 ATGAGAAGACCAATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCATCCCACTATGACC 1233

Qy 1686 CCATCTCTGTGATGTGACATCGCCATCTCTGAAGCTCTTAGACAAGGCCCGTATCAGCA 1745

Db 1234 CCATCTCTGTGATGTGACATCGCCATCTCTGAAGCTCTTAGACAAGGCCCGTATCAGCA 1293

Qy 1746 CCGAGTCCAGCCCATCTGCTCGCTCGAGTGGGATCTCAGCAGCTTCCTTCAGAGT 1805

Db 1294 CCGAGTCCAGCCCATCTGCTCGCTCGAGTGGGATCTCAGCAGCTTCCTTCAGAGT 1353

Qy 1806 CCACATCACTGTGGCTGGTGAATGTCTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGA 1865

Db 1354 CCACATCACTGTGGCTGGTGAATGTCTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGA 1413

Qy 1866 ACACACACTGCGCTCTGGGGTGGTCAAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGC 1925

Db 1414 ACACACACTGCGCTCTGGGGTGGTCAAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGC 1473

Qy 1926 ATGAGGACCATGGCATCCCATGAGTGTCACTGATTAACATGTTCTGTGCCAGCTGGGAAC 1985

Db 1474 ATGAGGACCATGGCATCCCATGAGTGTCACTGATTAACATGTTCTGTGCCAGCTGGGAAC 1533

Qy 1986 CCATGCGCCCTCTGATATCTGCATCGCAGACAGGAGGATCGCGGCTGTGTCTTCC 2045

Db 1534 CCATGCGCCCTCTGATATCTGCATCGCAGACAGGAGGATCGCGGCTGTGTCTTCC 1593

Qy 2046 CCGGACGAGCATCTCTGAGCCACGCTGGCATCTGATGGGATCGGTGAGCTGGAGCTATG 2105

Db 1594 CCGGACGAGCATCTCTGAGCCACGCTGGCATCTGATGGGATCGGTGAGCTGGAGCTATG 1653

Qy 2106 ATAAACATGAGCCACAGGCTCTCCACTGCTCCACAGGCTGCTCCCTTTTAAAGACT 2165

Db 1654 ATAAACATGAGCCACAGGCTCTCCACTGCTCCACAGGCTGCTCCCTTTTAAAGACT 1713

Qy 2166 GGATTGAAAGAAATATCAAAATGAACATGTCTATGCACTCTCTCAGAAAGTGTCTTCTGAT 2225

Db 1714 GGATTGAAAGAAATATCAAAATGAACATGTCTATGCACTCTCTCAGAAAGTGTCTTCTGAT 1773

Qy 2226 ATCCGCTGTGACGTGTCTCAATGCGTGAAGCAGTGTGGGCTGAAGTGTGATTTGGGCTG 2285

Db	1774	ATCCGCTCTGTACGTGTGTGTCATTGCGTGTGAAGCAGTGTGGGCGCTGAAGTGTGTGATTTTGGCGCTG	1833
Qy	2286	TGAACCTTGGCTGTGTCAGCGGGCTTCTGACCTTCAGGGACAAAACCTCAGTGTCAAGGGGTGAGTAG	2345
Db	1834	TGAACCTTGGCTGTGTCAGCGGGCTTCTGACCTTCAGGGACAAAACCTCAGTGTCAAGGGGTGAGTAG	1893
Qy	2346	ACCTCCATTTGCTGTGTAGGCTGATGCGCGGTCCACTACTAGAGACAGCCOATTTGGAAGATGC	2405
Db	1894	ACCTCCATTTGCTGTGTAGGCTGATGCGCGGTCCACTACTAGAGACAGCCOATTTGGAAGATGC	1953
Qy	2406	CAGGSCCTTGCAGAAGTAAGTTTCTTCAAAGAAGCACCATATACAAAAACCTCTCCACCTCCA	2465
Db	1954	CAGGSCCTTGCAGAAGTAAGTTTCTTCAAAGAAGCACCATATACAAAAACCTCTCCACCTCCA	2013
Qy	2466	CTGACCTGGTGGTCTTCTCCCAACTTTTCAGTTATACGAATGCCATCAGCTGTGACACAGGAA	2525
Db	2014	CTGACCTGGTGGTCTTCTCCCAACTTTTCAGTTATACGAATGCCATCAGCTGTGACACAGGAA	2073
Qy	2526	GATCTGGGCTTCATGAGGCCCTTTTGAGGGCTCTCAAGTTCTAGAGAGTGCCTGTGGGA	2585
Db	2074	GATCTGGGCTTCATGAGGCCCTTTTGAGGGCTCTCAAGTTCTAGAGAGTGCCTGTGGGA	2133
Qy	2586	CAGCCACAGGCAGCAGAGCTGGGATGTGTCATGCCCTTTGTGTACATGCCACAGTACA	2645
Db	2134	CAGCCACAGGCAGCAGAGCTGGGATGTGTCATGCCCTTTGTGTACATGCCACAGTACA	2193
Qy	2646	GTCGTGGTCTTTTCTTCTTCCCATCTCTGTGACACATTTTAATAAAATAAGGTTGGCTTC	2705
Db	2194	GTCGTGGTCTTTTCTTCTTCCCATCTCTGTGACACATTTTAATAAAATAAGGTTGGCTTC	2253
Qy	2706	TGAACCTCAA	2765
Db	2254	TGAACCTCAA	2313
Qy	2766	AA 2802	
Db	2314	AA 2350	
RESULT 10			
LOCUS	AR339478	2144 bp	DNA linear PAT 17-AUG-2003
DEFINITION	Sequence 969 from patent US 659662.		
ACCESSION	AR339478		
VERSION	AR339478.1 GI:33726335		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2144)		
AUTHORS	Tang, Y. T., Zhou, P. and Drmanac, R. T.		
TITLE	Nucleic acids and polypeptides		
JOURNAL	Patent: US 659662-A 969 27-MAY-2003;		
FEATURES	location/Qualifiers		
source	1..2144		
	/organism="unknown"		
	/mol_type="genomic DNA"		
ORIGIN			
Query Match	66.1%;	Score 1880;	DB 6; Length 2144;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 1880;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	846	TCCTTTGAAGAAAGAAACTGCTCAGACCTCGGGGCCAGTCAGTGGGTACAGAAAAATAA	905
Db	265	TCCTTTGAAGAAAGAAACTGCTCAGACCTCGGGGCCAGTCAGTGGGTACAGAAAAATAA	324
Qy	906	CAGGGGGCCCTGGGCTTATCAACGAGCGCCATGTCTAAATTTGGCACCGTGTCTTCT	965
Db	325	CAGGGGGCCCTGGGCTTATCAACGAGCGCCATGTCTAAATTTGGCACCGTGTCTTCT	384
Qy	966	TTTGTAAACACTCCTATGTTCTTAGTGGCAATGAGAAAGAACTTTCGACAGAAATCGAG	1025

Db	385	TTTGTAAACAATCCTATATGTTTCTTAGTGGCAATGAGAAAAGAACTTCCACGACGAGATGGAG	444
Qy	1026	AGTGGTCAGGGAAACAGCCCATCTGCATATAAGCCCTGCCGAGAACCAAGAATTTACAGACC	1085
Db	445	AGTGGTCAGGGAAACAGCCCATCTGCATATAAGCCCTGCCGAGAACCAAGAATTTACAGACC	504
Qy	1086	TGTTGAGAAAGAGATTTCTTCCGATGAGGTTCAAGTCAAGGGAGACACCATTTACACCAGC	1145
Db	505	TGTTGAGAAAGAGATTTCTTCCGATGAGGTTCAAGTCAAGGGAGACACCATTTACACCAGC	564
Qy	1146	TATACTCAGCGGCTTTCAGCAACGAGAACTGCAGAGTGCCTCTACCAAGAACCCAGCCC	1205
Db	565	TATACTCAGCGGCTTTCAGCAACGAGAACTGCAGAGTGCCTCTACCAAGAACCCAGCCC	624
Qy	1206	TTCCCTTTGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGT	1265
Db	625	TTCCCTTTGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGT	684
Qy	1266	GCATCTCACCCCTTCTACCGCGGCTGGGACGACGAGGAGACATCTGTAGGACCTGGGA	1325
Db	685	GCATCTCACCCCTTCTACCGCGGCTGGGACGACGAGGAGACATCTGTAGGACCTGGGA	744
Qy	1326	AGTGGAGTGGCGGGACCAATCTCTGCATCCCTATCTGCGGGAAAATTGAGAACATCACATG	1385
Db	745	AGTGGAGTGGCGGGACCAATCTCTGCATCCCTATCTGCGGGAAAATTGAGAACATCACATG	804
Qy	1386	CTCCAAAGACCCCAAGGGTTGCGCTGGCGGTGGCAGGCAGCCATCTACAGGAGACACAGCG	1445
Db	805	CTCCAAAGACCCCAAGGGTTGCGCTGGCGGTGGCAGGCAGCCATCTACAGGAGACACAGCG	864
Qy	1446	GGTGTGANTAGCGGAGCTTACACAAGGGAGCGTGGTTCTTAGTCTGACGGGTGCCCTGG	1505
Db	865	GGTGTGANTAGCGGAGCTTACACAAGGGAGCGTGGTTCTTAGTCTGACGGGTGCCCTGG	924
Qy	1506	TGAATGAGCGCATGTGTGGTGGTCCCATCTGTACTGACCTGGGGAGGTCACCA	1565
Db	925	TGAATGAGCGCATGTGTGGTGGTCCCATCTGTACTGACCTGGGGAGGTCACCA	984
Qy	1566	TGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAAATTCTACCGGGATGATGACCGGG	1625
Db	985	TGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAAATTCTACCGGGATGATGACCGGG	1044
Qy	1626	ATGAGAAGACCATCCAGAGCTTACAGATTTCTGCTATCATTTCTGATATCCAACTATGACC	1685
Db	1045	ATGAGAAGACCATCCAGAGCTTACAGATTTCTGCTATCATTTCTGATATCCAACTATGACC	1104
Qy	1686	CCATCTGCTTGATGTGACATCGCCATCTGTAAGCTCCTAGACAAGGCCCGTATCAGCA	1745
Db	1105	CCATCTGCTTGATGTGACATCGCCATCTGTAAGCTCCTAGACAAGGCCCGTATCAGCA	1164
Qy	1746	CCGAGTCCAGCCCATCTGCCTCGCTCCAGTCCGGATCTCAGCACTTCTTCCAGGAGT	1805
Db	1165	CCGAGTCCAGCCCATCTGCCTCGCTCCAGTCCGGATCTCAGCACTTCTTCCAGGAGT	1224
Qy	1806	CCACATCATGTGTGGCTGGAATGTCTTGCGACACGTGAGGAGCCCTGGCTTCAAAGA	1865
Db	1225	CCACATCATGTGTGGCTGGAATGTCTTGCGACACGTGAGGAGCCCTGGCTTCAAAGA	1284
Qy	1866	ACGACACATCGCCTCTGGGGTGGTCAGTGTGGTGGACCTCGCTGCTGTGTGAGGAGCAGC	1925
Db	1285	ACGACACATCGCCTCTGGGGTGGTCAGTGTGGTGGACCTCGCTGCTGTGTGAGGAGCAGC	1344
Qy	1926	ATGAGGACCATGGCATCCAGTGAGTGTCACTGATAACTGTTCTGTGCGAGCTGGGAAC	1985
Db	1345	ATGAGGACCATGGCATCCAGTGAGTGTCACTGATAACTGTTCTGTGCGAGCTGGGAAC	1404
Qy	1986	CCAATGCCCTTCTGATATCTGCATCTGCAGACAGGAGGCATTCGCGGCTGTGTCTTCC	2045
Db	1405	CCAATGCCCTTCTGATATCTGCATCTGCAGACAGGAGGCATTCGCGGCTGTGTCTTCC	1464
Qy	2046	CGGACGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCACTGGAGCTATG	2105
Db	1465	CGGACGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCACTGGAGCTATG	1524

```
QY 2106 ATAAACATGAGCCAGAGCTCTCCACTGCTTCAACAAAGGTGCTGCCCTTTAAAGACT 2165
DB 1525 ATAAACATGAGCCAGAGCTCTCCACTGCTTCAACAAAGGTGCTGCCCTTTAAAGACT 1584
QY 2166 GGATTGAAAGAAATATGAAATGAACACCATGCTATGCACTCTCTTGAGAAAGTGTTCCTAT 2225
DB 1585 GGATTGAAAGAAATATGAAATGAACACCATGCTATGCACTCTCTTGAGAAAGTGTTCCTAT 1644
QY 2226 ATCCGTCTGACGTGTGTCATTGGGTGAAGCAGTGTGGGCTGAAGTGTGATTTGGGCTG 2285
DB 1645 ATCCGTCTGACGTGTGTCATTGGGTGAAGCAGTGTGGGCTGAAGTGTGATTTGGGCTG 1704
QY 2286 TGAACCTTGGCTGTGCCAGGCTCTCTGACTTCAGGGAACAAACTCAGTGAAGGGTGAAGTAG 2345
DB 1705 TGAACCTTGGCTGTGCCAGGCTCTCTGACTTCAGGGAACAAACTCAGTGAAGGGTGAAGTAG 1764
QY 2346 ACCTCCATTGCTGGTAGGCTGATGCCGCTCCACTACTAGSACAGCCAAATTTGGAAGATGC 2405
DB 1765 ACCTCCATTGCTGGTAGGCTGATGCCGCTCCACTACTAGSACAGCCAAATTTGGAAGATGC 1824
QY 2406 CAGGGCTTGAAGAAAGTAAGTTCTTCAAGAGACCATATACAAACCTCTCCACTCCA 2465
DB 1825 CAGGGCTTGAAGAAAGTAAGTTCTTCAAGAGACCATATACAAACCTCTCCACTCCA 1884
QY 2466 CTGACCTGGTGGTCTTCCCAACTTTTCAGTTTATACGAATGCCATCAGCTTGACCAAGGAA 2525
DB 1885 CTGACCTGGTGGTCTTCCCAACTTTTCAGTTTATACGAATGCCATCAGCTTGACCAAGGAA 1944
QY 2526 GATCTGGGCTTCATGAGGCCCTTTTGGAGCTCTCAAGTTCTAGAGAGCTGCCCTGGGA 2585
DB 1945 GATCTGGGCTTCATGAGGCCCTTTTGGAGCTCTCAAGTTCTAGAGAGCTGCCCTGGGA 2004
QY 2586 CAGCCAGGGCAGCAGAGCTGGGATGGTGATGCTTGTGTACATGGCCACAGTACA 2645
DB 2005 CAGCCAGGGCAGCAGAGCTGGGATGGTGATGCTTGTGTACATGGCCACAGTACA 2064
QY 2646 GTCTGGTCTCTTCTTCCCATCTCTGTACACATTTTAAATAAAGGGTGGCTTC 2705
DB 2065 GTCTGGTCTCTTCTTCCCATCTCTGTACACATTTTAAATAAAGGGTGGCTTC 2124
QY 2706 TGAACACTAAAAAATAA 2725
DB 2125 TGAACACTAAAAAATAA 2144

RESULT 11
AR339515
LOCUS AR339515 2142 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1006 from patent US 6569662.
ACCESSION AR339515
VERSION AR339515.1 GI:33726372
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2142)
AUTHORS Tang,Y.T., Zhou,P. and Drmanac,R.T.
TITLE Nucleic acids and polypeptides
JOURNAL Patent: US 6569662-A 1006 27-MAY-2003;
FEATURES
source 1..2142
/mol_type="genomic DNA"

ORIGIN
Query Match 64.2%; Score 1827; DB 6; Length 2142;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1877; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 846 TCCTTGAAGAAAGAACTGCTCAGACCCCTGGGGCCCAAGTCAATGGGTACAGAAAAATAA 905
DB 265 TCCTTGAAGAAAGAACTGCTCAGACCCCTGGGGCCCAAGTCAATGGGTACAGAAAAATAA 324
```

```
QY 906 CAGGGGCCCTGGGCTTTATCAACGAGCGCCATGCTAAAAATTGGCACCGTGTGCTTTCT 965
DB 325 CAGGGGCCCTGGGCTTTATCAACGAGCGCCATGCTAAAAATTGGCACCGTGTGCTTTCT 384
QY 966 TTTGTAAACAATCTCTATGTTCTTAGTGGCAATGAGAAAAAACTTTGCCAGCAGAAATGGAG 1025
DB 385 TTTGTAAACAATCTCTATGTTCTTAGTGGCAATGAGAAAAAACTTTGCCAGCAGAAATGGAG 444
QY 1026 AGTGGTTCAGGGAACAGCCCATCTGCATAAAGCCTGCCGAGACCAAGATTTTCAGACC 1085
DB 445 AGTGGTTCAGGGAACAGCCCATCTGCATAAAGCCTGCCGAGAACCAAGATTTTCAGACC 504
QY 1086 TGGTGAAGAGAGAGTTCCTCCGATGCAAGTTCAGTCAAGGAGACACCAATTACACAGC 1145
DB 505 TGGTGAAGAGAGAGTTCCTCCGATGCAAGTTCAGTCAAGGAGACACCAATTACACAGC 564
QY 1146 TATATCTCAGCGGCTTCAGCAAGCAGAAACTGCAAGAGTGCCCTTACCAAGAACGACGCC 1205
DB 565 TATATCTCAGCGGCTTCAGCAAGCAGAAACTGCAAGAGTGCCCTTACCAAGAACGACGCC 624
QY 1206 TTCCCTTTGAGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAT 1265
DB 625 TTCCCTTTGAGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAT 684
QY 1266 GCATCTCACCTTCTACCGCGCTGGGAGCAGCAGGAGACATGCTGAGGACTGGGA 1325
DB 685 GCATCTCACCTTCTACCGCGCTGGGAGCAGCAGGAGACATGCTGAGGACTGGGA 744
QY 1326 AGTGGAGTGGCGGGCACCATCTGCATCTCTATCTGCGGGAAATTTGAGAACATCACTG 1385
DB 745 AGTGGAGTGGCGGGCACCATCTGCATCTCTATCTGCGGGAAATTTGAGAACATCACTG 804
QY 1386 CTCCAAAGACCCAGGGTTGGCTGGCGGTGGCAGGAGCCATCTACAGGAGGACGACG 1445
DB 805 CTCCAAAGACCCAGGGTTGGCTGGCGGTGGCAGGAGCCATCTACAGGAGGACGACG 864
QY 1446 GGGTGCATGACGGCAGCCTACAAAGGAGCGTGGTCTTAGTCTGCAGCGGTGCCCTGG 1505
DB 865 GGGTGCATGACGGCAGCCTACAAAGGAGCGTGGTCTTAGTCTGCAGCGGTGCCCTGG 924
QY 1506 TGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTTACTGACCTGGGGAAGTCAACA 1565
DB 925 TGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTTACTGACCTGGGGAAGTCAACA 984
QY 1566 TGATCAAGACAGCAGACCTGAAAGTGTGTTTGGGAAATTTCTACCGGAGTATGACCGGG 1625
DB 985 TGATCAAGACAGCAGACCTGAAAGTGTGTTTGGGAAATTTCTACCGGAGTATGACCGGG 1044
QY 1626 ATGAGAAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCATCCCAACTATGACC 1685
DB 1045 ATGAGAAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCATCCCAACTATGACC 1104
QY 1686 CCATCTCTGTGATGTGACATCGCCATCTCTGAAGCTCTTAGACAAGGCCCGTATCAGCA 1745
DB 1105 CCATCTCTGTGATGTGACATCGCCATCTCTGAAGCTCTTAGACAAGGCCCGTATCAGCA 1164
QY 1746 CCGAGTTCAGCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1805
DB 1165 CCGAGTTCAGCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1224
QY 1806 CCCACATCACTGTGGCTGGCTGGAATGCTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGA 1865
DB 1225 CCCACATCACTGTGGCTGGCTGGAATGCTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGA 1284
QY 1866 ACACACACTGCGCTCTGGGGTGGTCAAGTGTGGTGGACTCGCTGCTGTGTGAGAGCAGC 1925
DB 1285 ACACACACTGCGCTCTGGGGTGGTCAAGTGTGGTGGACTCGCTGCTGTGTGAGAGCAGC 1344
QY 1926 ATGAGGACCATGGCATCCCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1985
DB 1345 ATGAGGACCATGGCATCCCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1404
```


Db 1098 AGTGGTCAGGGAACAGCCCATCTGCATATAAAGCCTGCCAGAACCAAGATTTCAGACC 1157
QY 1086 TGGTGAGAGAGAGAGTTCTTCCGATGACAGGTTTCAGTCAAGGGAGACACCAATTACACAGC 1145
Db 1158 TGGTGAGAGAGAGAGTTCTTCCGATGACAGGTTTCAGTCAAGGGAGACACCAATTACACAGC 1217
QY 1146 TATATCTCAGCGGCTTCAGCAAGCAGAAATGTCAGAGTGGCCCTTACCAAGAAGCCAGCC 1205
Db 1218 TATATCTCAGCGGCTTCAGCAAGCAGAAATGTCAGAGTGGCCCTTACCAAGAAGCCAGCC 1277
QY 1206 TTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCAATCCAGCTCCAGTATGAGT 1265
Db 1278 TTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCAATCCAGCTCCAGTATGAGT 1337
QY 1266 GCATCTCACCTTCTACCGCGCTGGCGAGCAGCAGAGGAGACATGTCGAGGACTGGGA 1325
Db 1338 GCATCTCACCTTCTACCGCGCTGGCGAGCAGCAGAGGAGACATGTCGAGGACTGGGA 1397
QY 1326 AGTGGAGTGGGCGGCAACCATCTGCAATCCCTATCTCGGGGAAAATTGAGAACATCACTG 1385
Db 1398 AGTGGAGTGGGCGGCAACCATCTGCAATCCCTATCTCGGGGAAAATTGAGAACATCACTG 1457
QY 1386 CTCCAAAGACCCAAAGGTTGGCTGGCCGTGGCGAGGAGCCATCTACAGAGGAGCAGCG 1445
Db 1458 CTCCAAAGACCCAAAGGTTGGCTGGCCGTGGCGAGGAGCCATCTACAGAGGAGCAGCG 1517
QY 1446 GGGTGCAATGCGGAGCCTACACAAGGAGGCGTGGTTCCTAGTCTGACGCGGTGCCCTGG 1505
Db 1518 GGGTGCAATGCGGAGCCTACACAAGGAGGCGTGGTTCCTAGTCTGACGCGGTGCCCTGG 1577
QY 1506 TGAATGAGCGCACTGTGTGTGTGTGCTGCCCATCTGTGTTACTGACCTGGGGAAGTCAACA 1565
Db 1578 TGAATGAGCGCACTGTGTGTGTGTGCTGCCCATCTGTGTTACTGACCTGGGGAAGTCAACA 1637
QY 1566 TGATCAAGACAGCAGACTGAAAGTTGTTTGGGAAAATTCTACCGGAGTATGACCGGG 1625
Db 1638 TGATCAAGACAGCAGACTGAAAGTTGTTTGGGAAAATTCTACCGGAGTATGACCGGG 1697
QY 1626 ATGAGAGACCATCCAGAGCTACAGATTCTGCTATCATCTGCAATCTGCAATCCCACTATGACC 1685
Db 1698 ATGAGAGACCATCCAGAGCTACAGATTCTGCTATCATCTGCAATCTGCAATCCCACTATGACC 1757
QY 1686 CCATCTCTGTGATGCTGACATCGCCATCTCTGAAAGCTCTTAGACAAGGCCCGTATCAGCA 1745
Db 1758 CCATCTCTGTGATGCTGACATCGCCATCTCTGAAAGCTCTTAGACAAGGCCCGTATCAGCA 1817
QY 1746 CCCGAGTCCAGCCCATCTGCTCGCTCGCTGCGAGTGGGATCTCAGCACTTCTCTCAGAGT 1805
Db 1818 CCCGAGTCCAGCCCATCTGCTCGCTCGCTGCGAGTGGGATCTCAGCACTTCTCTCAGAGT 1877
QY 1806 CCCACATCACTGTGGCTGGCTGGGAATGTCCTGGCAGACGTCGAGGAGCCCTGGCTTCAAGA 1865
Db 1878 CCCACATCACTGTGGCTGGCTGGGAATGTCCTGGCAGACGTCGAGGAGCCCTGGCTTCAAGA 1937
QY 1866 ACAGACACTGCTGCTGGGTGGTTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGC 1925
Db 1938 ACAGACACTGCTGCTGGGTGGTTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGC 1997
QY 1926 ATGAGGCCATGGCATCCCACTGAGTGTCACTGATAAATGTTCTGTGCCAGCTGGGAAC 1985
Db 1998 ATGAGGCCATGGCATCCCACTGAGTGTCACTGATAAATGTTCTGTGCCAGCTGGGAAC 2057
QY 1986 CCATGCGCCCTTCTGATATCTGCACTGCGAGACAGGAGGATCGCGGCTGTGCTCTCC 2045
Db 2058 CCATGCGCCCTTCTGATATCTGCACTGCGAGACAGGAGGATCGCGGCTGTGCTCTCC 2117
QY 2046 CGGACGAGCATCTCTCTGAGCCAGCTGGCATCTGATGGGACTGCTGAGCTGGAGCTATG 2105
Db 2118 CGGACGAGCATCTCTCTGAGCCACGCTGGCATCTGATGGGACTGCTGAGCTGGAGCTATG 2177
QY 2106 ATAAAAATGAGCAGCAGAGCTCTCCACTGCGCTTCAACCAAGGCTGCTGCTTTAAAGACT 2165
Db 2178 ATAAAAATGAGCAGCAGAGCTCTCCACTGCGCTTCAACCAAGGCTGCTGCTTTAAAGACT 2237

QY 2166 GGATTGAAGAAATATCAATGAACCATGCTCATGCACTCCTTGAGAAGTGTTCCTAT 2225
Db 2238 GGATTGAAGAAATATCAATGAACCATGCTCATGCACTCCTTGAGAAGTGTTCCTAT 2297
QY 2226 ATCCGCTGTACGCTGTGTCATTCGCTGAAGCAGTGTGGGCTGAAGTGTGATTTGGCCTG 2285
Db 2298 ATCCGCTGTACGCTGTGTCATTCGCTGAAGCAGTGTGGGCTGAAGTGTGATTTGGCCTG 2357
QY 2286 TGAACCTTGGCTGTGCCAGGCTTCTGACTTCAGGGACAAAACTCAGTGAAGGGTGAAGTAG 2345
Db 2358 TGAACCTTGGCTGTGCCAGGCTTCTGACTTCAGGGACAAAACTCAGTGAAGGGTGAAGTAG 2417
QY 2346 ACCTCCATTTGCTGTGTAGCTGATGCCGCTCCACTACTAGGACAGCCAAATTGGAAGATGC 2405
Db 2418 ACCTCCATTTGCTGTGTAGCTGATGCCGCTCCACTACTAGGACAGCCAAATTGGAAGATGC 2477
QY 2406 CAGGGCTTGAAGAGTAAGTTCCTTCAAGAGAGACCATATACAAACCTCTCCACTCCA 2465
Db 2478 CAGGGCTTGAAGAGTAAGTTCCTTCAAGAGAGACCATATACAAACCTCTCCACTCCA 2537
QY 2466 CTGACCTGTGGTGTCTTCCCAACTTTTCAGTTATACGAATGCCATCAGC-TGACCCAGGGAA 2525
Db 2538 CTGACCTGTGGTGTCTTCCCAACTTTTCAGTTATACGAATGCCATCAGC-TGACCCAGGGAA 2596
QY 2526 GATCTGGGCTTCATGAGGCCCCCTTTTGAGGCTCTCAAGTTCTTAGAGAGTGCCTGTGGGA 2585
Db 2597 GATCTGGGCTTCATGAGGCCCCCTTTTGAGGCTCTCAAGTTCTTAGAGAGTGCCTGTGGGA 2656
QY 2586 CAGCCAGGCGCAGCAGAGCTGGGATGTGGTGCATGCCCTTTGTGTACATGSCCAGATACA 2645
Db 2657 CAGCCAGGCGCAGCAGAGCTGGGATGTGGTGCATGCCCTTTGTGTACATGSCCAGATACA 2716
QY 2646 GTCTGGTCTCTTCCCTTCCCATCTCTGTGTACATTTTAAATAAAGGTTGGCTTC 2705
Db 2717 GTCTGGTCTCTTCCCTTCCCATCTCTGTGTACATTTTAAATAAAGGTTGGCTTC 2776
QY 2706 TGAACCTAC 2713
Db 2777 TGAACCTAC 2784

RESULT 15

BD012234
LOCUS A novel gene encoding a serine protease-like protein.
DEFINITION A novel gene encoding a serine protease-like protein.
ACCESSION BD012234
VERSION BD012234.1 GI:22092423
KEYWORDS WO 0109349-A/1.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 2784)
Ota, T., Isegaki, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K., Otsuki, T., Yano, K.,
Murakami, K., Kanzaki, K., Inoue, Y., Hashimoto, B. and Kashima, A.
A novel gene encoding a serine protease-like protein
Patent: WO 0109349-A 1 08-FEB-2001;
HELIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA,
KOJI HAYASHI, KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, OMOYASU
SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI, KAZUHIRO YANO,
OJI MURAKAMI, KOJI KANZAKI, YOSHITAKA INOUE, EMI HASHIMOTO, AKIKO
KASHIMA

COMMENT

OS Homo sapiens (human)
PN WO 0109349-A/1
PD 08-FEB-2001
PF 28-JUL-2000 WO 2000JP005062
PR 29-JUL-1999 JP 99P 248036, 27-AUG-1999 JP 99P 300253 PR
11-JAN-2000 JP 00P 118776, 02-MAY-2000 JP 00P 183767 PR
18-OCT-1999 US 60/159590, 17-FEB-2000 US 60/183322 PI TOSHIO
OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, PI KAORU SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,

Db 2777 TGRACTAC 2784

Search completed: May 8, 2005, 15:25:31
Job time : 8150 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2005, 11:26:52 ; Search time 8099 Seconds
(without alignments)
17027.231 Million cell updates/sec

Title: US-10-063-692-37

Perfect score: 2846

Sequence: 1 cgcctgggcaccagccggc.....aaaaaaaaaaaaaaaaaaaaa 2846

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Maximum Match 100%

Listing first 1500 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hcg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_to.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2846	100.0	2846	6	AR252533 Sequence
2	2846	100.0	2846	6	AX092306 Sequence
3	2846	100.0	2846	6	AX376102 Sequence
4	2846	100.0	2846	6	AX403343 Sequence
5	2846	100.0	2846	9	AY358346 Homo sapi
6	2761.6	97.0	2768	9	AL832391 Homo sapi
7	2636.8	92.6	2784	6	BD157134 Primer fo
8	2636.8	92.6	2784	6	AX878296 Sequence
9	2636.8	92.6	2784	6	BD012234 A novel g
10	2636.8	92.6	2784	9	AK027841 Homo sapi
11	2292.4	80.5	2832	6	AX704692 Sequence
12	2259.4	79.4	2886	6	AR263926 Sequence
13	2223.8	78.1	2350	9	BC038457 Homo sapi
14	2197.6	77.2	2306	6	AX084209 Sequence
15	2197.6	77.2	2306	6	AX133839 Sequence
16	2142.2	75.3	2259	6	AR541687 Sequence
17	2095.8	73.6	2289	6	BD012236 A novel g
18	1988.4	69.9	2144	6	AR339478 Sequence
19	1984.8	69.7	2142	6	AR339515 Sequence

20	1831.4	64.3	2841	10	BC031841	BC031841	Mus muscu
21	1831.4	64.3	2841	10	BC057685	BC057685	Mus muscu
22	1722	60.5	1867	6	AX084207	AX084207	Sequence
23	1692.6	59.5	2244	6	BD012235	A novel g	
24	1667.4	58.6	1669	6	C0723377	Sequence	
25	1084.8	38.1	1088	9	HSMB00511	AL050214	Homo sapi
26	1070.4	37.6	141818	2	AL133389	AL133389	Homo sapi
27	1068.8	37.6	208659	2	AC067845	AC067845	Homo sapi
28	1059.4	37.2	142522	9	AC090625	AC090625	Homo sapi
29	1058.4	37.2	5735	5	BC075430	BC075430	Xenopus t
30	648	22.8	705	6	BD150061	Primer fo	
31	648	22.8	705	6	AX869999	Sequence	
32	546.4	19.2	217777	2	AC113891	AC113891	Rattus no
33	546.4	19.2	222330	2	AC096255	AC096255	Rattus no
34	546.4	19.2	246369	2	AC125707	AC125707	Rattus no
35	523.6	18.4	188958	10	AL844605	AL844605	Mouse DNA
36	479.4	16.8	505	6	AR264001	AR264001	Sequence
37	421	14.8	421	6	C0723379	C0723379	Sequence
38	417.8	14.7	73880	2	AC090728	AC090728	Homo sapi
39	408.2	14.3	532	6	BD155023	BD155023	Primer fo
40	408.2	14.3	532	6	AX874961	AX874961	Sequence
41	337	11.8	337	6	AX331347	AX331347	Sequence
42	337	11.8	337	6	AX331781	AX331781	Sequence
43	332	11.7	340	6	BD076812	BD076812	S' EST of
44	293.4	10.3	106657	9	AL354921	AL354921	Human DNA
45	279.4	9.8	297	6	C0667350	C0667350	Sequence
46	261.4	9.2	657	5	CR387267	CR387267	Gallus ga
47	213.6	7.5	369	6	AX395272	AX395272	Sequence
48	181	6.4	208659	2	AC067845	AC067845	Homo sapi
49	165	5.8	561	11	G91095	G91095	S210P6215RE
50	152	5.3	615	10	BC043668	BC043668	Mus muscu
51	149.8	5.3	1084	9	BC026265	BC026265	Homo sapi
52	148.8	5.2	1727	5	BC071446	BC071446	Danio rer
53	148.2	5.2	920	10	BC027780	BC027780	Mus muscu
54	147.8	5.2	4574	9	HSB803437	AL832130	Homo sapi
55	147.6	5.2	4619	9	HSB806714	AL832130	Homo sapi
56	146.8	5.2	5338	9	HSB808825	AX648674	Homo sapi
57	146.6	5.2	1132	10	BC060558	BC060558	Rattus no
58	146	5.1	1200	5	BC077122	BC077122	Danio rer
59	146	5.1	3723	9	HSB808835	AX648684	Homo sapi
60	145.8	5.1	446	3	AF146743	AF146743	Mesobuthu
61	145.8	5.1	1935	5	BC065678	BC065678	Danio rer
62	145.6	5.1	2005	9	HSB803426	AL832119	Homo sapi
63	145	5.1	1793	3	AK112657	AK112657	Ciona int
64	144.8	5.1	935	10	BC049693	BC049693	Mus muscu
65	144.8	5.1	2688	10	BC021912	BC021912	Mus muscu
66	144.6	5.1	1100	10	BC061092	BC061092	Mus muscu
67	144.6	5.1	3482	9	HSB800550	AL050393	Homo sapi
68	144.4	5.1	2674	10	BC083550	BC083550	Rattus no
69	144	5.1	381	6	CQ526814	CQ526814	Sequence
70	144	5.1	883	10	BC049726	BC049726	Mus muscu
71	144	5.1	1990	10	BC042668	BC042668	Mus muscu
72	144	5.1	4413	10	BC053035	BC053035	Mus muscu
73	143.8	5.1	375	6	CQ513063	CQ513063	Sequence
74	143.8	5.1	818	9	BC026261	BC026261	Homo sapi
75	143.8	5.1	1999	9	BC020684	BC020684	Homo sapi
76	143.8	5.1	2245	9	BC037547	BC037547	Homo sapi
77	143.8	5.1	2441	3	AK174351	AK174351	Ciona int
78	143.8	5.1	5517	9	HSB807238	AX647094	Homo sapi
79	143.6	5.0	1137	10	BC062232	BC062232	Rattus no
80	143.6	5.0	1388	9	BC016332	BC016332	Homo sapi
81	143.6	5.0	1424	5	BC063367	BC063367	Xenopus t
82	143.6	5.0	3796	5	BC066783	BC066783	Xenopus t
83	143.4	5.0	733	9	BC009801	BC009801	Homo sapi
84	143.4	5.0	1620	10	BC046622	BC046622	Mus muscu
85	143.4	5.0	3687	9	BC040431	BC040431	Homo sapi
86	143.2	5.0	1835	9	BC040063	BC040063	Homo sapi
87	143.2	5.0	2722	9	HSB806004	AX537897	Homo sapi
88	143.2	5.0	2804	9	HSB807489	AX647345	Homo sapi
89	143	5.0	701	5	BC075162	BC075162	Xenopus l
90	143	5.0	3623	10	BC034092	BC034092	Mus muscu
91	142.8	5.0	819	9	HSB807474	BD647330	Homo sapi
92	142.8	5.0	887	6	BD260630	BD260630	49 human

BC031841	Mus muscu
BC057685	Mus muscu
AX084207	Sequence
BD012235	A novel g
C0723377	Sequence
AL050214	Homo sapi
AL133389	Homo sapi
AL067845	Homo sapi
AC090625	Homo sapi
BC075430	Xenopus t
BD150061	Primer fo
AX869999	Sequence
AC113891	Rattus no
AC096255	Rattus no
AC125707	Rattus no
AL844605	Mouse DNA
AR264001	Sequence
C0723379	Sequence
AC090728	Homo sapi
BD155023	Primer fo
AX874961	Sequence
AX331347	Sequence
AX331781	Sequence
BD076812	5' EST of
AL354921	Human DNA
C0667350	Sequence
CR387267	Gallus ga
AX395272	Sequence
AC067845	Homo sapi
G91095	S210P6215RE
BC043668	Mus muscu
BC026265	Homo sapi
BC071446	Danio rer
BC027780	Mus muscu
AL832130	Homo sapi
AX40658	Homo sapi
AX48674	Homo sapi
BC060558	Rattus no
BC077122	Danio rer
AX48684	Homo sapi
AF146743	Mesobuthu
BC065678	Danio rer
AL832119	Homo sapi
AK112657	Ciona int
BC049693	Mus muscu
BC021912	Mus muscu
BC061092	Homo sapi
AL050393	Homo sapi
C0526814	Sequence
BC049726	Mus muscu
BC042668	Mus muscu
BC053035	Mus muscu
C0513063	Sequence
BC026261	Homo sapi
BC020684	Homo sapi
BC037547	Homo sapi
AX174351	Ciona int
AX47094	Homo sapi
BC062232	Rattus no
BC016332	Homo sapi
BC063367	Xenopus t
BC066783	Xenopus t
BC009801	Homo sapi
BC046622	Mus muscu
BC040431	Homo sapi
BC040063	Homo sapi
AX37897	Homo sapi
AX647345	Homo sapi
BC075162	Xenopus l
BC034092	Mus muscu
AX647330	Homo sapi
BD260630	49 human

93	142.8	5.0	3380	9	HSM807223	BX647079 Homo sapi	166	141	5.0	4154	9	HSM803629	AL832322 Homo sapi
94	142.6	5.0	1175	5	BC049447	BC049447 Danilo ter	167	141	5.0	4562	9	HSM805779	BX537704 Homo sapi
95	142.6	5.0	1409	9	BC049776	BC049776 Mus muscu	c 168	141	5.0	22338	2	AC087150	AC087150 Mus muscu
96	142.6	5.0	2922	6	CQ491282	CQ491282 Sequence	169	140.8	4.9	502	6	CQ525917	CQ525917 Sequence
97	142.6	5.0	3014	9	HSM803702	AL832394 Homo sapi	170	140.8	4.9	676	10	BC049769	BC049769 Mus muscu
98	142.4	5.0	1057	3	AY588476	AY588476 Ciona int	171	140.8	4.9	897	10	BC049625	BC049625 Mus muscu
99	142.4	5.0	1912	10	BC027060	BC027060 Mus muscu	172	140.8	4.9	1694	9	BC012597	BC012597 Homo sapi
100	142.4	5.0	1959	10	BC060504	BC060504 Mus muscu	173	140.8	4.9	1696	6	AR256293	AR256293 Sequence
101	142.4	5.0	2167	10	BC028325	BC028325 Mus muscu	174	140.8	4.9	2319	9	HSM805518	AL834428 Homo sapi
102	142.4	5.0	3229	9	HSM805883	BX537499 Homo sapi	175	140.8	4.9	7609	9	HSM807874	BX547728 Homo sapi
103	142.4	5.0	3870	9	HSM806049	BX537527 Homo sapi	c 176	140.8	4.9	8079	6	AX356488	AX356488 Sequence
104	142.2	5.0	544	6	CQ524776	CQ524776 Sequence	177	140.6	4.9	601	5	BC082926	BC082926 Xenopus l
105	142.2	5.0	2173	9	HSM806315	BX538120 Homo sapi	178	140.6	4.9	837	9	S78214	S78214 APC-tumor s
106	142.2	5.0	2975	9	HSM804650	AL833337 Homo sapi	179	140.6	4.9	1018	9	BC022044	BC022044 Homo sapi
107	142	5.0	705	10	BC059084	BC059084 Mus muscu	180	140.6	4.9	1472	9	BC017724	BC017724 Homo sapi
108	142	5.0	854	5	BC084189	BC084189 Xenopus t	181	140.6	4.9	1500	5	XLNAXATP	Y11587 X.laevis mR
109	142	5.0	900	10	BC035323	BC035323 Mus muscu	182	140.6	4.9	1562	5	BC054239	BC054239 Xenopus l
110	142	5.0	979	10	BC049752	BC049752 Mus muscu	183	140.6	4.9	1860	9	BC058897	BC058897 Homo sapi
111	142	5.0	1080	9	BC022354	BC022354 Homo sapi	184	140.6	4.9	2201	5	BC068355	BC068355 Danilo ter
112	142	5.0	1201	9	BC050586	BC050586 Homo sapi	185	140.6	4.9	2439	9	HSM807466	BX647322 Homo sapi
113	142	5.0	1696	5	BC067590	BC067590 Danilo ter	186	140.6	4.9	2549	10	BC061563	BC061563 Rattus no
114	142	5.0	2533	9	BC048340	BC048340 Homo sapi	187	140.6	4.9	2612	10	BC053749	BC053749 Mus muscu
115	142	5.0	2930	9	BC032304	BC032304 Homo sapi	188	140.6	4.9	2684	9	HSM805935	BX537504 Homo sapi
116	142	5.0	3269	5	BC073066	BC073066 Xenopus l	189	140.6	4.9	2688	9	BC021087	BC021087 Homo sapi
117	142	5.0	3660	10	BC051069	BC051069 Mus muscu	190	140.6	4.9	2809	9	HSM802470	AL157431 Homo sapi
118	142	5.0	12178	10	AP466694	AP466694 Rattus no	191	140.6	4.9	3226	9	AV189289	AV189289 Homo sapi
119	141.8	5.0	1333	10	BC010296	BC010296 Mus muscu	c 192	140.6	4.9	15954	6	AX344491	AX344491 Sequence
120	141.6	5.0	691	5	BC071138	BC071138 Xenopus l	c 193	140.6	4.9	15954	6	AX348900	AX348900 Sequence
121	141.6	5.0	805	10	BC063183	BC063183 Rattus no	194	140.4	4.9	1175	10	BC049596	BC049596 Mus muscu
122	141.6	5.0	1100	9	BC063599	BC063599 Homo sapi	195	140.4	4.9	1265	10	BC061243	BC061243 Mus muscu
123	141.6	5.0	1159	9	BC043507	BC043507 Homo sapi	196	140.4	4.9	1319	9	BC034528	BC034528 Homo sapi
124	141.6	5.0	1343	10	BC061103	BC061103 Mus muscu	197	140.4	4.9	1377	5	BC063336	BC063336 Xenopus t
125	141.6	5.0	2039	9	HSM806781	BX640711 Homo sapi	198	140.4	4.9	1405	9	BC044934	BC044934 Homo sapi
126	141.6	5.0	2214	9	HSM807772	BX647626 Homo sapi	199	140.4	4.9	2350	5	BC078091	BC078091 Xenopus l
127	141.6	5.0	2237	10	BC059191	BC059191 Mus muscu	200	140.4	4.9	2390	9	AF090900	AF090900 Homo sapi
128	141.6	5.0	3392	5	BC068927	BC068927 Xenopus l	201	140.4	4.9	2869	9	HSM804689	AL833376 Homo sapi
129	141.6	5.0	8392	6	AX346392	AX346392 Sequence	202	140.4	4.9	3159	10	BC030921	BC030921 Mus muscu
130	141.6	5.0	11416	6	AX251758	AX251758 Sequence	203	140.4	4.9	4362	9	HSM805498	AL834414 Homo sapi
131	141.6	5.0	11416	6	AX345020	AX345020 Sequence	204	140.4	4.9	4385	9	HSM806219	BX538049 Homo sapi
132	141.6	5.0	1416	6	AX348567	AX348567 Sequence	205	140.4	4.9	4494	10	BC063058	BC063058 Mus muscu
133	141.6	5.0	16033	6	AX346306	AX346306 Sequence	206	140.4	4.9	4828	9	HSM808886	BX648735 Homo sapi
134	141.4	5.0	1081	10	BC0649719	BC049719 Mus muscu	207	140.4	4.9	6644	6	E23356	E23356 Virus vecto
135	141.4	5.0	1409	5	BC064261	BC064261 Xenopus t	208	140.4	4.9	7372	6	E23357	E23357 Virus vecto
136	141.4	5.0	1883	10	BC022165	BC022165 Mus muscu	209	140.4	4.9	7797	6	E23355	E23355 Virus vecto
137	141.4	5.0	1946	5	BC077411	BC077411 Xenopus l	210	140.4	4.9	7996	6	E23359	E23359 Virus vecto
138	141.4	5.0	2194	10	BC031202	BC031202 Mus muscu	c 211	140.4	4.9	9747	9	HSM806689	BX640841 Homo sapi
139	141.4	5.0	2250	5	BC061708	BC061708 Danilo ter	c 212	140.4	4.9	11729	6	AX345797	AX345797 Sequence
140	141.4	5.0	2562	9	HSM808661	BX648513 Homo sapi	213	140.2	4.9	260	6	CQ695445	CQ695445 Sequence
141	141.4	5.0	2878	9	HSM805674	BX537379 Homo sapi	214	140.2	4.9	397	3	AF135818	AF135818 Mesobuthu
142	141.2	5.0	480	9	BC055410	BC055410 Homo sapi	215	140.2	4.9	812	10	BC061144	BC061144 Mus muscu
143	141.2	5.0	532	10	BC049701	BC049701 Mus muscu	216	140.2	4.9	848	5	BC062495	BC062495 Xenopus t
144	141.2	5.0	824	9	BC070291	BC070291 Homo sapi	217	140.2	4.9	860	9	BC039722	BC039722 Homo sapi
145	141.2	5.0	1038	10	BC013496	BC013496 Mus muscu	218	140.2	4.9	942	9	BC043511	BC043511 Homo sapi
146	141.2	5.0	1090	10	BC049543	BC049543 Mus muscu	219	140.2	4.9	1054	10	BC049758	BC049758 Mus muscu
147	141.2	5.0	1332	10	BC060992	BC060992 Mus muscu	220	140.2	4.9	1763	10	BC061098	BC061098 Mus muscu
148	141.2	5.0	1448	10	BC052344	BC052344 Mus muscu	221	140.2	4.9	1960	10	BC061459	BC061459 Mus muscu
149	141.2	5.0	1626	9	BC050587	BC050587 Homo sapi	222	140.2	4.9	1993	9	HSM803801	AL832493 Homo sapi
150	141.2	5.0	1806	9	BC025776	BC025776 Homo sapi	223	140.2	4.9	2054	10	BC039272	BC039272 Mus muscu
151	141.2	5.0	1986	10	BC050807	BC050807 Mus muscu	224	140.2	4.9	2202	10	BC052362	BC052362 Mus muscu
152	141.2	5.0	2284	9	AB055303	AB055303 Macaca fa	225	140.2	4.9	2316	10	BC064469	BC064469 Mus muscu
153	141.2	5.0	2593	9	HSM807470	BX647326 Homo sapi	226	140	4.9	240	6	I48979	I48979 Sequence 6
154	141.2	5.0	2724	9	HSM806666	BX641033 Homo sapi	227	140	4.9	749	9	BC008417	BC008417 Homo sapi
155	141.2	5.0	3245	9	HSM805849	BX374933 Homo sapi	228	140	4.9	760	6	CQ497632	CQ497632 Sequence
156	141.2	5.0	4725	9	BC040525	BC040525 Homo sapi	229	140	4.9	760	9	BC040885	BC040885 Homo sapi
157	141.2	5.0	6775	6	AX458643	AX458643 Sequence	230	140	4.9	889	10	BC049685	BC049685 Mus muscu
158	141.2	5.0	8900	6	CQ806977	CQ806977 Sequence	231	140	4.9	1093	9	BC043577	BC043577 Homo sapi
159	141.2	5.0	8900	6	CQ807251	CQ807251 Sequence	232	140	4.9	1119	9	BC070137	BC070137 Homo sapi
160	141	5.0	705	9	HSM800237	AL049452 Homo sapi	233	140	4.9	1139	9	HSM807844	BX647698 Homo sapi
161	141	5.0	1568	10	BC048399	BC048399 Mus muscu	234	140	4.9	1273	10	BC049640	BC049640 Mus muscu
162	141	5.0	2172	9	AB096991	AB096991 Macaca fa	235	140	4.9	1549	9	HSM808772	BX648621 Homo sapi
163	141	5.0	2627	9	BC027919	BC027919 Homo sapi	236	140	4.9	1603	6	CQ490224	CQ490224 Sequence
164	141	5.0	2972	9	BC023549	BC023549 Homo sapi	237	140	4.9	1603	6	CQ491236	CQ491236 Sequence
165	141	5.0	3454	9	HSM802993	AL713659 Homo sapi	238	140	4.9	1603	6	CQ496086	CQ496086 Sequence

239	140	4.9	1503	6	CQ497104	Sequence	CQ497104	Sequence	312	139.2	4.9	1271	9	AF090934	Homo sapi
240	140	4.9	1727	10	BC050800	Mus muscu	BC050800	Mus muscu	313	139.2	4.9	1403	9	BC043542	Homo sapi
241	140	4.9	1793	9	BC071757	Homo sapi	BC071757	Homo sapi	314	139.2	4.9	1786	9	AB070107	Macaca fa
242	140	4.9	3305	10	BC040407	Mus muscu	BC040407	Mus muscu	315	139.2	4.9	1827	9	AB070106	Macaca fa
243	140	4.9	3332	10	BC053922	Mus muscu	BC053922	Mus muscu	316	139.2	4.9	1891	9	BSM807589	Homo sapi
244	140	4.9	3558	9	BSM803467	Homo sapi	AL832160	Homo sapi	317	139.2	4.9	1944	9	BC028346	Homo sapi
245	140	4.9	3573	6	AX345073	Sequence	AX345073	Sequence	318	139.2	4.9	2604	8	BT009473	Triticum
c	246	140	4.9	4389	10	BC058345	Mus muscu	BC058345	319	139.2	4.9	2986	9	BSM807768	Homo sapi
c	247	140	4.9	5439	9	BSM805827	Sequence	AX537489	320	139.2	4.9	4237	6	BD057918	Secreted
c	248	140	4.9	40224	6	AX458633	Sequence	AX458633	321	139.2	4.9	21354	6	AX251544	Sequence
c	249	139.8	4.9	525	9	BC034020	Homo sapi	BC034020	322	139	4.9	439	6	C0525664	Sequence
c	250	139.8	4.9	738	9	BSM806309	Homo sapi	BSM806309	323	139	4.9	758	9	BC062750	Homo sapi
c	251	139.8	4.9	757	9	BC051791	Homo sapi	BC051791	324	139	4.9	819	10	BC064002	Mus muscu
c	252	139.8	4.9	881	10	BC049733	Mus muscu	BC049733	325	139	4.9	911	10	BC061108	Mus muscu
c	253	139.8	4.9	973	9	BC043578	Homo sapi	BC043578	326	139	4.9	1181	10	BC049768	Mus muscu
c	254	139.8	4.9	1030	5	BC054286	Mus muscu	BC054286	327	139	4.9	1652	9	BC028121	Homo sapi
c	255	139.8	4.9	1037	10	BC061131	Mus muscu	BC061131	328	139	4.9	1661	9	BC025755	Homo sapi
c	256	139.8	4.9	1047	9	BC027974	Homo sapi	BC027974	329	139	4.9	1684	9	BC064148	Homo sapi
c	257	139.8	4.9	1416	9	AF090943	Homo sapi	AF090943	330	139	4.9	1788	9	BSM806673	Homo sapi
c	258	139.8	4.9	1457	9	BC056863	Homo sapi	BC056863	331	139	4.9	2058	6	BD276055	48 Human
c	259	139.8	4.9	1500	9	BC056861	Homo sapi	BC056861	332	139	4.9	2312	9	BSM803723	Homo sapi
c	260	139.8	4.9	1576	9	BSM806260	Homo sapi	BSM806260	333	139	4.9	2334	3	AK116665	Ciona int
c	261	139.8	4.9	1598	9	BC013323	Homo sapi	BC013323	334	139	4.9	3230	9	BC063118	Homo sapi
c	262	139.8	4.9	1506	10	BC053176	Mus muscu	BC053176	335	139	4.9	5365	9	BSM807518	Homo sapi
c	263	139.8	4.9	2040	9	BSM807056	Sequence	AX640916	336	139	4.9	5845	6	AX346564	Sequence
c	264	139.8	4.9	2235	9	BC022267	Homo sapi	BC022267	337	139	4.9	6719	9	BSM803507	Homo sapi
c	265	139.8	4.9	2280	9	BC047310	Homo sapi	BC047310	338	139	4.9	7306	6	AX346539	Sequence
c	266	139.8	4.9	2356	10	BC061208	Mus muscu	BC061208	339	139	4.9	12007	6	AX345619	Sequence
c	267	139.8	4.9	2832	10	BC052176	Mus muscu	BC052176	340	139	4.9	34980	6	AX344553	Sequence
c	268	139.8	4.9	3005	10	BC032271	Mus muscu	BC032271	341	138.8	4.9	685	10	BC049720	Mus muscu
c	269	139.8	4.9	3080	9	BSM807488	Sequence	AX647344	342	138.8	4.9	936	6	BD107846	36 human
c	270	139.8	4.9	3645	10	BC062916	Mus muscu	BC062916	343	138.8	4.9	1044	10	BC049565	Mus muscu
c	271	139.8	4.9	4043	10	BC020177	Mus muscu	BC020177	344	138.8	4.9	1084	9	BC022290	Homo sapi
c	272	139.8	4.9	4518	9	BSM802971	Homo sapi	AL713745	345	138.8	4.9	1124	9	BC025950	Homo sapi
c	273	139.8	4.9	5205	9	BSM805958	Homo sapi	BSM805958	346	138.8	4.9	1248	5	BC071085	Xenopus l
c	274	139.6	4.9	490	6	CQ525211	Sequence	CQ525211	347	138.8	4.9	1250	9	BC051908	Homo sapi
c	275	139.6	4.9	901	10	BC053108	Mus muscu	BC053108	348	138.8	4.9	1251	10	BC038552	Mus muscu
c	276	139.6	4.9	1782	10	BC030946	Mus muscu	BC030946	349	138.8	4.9	1384	10	BC052146	Mus muscu
c	277	139.6	4.9	1971	10	BC050802	Mus muscu	BC050802	350	138.8	4.9	1625	9	BSM806623	Homo sapi
c	278	139.6	4.9	2302	5	BC079972	Xenopus l	BC079972	351	138.8	4.9	1877	5	BC066464	Danio rer
c	279	139.6	4.9	2499	9	BSM801350	Homo sapi	AL133016	352	138.8	4.9	2035	9	BSM807574	Homo sapi
c	280	139.6	4.9	2777	5	BC063344	Xenopus t	BC063344	353	138.8	4.9	2244	9	BSM807352	Homo sapi
c	281	139.6	4.9	3001	6	CQ787448	Sequence	CQ787448	354	138.8	4.9	2453	9	BSM807676	Homo sapi
c	282	139.6	4.9	3180	10	BC041774	Mus muscu	BC041774	355	138.8	4.9	2507	10	BC053747	Homo sapi
c	283	139.6	4.9	3353	9	BSM803622	Mus muscu	AL832315	356	138.8	4.9	2730	9	BC053349	Homo sapi
c	284	139.6	4.9	4436	10	BC058961	Mus muscu	BC058961	357	138.8	4.9	2782	9	BSM803706	Homo sapi
c	285	139.6	4.9	5359	10	BC054082	Mus muscu	BC054082	358	138.8	4.9	2943	10	BC005526	Mus muscu
c	286	139.6	4.9	6458	9	BSM806837	Sequence	AX641067	359	138.8	4.9	2977	5	BC070986	Xenopus l
c	287	139.4	4.9	667	6	BD249950	50 human	BD249950	360	138.8	4.9	3178	9	BSM803719	Homo sapi
c	288	139.4	4.9	686	10	BC064030	Rattus no	BC064030	361	138.8	4.9	3394	9	BC050550	Homo sapi
c	289	139.4	4.9	1080	9	BC063605	Homo sapi	BC063605	362	138.8	4.9	4838	10	BC082542	Mus muscu
c	290	139.4	4.9	1122	10	BC049644	Mus muscu	BC049644	363	138.8	4.9	5155	9	BSM805801	Homo sapi
c	291	139.4	4.9	1124	3	AK174947	Ciona int	AK174947	364	138.8	4.9	15832	6	AX277943	Sequence
c	292	139.4	4.9	1906	10	BC063161	Rattus no	BC063161	365	138.8	4.9	15832	6	AX323630	Sequence
c	293	139.4	4.9	1974	10	BC083571	Rattus no	BC083571	366	138.6	4.9	309	6	CQ513146	Sequence
c	294	139.4	4.9	2004	9	BC043556	Homo sapi	BC043556	367	138.6	4.9	746	10	BC061195	Mus muscu
c	295	139.4	4.9	2046	9	BSM808718	Homo sapi	BSM808718	368	138.6	4.9	789	9	BC061900	Homo sapi
c	296	139.4	4.9	2132	9	AB072776	Macaca fa	AB072776	369	138.6	4.9	893	6	CQ472917	Sequence
c	297	139.4	4.9	2420	5	BC066695	Danio rer	BC066695	370	138.6	4.9	1000	10	BC038055	Mus muscu
c	298	139.4	4.9	2470	10	BC027800	Mus muscu	BC027800	371	138.6	4.9	1373	10	BC049731	Mus muscu
c	299	139.4	4.9	2648	10	BC031180	Mus muscu	BC031180	372	138.6	4.9	1610	9	BC064141	Homo sapi
c	300	139.4	4.9	2846	9	BSM802834	Homo sapi	AL442082	373	138.6	4.9	1876	10	BC053422	Mus muscu
c	301	139.4	4.9	2910	9	BC042070	Homo sapi	BC042070	374	138.6	4.9	1985	5	BC053414	Danio rer
c	302	139.4	4.9	3084	10	BC058950	Mus muscu	BC058950	375	138.6	4.9	1985	10	BC049351	Mus muscu
c	303	139.4	4.9	3134	9	BSM805794	Homo sapi	BSM805794	376	138.6	4.9	1995	10	BC050759	Mus muscu
c	304	139.4	4.9	4116	9	BSM807269	Homo sapi	BSM807269	377	138.6	4.9	2098	9	BC017717	Homo sapi
c	305	139.4	4.9	5695	10	BC082548	Mus muscu	BC082548	378	138.6	4.9	2321	9	BC058898	Homo sapi
c	306	139.4	4.9	25673	2	AC087146	Sequence	AC087146	379	138.6	4.9	2815	9	BC038597	Homo sapi
c	307	139.4	4.9	349980	6	AX344573	Sequence	AX344573	380	138.6	4.9	2886	10	BC025599	Mus muscu
c	308	139.2	4.9	658	6	BD275413	50 Human	BD275413	381	138.6	4.9	3189	9	BC002830	Homo sapi
c	309	139.2	4.9	1062	5	BC084361	Xenopus l	BC084361	382	138.6	4.9	3502	9	BSM807726	Homo sapi
c	310	139.2	4.9	1071	9	AF078844	Homo sapi	AF078844	383	138.6	4.9	4155	5	BC074405	Xenopus l
c	311	139.2	4.9	1129	10	BC060535	Rattus no	BC060535	384	138.6	4.9				

385	138.6	4.9	4946	9	HSMB05863	138	4.8	113515	6	AX347076	Sequence
386	138.6	4.9	5344	9	HSMB07425	138	4.8	349980	6	AX344559	Sequence
387	138.6	4.9	7216	9	HSMB05762	138	4.8	349980	6	AX344565	Sequence
C 388	138.6	4.9	14006	6	AX346860	138	4.8	349980	6	AX344572	Sequence
C 389	138.4	4.9	396	6	AR391230	462	137.8	4.8	384	3	AF155365
C 390	138.4	4.9	396	6	AR392935	463	137.8	4.8	48	4.8	393
C 391	138.4	4.9	396	6	AR489665	464	137.8	4.8	596	9	BC008387
C 392	138.4	4.9	396	6	AR493906	465	137.8	4.8	675	10	BC059112
C 393	138.4	4.9	396	6	AX093235	466	137.8	4.8	686	10	BC060302
394	138.4	4.9	704	10	BC043749	467	137.8	4.8	879	9	BC007021
395	138.4	4.9	863	10	BC061014	468	137.8	4.8	1219	10	BC049717
396	138.4	4.9	935	3	AK174210	469	137.8	4.8	1493	9	BC042547
397	138.4	4.9	1080	10	BC049655	470	137.8	4.8	1770	9	BC025717
398	138.4	4.9	1493	9	BC032462	471	137.8	4.8	1798	6	AR366535
399	138.4	4.9	1671	10	BC022180	472	137.8	4.8	2464	9	HSMB07471
400	138.4	4.9	2030	10	BC058229	473	137.8	4.8	2770	9	HSMB07752
401	138.4	4.9	2553	10	BC061558	C 474	137.8	4.8	4316	6	CQ0806814
402	138.4	4.9	4259	9	HSMB05206	C 475	137.8	4.8	4316	6	AX795752
403	138.4	4.9	4421	10	BC042512	C 476	137.8	4.8	4316	6	AX822260
404	138.4	4.9	4930	9	HSMB03373	C 477	137.8	4.8	4316	6	AX825900
405	138.4	4.9	4940	9	HSMB06769	C 478	137.8	4.8	4636	10	BC057352
406	138.4	4.9	5402	9	HSMB04677	C 479	137.8	4.8	5195	6	AX345823
C 407	138.4	4.9	6486	6	AX458534	480	137.8	4.8	5355	9	HSMB06819
C 408	138.4	4.9	7369	6	AX598791	C 481	137.8	4.8	6944	6	AX347467
C 409	138.4	4.9	7369	6	AX705365	C 482	137.8	4.8	6944	6	AX349188
C 410	138.4	4.9	10369	6	AX251057	C 483	137.8	4.8	6944	6	AX657867
C 411	138.4	4.9	10369	6	AX345294	C 484	137.8	4.8	6944	6	AX659141
C 412	138.4	4.9	70389	2	AC135859	C 485	137.8	4.8	73778	6	AX344575
413	138.4	4.9	153567	2	AC087145	C 486	137.6	4.8	406	6	CQ397829
C 414	138.4	4.9	212273	10	AC104920	C 487	137.6	4.8	406	6	CQ404124
C 415	138.2	4.9	351	6	CQ410508	488	137.6	4.8	556	6	CQ508215
416	138.2	4.9	625	10	BC059134	489	137.6	4.8	556	6	CQ510257
417	138.2	4.9	687	10	BC049765	490	137.6	4.8	556	6	CQ511753
418	138.2	4.9	788	5	BC072244	491	137.6	4.8	809	6	BD252094
419	138.2	4.9	794	9	BC058920	492	137.6	4.8	845	9	BC044653
420	138.2	4.9	940	10	BC060548	493	137.6	4.8	873	6	AX780227
421	138.2	4.9	1289	10	BC049691	494	137.6	4.8	1071	9	HSMB05733
422	138.2	4.9	1382	10	BC066858	495	137.6	4.8	1433	3	AX174181
423	138.2	4.9	1500	10	BC049755	496	137.6	4.8	1433	5	BC082836
424	138.2	4.9	1954	6	BD270057	497	137.6	4.8	1802	9	AX071113
425	138.2	4.9	2621	10	MUSBRD	498	137.6	4.8	1933	9	HSMB06724
426	138.2	4.9	3149	10	BC040763	499	137.6	4.8	2003	9	BC051760
427	138.2	4.9	3275	6	BD237099	500	137.6	4.8	2439	10	BC061540
428	138.2	4.9	3275	6	AR225499	501	137.6	4.8	2556	9	HSMB05953
429	138.2	4.9	3275	6	AR562922	502	137.6	4.8	2917	9	BC054514
430	138.2	4.9	3275	6	AX321620	503	137.6	4.8	2986	5	BC084243
431	138.2	4.9	3518	9	HSMB07510	C 504	137.6	4.8	231	6	CQ685486
432	138.2	4.9	3564	10	BC065123	C 505	137.6	4.8	431	9	BC070144
433	138.2	4.9	3924	10	MUSBRD	506	137.4	4.8	664	10	BC061046
434	138.2	4.9	4286	9	HSMB07052	507	137.4	4.8	720	10	BC083088
435	138.2	4.9	4345	9	HSMB089518	508	137.4	4.8	749	10	BC060563
436	138.2	4.9	5154	9	HSMB05947	509	137.4	4.8	760	9	BC032326
437	138.2	4.9	5280	10	BC052198	510	137.4	4.8	953	10	BC049732
438	138.2	4.9	5763	9	HSMB08699	511	137.4	4.8	1109	10	BC063150
C 439	138.2	4.9	6436	6	AX3445583	512	137.4	4.8	1381	5	BC063358
C 440	138.2	4.9	349980	6	AX344558	513	137.4	4.8	1432	10	BC062239
441	138	4.8	1173	10	BC061094	514	137.4	4.8	1820	8	BT009533
442	138	4.8	1464	9	IR2005397	515	137.4	4.8	2387	10	BC048933
443	138	4.8	1589	9	BC043543	516	137.4	4.8	2545	9	BC063430
444	138	4.8	1725	9	HSMB06934	517	137.4	4.8	5241	6	AX252153
445	138	4.8	1740	9	BC042437	518	137.4	4.8	5241	6	AX348924
446	138	4.8	2073	9	BC068024	519	137.4	4.8	2909	3	AX116710
447	138	4.8	2158	5	BC082415	520	137.4	4.8	2936	5	BC077828
448	138	4.8	2329	10	BC050816	521	137.4	4.8	3006	9	BC039068
449	138	4.8	2700	9	BC064849	522	137.4	4.8	3117	10	BC043717
450	138	4.8	2789	10	BC026672	523	137.4	4.8	3183	9	BC044242
451	138	4.8	2929	10	BC053441	C 524	137.4	4.8	5241	6	AX248924
C 452	138	4.8	3001	6	CQ787464	C 525	137.4	4.8	5241	6	AX348924
453	138	4.8	3532	9	HSMB07372	C 526	137.4	4.8	227273	2	AC141526
454	138	4.8	4457	10	BC070435	527	137.2	4.8	539	10	BC061539
455	138	4.8	5395	9	BC078662	528	137.2	4.8	932	9	BC043537
456	138	4.8	5627	9	HSMB07499	529	137.2	4.8	950	9	BC063550
C 457	138	4.8	8946	6	AX345813	530	137.2	4.8	1001	10	BC049605

531	137.2	4.8	1115	10	BC049678	BC049678 Mus muscu	604	136.6	4.8	2262	6	AR487911	Sequence
532	137.2	4.8	1119	9	BC071717	BC071717 Homo sapi	605	136.6	4.8	2271	9	AB056809	Macaca fa
533	137.2	4.8	1267	10	BC049715	BC049715 Mus muscu	606	136.6	4.8	2282	9	BC033689	BC033689 Homo sapi
534	137.2	4.8	1684	10	BC055910	BC055910 Mus muscu	607	136.6	4.8	2328	9	BC043587	BC043587 Homo sapi
535	137.2	4.8	1808	6	AX535019	AX535019 Sequence	608	136.6	4.8	2666	9	BC027972	BC027972 Homo sapi
536	137.2	4.8	1966	9	HSB808069	AX535019 Sequence	609	136.6	4.8	2991	9	BC030556	BC030556 Homo sapi
537	137.2	4.8	2019	10	BC063758	BC063758 Mus muscu	610	136.6	4.8	3141	3	AX116783	BC030556 Homo sapi
538	137.2	4.8	2104	9	HSB806838	BC063758 Mus muscu	611	136.6	4.8	3375	10	HSB806652	AX116783 Ciona int
539	137.2	4.8	3883	9	HSB808647	BC0649181 Homo sapi	612	136.6	4.8	4358	10	BC060187	BC060187 Mus muscu
540	137.2	4.8	4726	9	HSB808819	BC0648499 Homo sapi	613	136.6	4.8	4942	9	HSB808887	BC0647062 Homo sapi
541	137.2	4.8	12177	6	AX345553	BC0648668 Homo sapi	614	136.6	4.8	5703	10	BC054080	BC0648736 Homo sapi
542	137	4.8	497	6	CQ526425	AX345553 Sequence	c 615	136.6	4.8	11394	6	AX323608	BC054080 Mus muscu
543	137	4.8	732	5	AY522586	CQ526425 Sequence	c 616	136.6	4.8	39980	6	AX344551	AX323608 Sequence
544	137	4.8	865	10	BC060948	AY522586 Oreochrom	617	136.4	4.8	510	9	BC070217	AX344551 Sequence
545	137	4.8	900	10	BC049654	BC060948 Mus muscu	618	136.4	4.8	516	6	CQ524041	BC070217 Homo sapi
546	137	4.8	910	10	BC049687	BC049654 Mus muscu	c 619	136.4	4.8	539	6	CQ410791	CQ524041 Sequence
547	137	4.8	1222	9	BC035237	BC049687 Mus muscu	620	136.4	4.8	549	10	BC048536	CQ410791 Sequence
548	137	4.8	1368	10	BC0383654	BC035237 Homo sapi	621	136.4	4.8	645	3	AX168768	BC048536 Mus muscu
549	137	4.8	1383	9	BC032432	BC0383654 Rattus no	622	136.4	4.8	679	9	BC052814	AX168768 Branchios
550	137	4.8	1493	9	HSB805897	BC032432 Homo sapi	623	136.4	4.8	693	10	BC049621	BC052814 Homo sapi
551	137	4.8	1730	9	BC033615	BSX538346 Homo sapi	624	136.4	4.8	705	10	BC049708	BC049621 Mus muscu
552	137	4.8	1890	9	HSB807434	BC033615 Homo sapi	625	136.4	4.8	827	10	BC049739	BC049708 Mus muscu
553	137	4.8	2039	10	BC050804	BC047290 Homo sapi	626	136.4	4.8	970	10	BC061464	BC049739 Mus muscu
554	137	4.8	2447	6	AR079032	BC050804 Mus muscu	627	136.4	4.8	1030	10	BC049544	BC061464 Mus muscu
555	137	4.8	2447	6	BD190886	AR079032 Sequence	628	136.4	4.8	1048	9	BC063640	BC049544 Mus muscu
556	137	4.8	2598	5	BC044109	BD190886 Secreted	629	136.4	4.8	1580	5	BC067146	BC063640 Homo sapi
557	137	4.8	2752	9	HSB806735	BC044109 Xenopus l	630	136.4	4.8	1762	9	AF258575	BC067146 Homo rer
558	137	4.8	3232	9	AX7090901	BC641046 Homo sapi	631	136.4	4.8	1931	10	BC036150	AF258575 Homo sapi
559	137	4.8	6172	6	AX281462	AF090901 Homo sapi	632	136.4	4.8	1941	9	BC051758	BC036150 Mus muscu
560	137	4.8	65326	2	AC124815	AX281462 Sequence	633	136.4	4.8	2521	10	BC026021	BC051758 Homo sapi
561	137	4.8	191531	2	AC113984	AC124815 Mus muscu	c 634	136.4	4.8	4316	6	CQ807088	BC026021 Mus muscu
562	136.8	4.8	570	6	CQ527266	AC113984 Mus muscu	c 635	136.4	4.8	4316	6	AX795868	CQ807088 Sequence
563	136.8	4.8	589	10	BC049706	BC049706 Mus muscu	636	136.4	4.8	4316	6	AX822388	AX795868 Sequence
564	136.8	4.8	1017	9	HSB807298	BC049706 Mus muscu	c 637	136.4	4.8	4316	6	AX826028	AX822388 Sequence
565	136.8	4.8	1591	9	HSB807298	BC647154 Homo sapi	638	136.4	4.8	4659	9	HSB806121	AX826028 Sequence
566	136.8	4.8	1640	9	AB070034	AB070034 Macaca fa	c 639	136.4	4.8	5368	6	AX344691	BSX537988 Homo sapi
567	136.8	4.8	1743	10	BC051150	BC051150 Mus muscu	c 640	136.4	4.8	5586	6	AX348391	AX344691 Sequence
568	136.8	4.8	1746	9	BC025377	BC025377 Homo sapi	c 641	136.4	4.8	24259	6	AX251448	AX348391 Sequence
569	136.8	4.8	1803	9	HSB807650	BC647504 Homo sapi	642	136.4	4.8	31656	2	AC149363	AX251448 Sequence
570	136.8	4.8	1885	9	HSB807866	BC647720 Homo sapi	643	136.2	4.8	459	6	CQ522436	AC149363 Phakopsor
571	136.8	4.8	1913	3	AX069281	AX069281 Drosophil	644	136.2	4.8	481	6	CQ524400	CQ522436 Sequence
572	136.8	4.8	2217	9	AX069281	BC073932 Homo sapi	645	136.2	4.8	828	10	BC049756	CQ524400 Sequence
573	136.8	4.8	2313	10	BC021410	BC073932 Homo sapi	646	136.2	4.8	890	8	AY735693	BC049756 Mus muscu
574	136.8	4.8	2835	9	BC068211	BC021410 Mus muscu	647	136.2	4.8	1038	9	BC038366	AY735693 Arabidopp
575	136.8	4.8	3525	10	BC034207	BC034207 Mus muscu	648	136.2	4.8	1245	5	BC049747	BC038366 Homo sapi
576	136.8	4.8	3530	10	BC053732	BC053732 Mus muscu	649	136.2	4.8	1430	5	BC064202	BC049747 Mus muscu
577	136.8	4.8	4081	9	HSB807531	BC647386 Homo sapi	650	136.2	4.8	1657	10	BC057688	BC064202 Xenopus t
578	136.8	4.8	4597	10	BC043313	BC043313 Mus muscu	651	136.2	4.8	1719	10	BC045148	BC057688 Mus muscu
579	136.8	4.8	6161	6	AX345313	AX345313 Sequence	652	136.2	4.8	1887	10	BC050801	BC045148 Mus muscu
580	136.8	4.8	6192	6	AX251440	AX251440 Sequence	653	136.2	4.8	2048	9	BC044243	BC050801 Mus muscu
581	136.8	4.8	7369	6	AX598937	AX598937 Sequence	654	136.2	4.8	2370	10	BC034555	BC044243 Homo sapi
582	136.8	4.8	7369	6	AX705387	AX705387 Sequence	655	136.2	4.8	2776	10	BC034120	BC034555 Mus muscu
583	136.8	4.8	15528	6	A93016	A93016 Sequence 4	656	136.2	4.8	2968	10	BC058408	BC034120 Mus muscu
584	136.8	4.8	15528	12	FEAVGEN	Y07862 Cloning vec	657	136.2	4.8	3329	10	BC054371	BC058408 Mus muscu
585	136.6	4.8	212	6	CQ677317	CQ677317 Sequence	658	136.2	4.8	4661	5	BC068849	BC054371 Mus muscu
586	136.6	4.8	368	10	BC049735	BC049735 Mus muscu	659	136.2	4.8	4753	10	BC058514	BC068849 Xenopus l
587	136.6	4.8	394	6	CQ481688	CQ481688 Sequence	c 660	136.2	4.8	5249	9	HSB803431	BC058514 Mus muscu
588	136.6	4.8	408	6	CQ502830	CQ502830 Sequence	c 661	136.2	4.8	5387	6	AX344633	AL832124 Homo sapi
589	136.6	4.8	408	6	CQ511687	CQ511687 Sequence	c 662	136.2	4.8	24259	6	AX251447	AX344633 Sequence
590	136.6	4.8	484	6	CQ526160	CQ526160 Sequence	c 663	136	4.8	138	6	CQ705290	AX251447 Sequence
591	136.6	4.8	661	10	BC051629	BC051629 Mus muscu	664	136	4.8	481	9	CQ705290	CQ705290 Sequence
592	136.6	4.8	907	10	BC064826	BC064826 Mus muscu	665	136	4.8	481	5	BC082915	BC070219 Homo sapi
593	136.6	4.8	1017	10	BC034217	BC034217 Mus muscu	666	136	4.8	671	5	BC082915	BC082915 Xenopus l
594	136.6	4.8	1065	10	BC049634	BC049634 Mus muscu	667	136	4.8	1024	9	BC012602	BC012602 Homo sapi
595	136.6	4.8	1150	5	BC066608	BC049634 Mus muscu	668	136	4.8	1419	9	BC032340	BC032340 Homo sapi
596	136.6	4.8	1182	10	BC049567	BC066608 Danio rer	669	136	4.8	1500	3	AX174058	AX174058 Ciona int
597	136.6	4.8	1310	9	HSB807559	BC049567 Mus muscu	670	136	4.8	1913	3	AX174058	AX174058 Ciona int
598	136.6	4.8	1414	10	BC049767	BC647414 Homo sapi	671	136	4.8	2435	5	BC050387	BC012362 Homo sapi
599	136.6	4.8	1501	5	BC080019	BC049767 Mus muscu	c 672	136	4.8	2725	9	BC077764	BC050387 Homo sapi
600	136.6	4.8	1545	10	BC062173	BC080019 Xenopus l	c 673	136	4.8	3030	3	AX116919	BC077764 Sequence
601	136.6	4.8	1647	9	HSB806170	BC062173 Mus muscu	c 674	135.8	4.8	34980	6	AX344566	AX116919 Ciona int
602	136.6	4.8	2016	10	BC063147	BSX37936 Homo sapi	675	135.8	4.8	396	6	CQ525748	AX344566 Sequence
603	136.6	4.8	2233	9	BC040959	BC063147 Rattus no	c 676	135.8	4.8	509	6	BC017744	CQ525748 Sequence
						BC040959 Homo sapi	c 676	135.8	4.8	549	6	CQ524814	BC017744 Homo sapi

677	135.8	4.8	711	9	BC051802	BC051802 Homo sapi	C 750	135.2	4.8	9580	14	AF054250	AF054250 Hepatitis
678	135.8	4.8	781	10	BC049734	BC049734 Mus muscu	C 751	135.2	4.8	349980	6	AX344563	AX344563 Sequence
679	135.8	4.8	1035	10	BC055104	BC055104 Mus muscu	752	135	4.7	240	6	CQ663206	CQ663206 Sequence
680	135.8	4.8	1528	9	BC043317	BC043317 Homo sapi	C 753	135	4.7	417	6	CQ477248	CQ477248 Sequence
681	135.8	4.8	1832	5	BC084269	BC084269 Xenopus l	754	135	4.7	612	10	BC061085	BC061085 Mus muscu
682	135.8	4.8	1939	5	BC079974	BC079974 Xenopus l	755	135	4.7	1329	9	AF544398	AF544398 Homo sapi
683	135.8	4.8	2074	9	BC014433	BC014433 Homo sapi	756	135	4.7	1872	9	BC038952	BC038952 Homo sapi
684	135.8	4.8	2081	9	HS0806272	BX537592 Homo sapi	757	135	4.7	1933	6	BD270058	BD270058 Secreted
685	135.8	4.8	2112	5	BC076765	BC076765 Xenopus l	758	135	4.7	3255	9	HS0803224	AL831898 Homo sapi
686	135.8	4.8	2116	9	BC034379	BC034379 Homo sapi	759	135	4.7	6163	10	BC052150	BC052150 Mus muscu
C 687	135.8	4.8	2501	6	AX598878	AX598878 Sequence	760	134.8	4.7	515	6	CQ522671	CQ522671 Sequence
C 688	135.8	4.8	2501	6	AX599024	AX599024 Sequence	761	134.8	4.7	547	9	BC070202	BC070202 Homo sapi
C 689	135.8	4.8	2612	9	BC063856	BC063856 Homo sapi	762	134.8	4.7	1090	5	BC066372	BC066372 Danio rer
C 690	135.8	4.8	4001	6	AX347363	AX347363 Sequence	763	134.8	4.7	1793	10	BC062171	BC062171 Mus muscu
C 691	135.8	4.8	4001	6	AX349084	AX349084 Sequence	764	134.8	4.7	1812	10	BC055113	BC055113 Mus muscu
C 692	135.8	4.8	4001	6	AX657851	AX657851 Sequence	765	134.8	4.7	2511	3	AK174016	AK174016 Ciona int
C 693	135.8	4.8	4001	6	AX659125	AX659125 Sequence	766	134.8	4.7	2905	3	AK174395	AK174395 Ciona int
C 694	135.8	4.8	4265	9	HS0807603	BX647458 Homo sapi	767	134.8	4.7	3422	9	HS0805920	BX537826 Homo sapi
C 695	135.8	4.8	4863	9	HS0808808	BX648657 Homo sapi	768	134.8	4.7	173854	2	AC073047	AC073047 Homo sapi
C 696	135.8	4.8	5306	6	AX345413	AX345413 Sequence	769	134.8	4.7	349980	6	AX344570	AX344570 Sequence
C 697	135.8	4.8	6134	6	AX458624	AX458624 Sequence	C 770	134.6	4.7	360	6	CQ527206	CQ527206 Sequence
C 698	135.8	4.8	7061	6	AX251886	AX251886 Sequence	C 771	134.6	4.7	391	6	CQ476273	CQ476273 Sequence
C 699	135.8	4.8	7061	6	AX345898	AX345898 Sequence	772	134.6	4.7	579	6	CQ526842	CQ526842 Sequence
C 700	135.8	4.8	7061	6	AX348679	AX348679 Sequence	773	134.6	4.7	6976	9	HS0808639	AB125184 Macaca fa
C 701	135.8	4.8	14798	6	AX345934	AX345934 Sequence	774	134.6	4.7	887	9	AB125184	AB125184 Macaca fa
C 702	135.8	4.8	14920	6	AX344738	AX344738 Sequence	775	134.6	4.7	981	9	BC041179	BC041179 Homo sapi
C 703	135.8	4.8	16633	6	AX344576	AX344576 Sequence	776	134.6	4.7	1562	10	BC063181	BC063181 Rattus no
C 704	135.8	4.8	17934	6	AX346621	AX346621 Sequence	777	134.6	4.7	1853	10	BC052346	BC052346 Mus muscu
C 705	135.8	4.8	35962	6	AX598758	AX598758 Sequence	778	134.6	4.7	3181	5	BC070985	BC070985 Xenopus l
C 706	135.8	4.8	35962	6	AX598904	AX598904 Sequence	779	134.6	4.7	6976	9	HS0808639	BX648491 Homo sapi
C 707	135.8	4.8	66993	2	AC138074	AC138074 Homo sapi	780	134.6	4.7	13054	2	AC149986	AC149986 Strongylo
C 708	135.8	4.8	110000	8	CR382134 ¹²	Continuation (13 o	C 781	134.6	4.7	45685	2	AC087168	AC087168 Homo sapi
C 709	135.8	4.8	193988	2	AC102269	AC102269 Mus muscu	C 782	134.4	4.7	416	6	CQ484252	CQ484252 Sequence
C 710	135.6	4.8	800	10	BC034163	BC034163 Mus muscu	C 783	134.4	4.7	608	6	CQ398119	CQ398119 Sequence
C 711	135.6	4.8	831	6	CQ423554	CQ423554 Sequence	784	134.4	4.7	766	8	AF531371	AF531371 Gossypium
C 712	135.6	4.8	1053	10	BC049595	BC049595 Mus muscu	785	134.4	4.7	2237	3	AK112710	AK112710 Ciona int
C 713	135.6	4.8	1459	6	BD270519	BD270519 Novel mai	C 791	134.4	4.7	2548	9	BC040371	BC040371 Homo sapi
C 714	135.6	4.8	1459	6	AR494847	AR494847 Sequence	787	134.4	4.7	2922	9	BC032692	BC032692 Homo sapi
C 715	135.6	4.8	1459	6	AX046603	AX046603 Sequence	788	134.4	4.7	2943	9	HS0803526	AL832219 Homo sapi
C 716	135.6	4.8	1985	3	AX118692	AX118692 Drosophil	C 789	134.4	4.7	11097	6	AX826974	AX826974 Sequence
C 717	135.6	4.8	2395	9	AF090903	AF090903 Homo sapi	C 790	134.4	4.7	240657	2	AC111675	AC111675 Rattus no
C 718	135.6	4.8	2585	9	HS0805677	BX537382 Homo sapi	C 791	134.4	4.7	349980	6	AX344554	AX344554 Sequence
C 719	135.6	4.8	2915	10	BC061479	BC061479 Mus muscu	C 792	134.4	4.7	349980	6	AX344555	AX344555 Sequence
C 720	135.6	4.8	6484	6	AX344730	AX344730 Sequence	C 793	134.2	4.7	501	6	CNS01D7J	CNS01D7J Sequence
C 721	135.6	4.8	9095	6	AX458545	AX458545 Sequence	C 794	134.2	4.7	720	8	BC072684	BC072684 Homo sapi
C 722	135.6	4.8	15649	6	AX348976	AX348976 Sequence	C 795	134.2	4.7	1269	9	BC063419	BC063419 Homo sapi
C 723	135.6	4.8	40862	6	AX346974	AX346974 Sequence	796	134.2	4.7	1770	9	HS0806048	BX537929 Homo sapi
C 724	135.4	4.8	412	6	CQ522434	CQ522434 Sequence	797	134.2	4.7	1933	9	HS0806048	AB056420 Macaca fa
C 725	135.4	4.8	774	10	BC013457	BC013457 Mus muscu	C 799	134.2	4.7	7657	6	AX278022	AX278022 Sequence
C 726	135.4	4.8	859	9	BC043551	BC043551 Homo sapi	C 800	134.2	4.7	7657	6	AX346924	AX346924 Sequence
C 727	135.4	4.8	872	6	AX068322	AX068322 Sequence	C 801	134.2	4.7	9814	6	AX344425	AX344425 Sequence
C 728	135.4	4.8	1004	10	BC025458	BC025458 Mus muscu	C 802	134.2	4.7	37973	6	AX347098	AX347098 Sequence
C 729	135.4	4.8	1198	10	BC033305	BC033305 Mus muscu	C 803	134.2	4.7	63365	2	AC087437	AC087437 Homo sapi
C 730	135.4	4.8	1648	9	HS0808551	BX648403 Homo sapi	C 804	134.2	4.7	75689	2	AC018536	AC018536 Homo sapi
C 731	135.4	4.8	1732	9	HS0806991	BX648074 Homo sapi	C 805	134.2	4.7	349980	6	AX344567	AX344567 Sequence
C 732	135.4	4.8	1743	9	AB070131	AB070131 Macaca fa	C 806	134	4.7	472	6	CQ525172	CQ525172 Sequence
C 733	135.4	4.8	2026	9	BC022399	BC022399 Homo sapi	C 807	134	4.7	756	6	CQ399155	CQ399155 Sequence
C 734	135.4	4.8	2027	9	BC063512	BC063512 Homo sapi	C 808	134	4.7	756	6	CQ405433	CQ405433 Sequence
C 735	135.4	4.8	2371	9	HS0805927	BX537833 Homo sapi	C 809	134	4.7	844	9	BC009571	BC009571 Homo sapi
C 736	135.4	4.8	2563	9	AF125949	AF125949 Homo sapi	C 810	134	4.7	1339	9	BC016710	BC016710 Homo sapi
C 737	135.4	4.8	3186	5	BC068331	BC068331 Danio rer	C 811	134	4.7	1701	9	BC071665	BC071665 Homo sapi
C 738	135.4	4.8	3758	9	HS0801755	AL136787 Homo sapi	C 812	134	4.7	1742	9	HS0806670	BX640624 Homo sapi
C 739	135.4	4.8	3836	9	BC063854	BC063854 Homo sapi	C 813	134	4.7	2207	10	BC066857	BC066857 Mus muscu
C 740	135.4	4.8	4086	9	HS0803439	AL832132 Homo sapi	C 814	134	4.7	2610	9	BC038448	BC038448 Homo sapi
C 741	135.2	4.8	385	6	CQ522393	CQ522393 Sequence	C 815	134	4.7	2734	5	BC076749	BC076749 Xenopus l
C 742	135.2	4.8	522	6	CQ518047	CQ518047 Sequence	C 816	134	4.7	3274	9	HS0807371	BX647227 Homo sapi
C 743	135.2	4.8	682	10	BC049545	BC049545 Mus muscu	C 817	134	4.7	3916	10	BC018439	BC018439 Mus muscu
C 744	135.2	4.8	1138	10	BC062234	BC062234 Rattus no	C 818	134	4.7	4062	5	BC070004	BC070004 Danio rer
C 745	135.2	4.8	1963	10	BC083817	BC083817 Rattus no	C 819	134	4.7	5152	6	AX453070	AX453070 Sequence
C 746	135.2	4.8	1999	9	HS08242859	AJ242859 Homo sapi	C 820	134	4.7	5152	6	AX281182	AX281182 Sequence
C 747	135.2	4.8	2394	6	AK374733	AK374733 Sequence	C 821	134	4.7	8899	6	AX345739	AX345739 Sequence
C 748	135.2	4.8	2789	3	AK114441	AK114441 Ciona int	C 822	134	4.7	8899	6	AX348461	AX348461 Sequence
C 749	135.2	4.8	3681	9	HS0806036	BX537922 Homo sapi	C 822	134	4.7	8899	6	AX348461	AX348461 Sequence

C-823	134	4.7	64789	2	AC083839	AC083839 Homo sapi	C 896	133	4.7	6794	6	AX251872	Sequence
C 824	134	4.7	165563	2	AC083752	AC083752 Mus muscu	C 897	133	4.7	6794	6	AX344260	Sequence
825	133.8	4.7	474	6	CQ522390	CQ522390 Sequence	C 898	133	4.7	6794	6	AX348651	Sequence
826	133.8	4.7	500	9	BC070218	BC070218 Homo sapi	C 899	133	4.7	14568	6	AX345132	Sequence
827	133.8	4.7	761	11	CNS06KKG	AL042998 T7 end of	C 900	132.8	4.7	420	6	CQ476954	Sequence
C 828	133.8	4.7	817	6	CQ423543	CQ423543 Sequence	C 901	132.8	4.7	1078	9	BC035314	Sequence
C 829	133.8	4.7	859	9	AC026608	AC026608 Homo sapi	C 902	132.8	4.7	1142	8	AJ840525	Sequence
C 830	133.8	4.7	874	6	CQ414670	CQ414670 Sequence	C 903	132.8	4.7	1456	5	BC077897	Sequence
C 831	133.8	4.7	931	10	BC049725	BC049725 Mus muscu	C 904	132.8	4.7	1968	10	BC006016	Sequence
C 832	133.8	4.7	1197	8	AJ840663	AJ840663 Arabidops	C 905	132.8	4.7	1982	3	AK112713	Ciona int
C 833	133.8	4.7	1328	8	AJ840631	AJ840631 Arabidops	C 906	132.8	4.7	1983	10	BC005510	Mus muscu
C 834	133.8	4.7	2030	9	BC063602	BC063602 Homo sapi	C 907	132.8	4.7	1985	6	BD172402	Secreted
835	133.8	4.7	2566	6	CQ834011	CQ834011 Sequence	C 908	132.8	4.7	1985	6	BD172421	Secreted
C 836	133.8	4.7	3341	9	BC032308	BC032308 Homo sapi	C 909	132.8	4.7	1985	6	BD173040	Secreted
C 837	133.8	4.7	6115	6	AX346703	AX346703 Sequence	C 910	132.8	4.7	1985	6	BD173359	Secreted
C 838	133.8	4.7	8712	6	AX344694	AX344694 Sequence	C 911	132.8	4.7	1985	6	BD175393	Secretory
C 839	133.8	4.7	61940	2	AC109312	AC109312 Homo sapi	C 912	132.8	4.7	1985	6	CQ881212	Sequence
C 840	133.8	4.7	64767	2	AC102701	AC102701 Mus muscu	C 913	132.8	4.7	1985	6	AR410771	Sequence
841	133.8	4.7	133276	2	AC087147	AC087147 Homo sapi	C 914	132.8	4.7	1985	6	AR439135	Sequence
842	133.8	4.7	167711	2	AC007629	AC007629 Mus muscu	C 915	132.8	4.7	1985	6	AR473155	Sequence
843	133.6	4.7	562	10	BC049688	BC049688 Homo sapi	C 916	132.8	4.7	1985	6	AR527141	Sequence
844	133.6	4.7	763	9	BC040916	BC040916 Homo sapi	C 917	132.8	4.7	1985	6	AR566174	Sequence
845	133.6	4.7	967	9	HSN802777	AL390167 Homo sapi	C 918	132.8	4.7	1985	6	AX375960	Sequence
846	133.6	4.7	1352	3	AK115954	AK115954 Ciona int	C 919	132.8	4.7	1985	6	AX697621	Sequence
847	133.6	4.7	1408	10	BC048693	BC048693 Mus muscu	C 920	132.8	4.7	1985	6	BD075542	Secretory
848	133.6	4.7	1788	9	BC044944	BC044944 Homo sapi	C 921	132.8	4.7	1985	9	AX358500	Homo sapi
849	133.6	4.7	1816	9	BC050396	BC050396 Homo sapi	C 922	132.8	4.7	6668	6	AX346598	Sequence
850	133.6	4.7	1889	9	HSN805887	BS537794 Homo sapi	C 923	132.8	4.7	11097	6	AX826972	Sequence
851	133.6	4.7	2178	6	AX099370	AX099370 Sequence	C 924	132.8	4.7	12138	6	AX346530	Sequence
852	133.6	4.7	2514	9	BC044863	BC044863 Homo sapi	C 925	132.8	4.7	12138	6	AX348420	Sequence
853	133.6	4.7	2641	9	BC020219	BC020219 Homo sapi	C 926	132.6	4.7	602	9	BC008488	Homo sapi
854	133.6	4.7	3375	9	BC038406	BC038406 Homo sapi	C 927	132.6	4.7	972	10	BC049738	Mus muscu
C 855	133.6	4.7	6025	6	AX277881	AX277881 Sequence	C 928	132.6	4.7	1590	9	HSN803698	Homo sapi
C 856	133.6	4.7	56153	6	AX251552	AX251552 Sequence	C 929	132.6	4.7	1634	9	HSN807708	Homo sapi
857	133.6	4.7	213641	2	AC114620	AC114620 Mus muscu	C 930	132.6	4.7	2679	10	BC006021	Mus muscu
858	133.4	4.7	202	6	BD190570	BD190570 Secretory	C 931	132.6	4.7	2827	6	CQ491125	Sequence
859	133.4	4.7	202	6	AX099441	AX099441 Sequence	C 932	132.6	4.7	2827	6	CQ496990	Sequence
860	133.4	4.7	358	6	CQ671266	CQ671266 Sequence	C 933	132.6	4.7	3586	6	AX339195	Sequence
861	133.4	4.7	565	6	CQ526051	CQ526051 Sequence	C 934	132.6	4.7	5586	6	AX345551	Sequence
C 862	133.4	4.7	597	6	AX187052	AX187052 Sequence	C 935	132.6	4.7	5893	6	AX345761	Sequence
C 863	133.4	4.7	621	6	AX187131	AX187131 Sequence	C 936	132.6	4.7	6171	6	AX345691	Sequence
C 864	133.4	4.7	1083	9	HSN800561	AL080060 Homo sapi	C 937	132.6	4.7	34980	6	AX344571	Sequence
865	133.4	4.7	1570	10	BC049624	BC049624 Mus muscu	C 938	132.4	4.7	1000	9	HSN806624	Homo sapi
866	133.4	4.7	1941	5	BC053250	BC053250 Danio rer	C 939	132.4	4.7	1012	10	BC049579	Mus muscu
867	133.4	4.7	2164	10	BC005513	BC005513 Mus muscu	C 940	132.4	4.7	1073	5	BC084065	Xenopus l
868	133.4	4.7	2790	9	BC048292	BC048292 Homo sapi	C 941	132.4	4.7	1468	10	BC068202	Rattus no
869	133.2	4.7	1372	9	BC024221	BC024221 Homo sapi	C 942	132.4	4.7	2417	9	HSN800967	Sequence
870	133.2	4.7	1383	5	BC056115	BC056115 Xenopus l	C 943	132.4	4.7	2500	10	BC058946	Mus muscu
871	133.2	4.7	1756	9	BC069223	BC069223 Homo sapi	C 944	132.4	4.7	2607	5	BC0584610	Danio rer
C 872	133.2	4.7	4459	9	HSN804634	AL833321 Homo sapi	C 945	132.4	4.7	2788	9	AF111847	Homo sapi
C 873	133.2	4.7	8186	6	AX344682	AX344682 Sequence	C 946	132.4	4.7	3383	9	HSN803701	Homo sapi
C 874	133.2	4.7	9021	6	AX347134	AX347134 Sequence	C 947	132.4	4.7	3491	5	BC059285	Xenopus l
C 875	133.2	4.7	9021	6	AX347426	AX347426 Sequence	C 948	132.4	4.7	4169	10	BC053919	Mus muscu
C 876	133.2	4.7	9021	6	AX348462	AX348462 Sequence	C 949	132.4	4.7	4969	9	HSN806817	Homo sapi
C 877	133.2	4.7	9021	6	AX349147	AX349147 Sequence	C 950	132.4	4.7	61155	2	AC074069	Homo sapi
C 878	133.2	4.7	9021	6	AX657808	AX657808 Sequence	C 951	132.2	4.6	539	6	CQ523463	Sequence
C 879	133.2	4.7	9021	6	AX659082	AX659082 Sequence	C 952	132.2	4.6	878	6	AX482482	Sequence
C 880	133.2	4.7	203657	2	BS927302	BS927302 Danio rer	C 953	132.2	4.6	1359	5	BC053194	Danio rer
881	133.2	4.7	231972	2	AC068055	AC068055 Homo sapi	C 954	132.2	4.6	2161	6	CQ414527	Sequence
C 882	133.2	4.7	340089	2	AC104922	AC104922 Mus muscu	C 955	132	4.6	390	6	CQ410737	Sequence
C 883	133.2	4.7	349980	6	AX344560	AX344560 Sequence	C 956	132	4.6	545	6	AX185705	Sequence
C 884	133	4.7	425	6	CQ506214	CQ506214 Sequence	C 957	132	4.6	681	5	BC055187	Danio rer
C 885	133	4.7	587	9	HSN337540	AJ337540 Homo sapi	C 958	132	4.6	1166	9	BC043545	Homo sapi
886	133	4.7	656	10	BC049555	BC049555 Mus muscu	C 959	132	4.6	2009	3	AK116580	Ciona int
C 887	133	4.7	843	6	CQ484198	CQ484198 Sequence	C 960	132	4.6	2350	9	BC063427	Homo sapi
888	133	4.7	1257	9	BC043535	BC043535 Homo sapi	C 961	132	4.6	71532	2	AC023655	Homo sapi
889	133	4.7	1337	3	AY118704	AY118704 Drosophill	C 962	132	4.6	200124	2	AC111061	Mus muscu
890	133	4.7	1489	9	AB048953	AB048953 Macaca fa	C 963	131.8	4.6	329	6	CQ518231	Sequence
891	133	4.7	2090	9	BC049196	BC049196 Homo sapi	C 964	131.8	4.6	768	9	CQ432402	Sequence
892	133	4.7	2216	5	BC054636	BC054636 Danio rer	C 965	131.8	4.6	1094	9	BC039173	Homo sapi
893	133	4.7	2293	5	BC070538	BC070538 Xenopus l	C 966	131.8	4.6	1661	9	BC025753	Homo sapi
894	133	4.7	2722	10	BC075615	BC075615 Mus muscu	C 967	131.8	4.6	2674	6	AK183261	Sequence
895	133	4.7	4185	9	BC050532	BC050532 Homo sapi	C 968	131.8	4.6	2674	6	AR456323	Sequence

969	131.8	4.6	3345	9	BC041132	Homo sapi	1042	130.6	4.6	1560	9	BC032420	Homo sapi
970	131.8	4.6	4670	9	AF104032		1043	130.6	4.6	1985	5	BD275145	48 Human
971	131.6	4.6	308	6	C0517578		1044	130.6	4.6	2690	5	BC077100	Danio rer
972	131.6	4.6	720	10	BC061086		1045	130.6	4.6	5165	6	C0413028	Sequence
973	131.6	4.6	1051	6	AR164814	Sequence	c1046	130.6	4.6	9770	6	AX344934	Sequence
974	131.6	4.6	1051	6	AR490614	Sequence	1047	130.6	4.6	132374	2	AC026503	Homo sapi
975	131.6	4.6	1051	6	AR532388	Sequence	1048	130.6	4.6	420	6	C0526488	Sequence
976	131.6	4.6	1728	9	AB070110	Macaca fa	1049	130.4	4.6	466	6	C0526037	Sequence
977	131.6	4.6	1773	9	BC037559	Homo sapi	c1050	130.4	4.6	668	6	C0397705	Sequence
978	131.6	4.6	6668	6	AX346599	Sequence	c1051	130.4	4.6	668	6	C0404002	Sequence
979	131.6	4.6	186882	2	AC107855	Mus muscu	c1052	130.4	4.6	749	9	HS4336745	Homo sapi
980	131.4	4.6	351	6	C0526060	Sequence	1053	130.4	4.6	1665	9	BC041446	Homo sapi
981	131.4	4.6	453	6	C0524875	Sequence	1054	130.4	4.6	1738	6	AR560934	Sequence
982	131.4	4.6	586	6	C0524455	Sequence	1055	130.4	4.6	1738	8	BT009079	Triticum
983	131.4	4.6	2165	5	BC054602	Danio rer	1056	130.4	4.6	3399	9	BC063840	Homo sapi
984	131.4	4.6	2747	9	BC025706	Homo sapi	1057	130.4	4.6	3582	10	BC053927	Mus muscu
985	131.4	4.6	4606	10	BC058089		c1058	130.4	4.6	8607	6	AR453095	Sequence
986	131.4	4.6	58890	2	AC110050	Homo sapi	c1059	130.4	4.6	8607	6	AX281207	Sequence
987	131.4	4.6	126038	2	AC016068	Homo sapi	c1060	130.4	4.6	8607	6	AX356478	Sequence
988	131.4	4.6	173585	2	AC021113	Homo sapi	c1061	130.4	4.6	9547	6	AX346406	Sequence
989	131.2	4.6	490	6	C0523744	Sequence	c1062	130.4	4.6	45210	2	AC087043	Homo sapi
990	131.2	4.6	543	6	C0524637	Sequence	c1063	130.4	4.6	57121	2	AC084255	Homo sapi
991	131.2	4.6	1232	10	BC060554	Rattus no	c1064	130.4	4.6	193988	2	AC102269	Mus muscu
992	131.2	4.6	1673	6	AX772808	Sequence	c1065	130.2	4.6	510	6	C0399174	Sequence
993	131.2	4.6	1775	5	BC053257	Danio rer	1067	130.2	4.6	561	10	BC049674	Mus muscu
994	131.2	4.6	1882	5	BC068036	Xenopus t	1068	130.2	4.6	2270	9	HS806047	Homo sapi
995	131.2	4.6	2000	9	BC063423	Homo sapi	1069	130.2	4.6	2728	5	BC081123	Xenopus t
996	131.2	4.6	2080	10	BC013564	Mus muscu	1070	130	4.6	407	6	C0522526	Sequence
997	131.2	4.6	3050	5	BC066571	Danio rer	1071	130	4.6	1265	9	BC033301	Homo sapi
998	131.2	4.6	3640	9	HS806825	Homo sapi	1072	130	4.6	1715	5	BC067176	Danio rer
999	131.2	4.6	4744	5	BC066770	Xenopus l	1073	130	4.6	2246	9	BC051820	Homo sapi
1000	131.2	4.6	147499	2	AX178788	Canis fam	c1074	130	4.6	56857	2	AC021917	Homo sapi
1001	131	4.6	383	6	C0502211	Sequence	c1075	130	4.6	91034	2	AC025911	Mus muscu
1002	131	4.6	383	6	C0511079	Sequence	1076	130	4.6	26970	2	AC098406	Rattus no
1003	131	4.6	423	6	C0523358	Sequence	c1077	129.8	4.6	173	6	AX185626	Sequence
1004	131	4.6	470	6	C0514078	Sequence	1078	129.8	4.6	1156	5	BC049488	Danio rer
1005	131	4.6	498	6	C0481059	Sequence	1079	129.8	4.6	2029	10	BC050265	Mus muscu
1006	131	4.6	574	6	C0525654	Sequence	1080	129.8	4.6	2709	10	BC054846	Mus muscu
1007	131	4.6	1243	9	HS802621	Homo sapi	1081	129.8	4.6	2759	10	BC055046	Mus muscu
1008	131	4.6	1348	9	BC070154	Homo sapi	1082	129.8	4.6	3300	9	BC011656	Homo sapi
1009	131	4.6	3420	10	BC074017	Rattus no	1083	129.8	4.6	3326	9	HS808512	Homo sapi
1010	131	4.6	3626	9	BC012147	Homo sapi	1084	129.8	4.6	3850	10	BC063749	Mus muscu
1011	131	4.6	4180	10	BC042645	Mus muscu	c1085	129.8	4.6	141003	2	AC016463	Homo sapi
1012	131	4.6	5198	6	AX345181	Sequence	1086	129.6	4.6	1128	9	BC071732	Homo sapi
1013	131	4.6	5750	6	AX251465	Sequence	1087	129.6	4.6	1175	9	BC049386	Homo sapi
1014	131	4.6	5750	6	AX346910	Sequence	1088	129.6	4.6	1287	3	BT009948	Drosophil
1015	131	4.6	6027	6	AX344764	Sequence	1089	129.6	4.6	1397	6	C0491382	Sequence
1016	131	4.6	6577	6	AX251920	Sequence	1090	129.6	4.6	1402	9	BC040630	Homo sapi
1017	131	4.6	6577	6	AX346258	Sequence	1091	129.6	4.6	1487	4	AY423736	Tachyglos
1018	131	4.6	6577	6	AX348993	Sequence	1092	129.6	4.6	2247	9	BC009648	Homo sapi
1019	131	4.6	68280	2	AC116016	Homo sapi	1093	129.6	4.6	3038	9	HS806221	Sequence
1020	131	4.6	73778	6	AX344562	Sequence	1094	129.6	4.6	5277	9	HS8086645	Homo sapi
1021	131	4.6	173224	2	AC116813	Mus muscu	c1095	129.6	4.6	8342	6	AX345403	Sequence
1022	131	4.6	263319	2	AC125258	Mus muscu	1096	129.6	4.6	211348	2	EX927237	Danio rer
1023	131	4.6	349980	6	AX344561	Sequence	1097	129.4	4.5	603	6	C0526797	Sequence
1024	130.8	4.6	364	6	C0399251	Sequence	c1098	129.4	4.5	743	9	HS4335471	Homo sapi
1025	130.8	4.6	364	6	C0405529	Sequence	1099	129.4	4.5	1130	10	BC043698	Mus muscu
1026	130.8	4.6	1447	6	AR237880	Sequence	1100	129.4	4.5	1429	10	BC022900	Mus muscu
1027	130.8	4.6	1651	10	BC024872	Mus muscu	1101	129.4	4.5	1499	9	BC042195	Homo sapi
1028	130.8	4.6	1850	9	BC040123	Homo sapi	1102	129.4	4.5	1711	9	BC032509	Homo sapi
1029	130.8	4.6	1905	9	BC032703	Homo sapi	1103	129.4	4.5	1760	9	BC051807	Homo sapi
1030	130.8	4.6	2053	9	BC030196	Homo sapi	1104	129.4	4.5	1789	9	BC070134	Homo sapi
1031	130.8	4.6	2265	10	BC051639	Mus muscu	1105	129.4	4.5	1946	9	HS808123	Sequence
1032	130.8	4.6	2336	5	BC072340	Xenopus l	1106	129.4	4.5	1994	3	AX116078	Ciona int
1033	130.8	4.6	3941	9	HS8083636	Homo sapi	1107	129.4	4.5	2150	6	C0882012	Sequence
1034	130.8	4.6	7906	6	AX277935	Sequence	1108	129.4	4.5	2287	6	C0882010	Sequence
1035	130.8	4.6	7906	6	AX323622	Sequence	1109	129.4	4.5	2287	6	BC044220	Homo sapi
1036	130.8	4.6	7906	6	AX344771	Sequence	1110	129.4	4.5	2367	9	HS801757	Sequence
1037	130.6	4.6	501	6	C0411817	Sequence	1111	129.4	4.5	2508	10	BC079036	Rattus no
1038	130.6	4.6	580	10	BC006049	Mus muscu	1112	129.4	4.5	2610	10	BC083267	Mus muscu
1039	130.6	4.6	870	6	BD231669	31 human	1113	129.4	4.5	2922	3	AF479582	Boophilus
1040	130.6	4.6	977	9	BC051846	Homo sapi	1114	129.4	4.5	4651	9	BC042656	Homo sapi
1041	130.6	4.6	1280	9	BC047365	Homo sapi							

c1115	129.4	4.5	4990	6	CQ493127	Sequence	1188	128.4	4.5	1976	9	BC040113	Homo sapi
c1116	129.4	4.5	4990	6	CQ493522	Sequence	1189	128.4	4.5	1978	9	BC012750	Homo sapi
c1117	129.4	4.5	5908	6	AX251914	Sequence	1190	128.4	4.5	1990	9	AK000212	Homo sapi
c1118	129.4	4.5	5908	6	AX277930	Sequence	c1191	128.4	4.5	113515	6	AX347077	Sequence
c1119	129.4	4.5	5908	6	AX323617	Sequence	1192	128.2	4.5	299	6	CQ669036	Sequence
c1120	129.4	4.5	6112	6	AX345565	Sequence	1193	128.2	4.5	335	10	BC048511	Mus muscu
c1121	129.4	4.5	6338	6	AX346028	Sequence	c1194	128.2	4.5	385	6	CQ398297	Sequence
c1122	129.4	4.5	7058	6	AX348438	Sequence	c1195	128.2	4.5	385	6	CQ404584	Sequence
c1123	129.4	4.5	8298	6	AX344783	Sequence	1196	128.2	4.5	1004	9	BC043536	Homo sapi
c1124	129.4	4.5	9268	6	AX346503	Sequence	1197	128.2	4.5	1350	10	BC072695	Rattus no
c1125	129.4	4.5	9515	6	AX277997	Sequence	1198	128.2	4.5	1846	9	BC038379	Homo sapi
c1126	129.4	4.5	9515	6	AX323694	Sequence	1199	128.2	4.5	2035	9	BC063696	Homo sapi
c1127	129.4	4.5	9515	6	AX344837	Sequence	1200	128.2	4.5	2085	5	BC077186	Xenopus l
1128	129.4	4.5	185292	2	BX957342	Danio rer	1201	128.2	4.5	2139	5	BC054626	Danio rer
1129	129.2	4.5	267	6	CQ525163	Sequence	1202	128.2	4.5	2633	9	AL833388	Homo sapi
1130	129.2	4.5	567	6	CQ527262	Sequence	1203	128.2	4.5	2946	5	BC076976	Xenopus t
1131	129.2	4.5	1926	5	BC084091	Sequence	c1204	128.2	4.5	6960	6	AX347301	Sequence
1132	129.2	4.5	2840	5	BC056558	Danio rer	c1205	128.2	4.5	62359	2	AC116167	Homo sapi
1133	129.2	4.5	3110	10	BC057617	Sequence	1206	128	4.5	504	6	CQ526419	Sequence
c1134	129.2	4.5	70511	2	AC091083	Sequence	1207	128	4.5	539	6	CQ526970	Sequence
c1135	129.2	4.5	257700	2	AC147391	Pan trogl	1208	128	4.5	606	6	CQ524188	Sequence
1136	129	4.5	247	6	CQ677559	Sequence	1209	128	4.5	1347	10	BC008980	Mus muscu
1137	129	4.5	317	6	CQ526915	Sequence	1210	128	4.5	1469	6	BD260697	50 human
1138	129	4.5	1414	10	BC005487	Mus muscu	1211	128	4.5	1470	9	BC072387	Homo sapi
1139	129	4.5	1527	5	BC064182	Xenopus t	1212	128	4.5	1627	9	BC039584	Homo sapi
1140	129	4.5	1615	9	AF218014	Homo sapi	1213	128	4.5	2002	9	BC068030	Homo sapi
1141	129	4.5	1817	10	BC083562	Sequence	1214	128	4.5	2212	10	BC046775	Mus muscu
1142	129	4.5	2630	9	BC038222	Homo sapi	1215	128	4.5	2500	9	BC065207	Mus muscu
1143	129	4.5	3446	9	HSN802955	Homo sapi	1216	128	4.5	2754	10	BC066817	Mus muscu
c1144	129	4.5	145992	2	CR339064	Danio rer	1217	128	4.5	3060	6	AR252731	Sequence
1145	128.8	4.5	208	6	CQ677600	Sequence	1218	128	4.5	3060	6	AX055476	Sequence
1146	128.8	4.5	373	6	CQ526228	Sequence	1219	128	4.5	3060	6	AX089948	Sequence
1147	128.8	4.5	471	6	CQ515907	Sequence	1220	128	4.5	3060	6	AX358962	Sequence
1148	128.8	4.5	1010	10	BC061971	Rattus no	1221	128	4.5	3060	6	AX362455	Sequence
1149	128.8	4.5	1011	9	BC020756	Homo sapi	1222	128	4.5	3060	6	AX403617	Sequence
1150	128.8	4.5	1462	10	BC006018	Mus muscu	1223	128	4.5	3060	6	AX454694	Sequence
1151	128.8	4.5	1588	9	BC070183	Homo sapi	1224	128	4.5	3060	6	AX491172	Sequence
1152	128.8	4.5	1706	5	BC082351	Xenopus l	c1225	128	4.5	81120	2	AC022851	Homo sapi
1153	128.8	4.5	1838	10	BC083573	Rattus no	1226	127.8	4.5	223	6	CQ523534	Sequence
1154	128.8	4.5	2245	9	HSN803715	Homo sapi	1227	127.8	4.5	439	6	CQ518358	Sequence
1155	128.8	4.5	3251	5	BC074658	Xenopus t	1228	127.8	4.5	535	6	CQ471891	Sequence
1156	128.8	4.5	3894	10	BC053925	Mus muscu	c1229	127.8	4.5	660	8	CNS01C1X	Botrytis
c1157	128.8	4.5	109082	2	AC026133	Homo sapi	1230	127.8	4.5	935	10	BC061157	Mus muscu
c1158	128.8	4.5	258622	2	AC020877	Homo sapi	c1231	127.8	4.5	936	8	AJ840640	Arabidops
1159	128.6	4.5	319	6	CQ5270102	Sequence	1232	127.8	4.5	1408	9	BC065718	Homo sapi
1160	128.6	4.5	332	6	CQ523998	Sequence	1233	127.8	4.5	1765	9	BC063438	Homo sapi
c1161	128.6	4.5	360	6	CQ427909	Sequence	1234	127.8	4.5	1880	6	CQ769491	Sequence
c1162	128.6	4.5	363	6	CQ397318	Sequence	1235	127.8	4.5	2445	9	BC019562	Homo sapi
c1163	128.6	4.5	363	6	CQ403817	Sequence	1236	127.8	4.5	2530	9	BC036868	Homo sapi
1164	128.6	4.5	527	10	BC049658	Mus muscu	1237	127.8	4.5	2750	5	BC084264	Xenopus l
1165	128.6	4.5	607	5	BC049055	Danio rer	c1238	127.8	4.5	3223	6	CQ806938	Sequence
c1166	128.6	4.5	768	6	CQ432391	Sequence	c1239	127.8	4.5	3223	6	CQ807212	Sequence
1167	128.6	4.5	1076	10	BC062802	Rattus no	1240	127.8	4.5	3307	9	BC025714	Homo sapi
1168	128.6	4.5	1205	9	BC039058	Homo sapi	c1241	127.8	4.5	67776	2	AC101220	Mus muscu
1169	128.6	4.5	1426	5	BC0543250	Xenopus l	c1242	127.8	4.5	83440	2	AC024285	Homo sapi
1170	128.6	4.5	1567	9	HSN806640	Homo sapi	c1243	127.8	4.5	301026	2	BX004844	Danio rer
1171	128.6	4.5	1608	9	AX358187	Homo sapi	1244	127.6	4.5	674	6	AR283453	Sequence
1172	128.6	4.5	1690	9	BC049211	Homo sapi	1245	127.6	4.5	674	6	AR344221	Sequence
1173	128.6	4.5	1722	5	BC063371	Xenopus t	1246	127.6	4.5	674	6	AR351422	Sequence
1174	128.6	4.5	2085	9	BC029120	Homo sapi	1247	127.6	4.5	674	6	AR454002	Sequence
1175	128.6	4.5	2337	9	HSN800876	Homo sapi	1248	127.6	4.5	674	6	AR561590	Sequence
1176	128.6	4.5	2377	8	AY080711	Arabidops	1249	127.6	4.5	674	6	AX282972	Sequence
1177	128.6	4.5	3676	10	BC062923	Mus muscu	1250	127.6	4.5	674	6	AX303145	Sequence
1178	128.6	4.5	4818	9	HSN807492	Homo sapi	1251	127.6	4.5	745	10	BC049606	Mus muscu
1179	128.4	4.5	458	10	BC061002	Sequence	1252	127.6	4.5	2661	10	BC026137	Mus muscu
1180	128.4	4.5	569	6	BD223440	94 human	1253	127.6	4.5	3856	9	HSN805531	Sequence
1181	128.4	4.5	569	6	AR243074	Sequence	c1254	127.6	4.5	8305	6	AX346470	Sequence
1182	128.4	4.5	569	6	AR404255	Sequence	c1255	127.6	4.5	56693	2	AC084077	Homo sapi
1183	128.4	4.5	633	5	BC057512	Danio rer	c1256	127.6	4.5	60565	2	AC023852	Homo sapi
1184	128.4	4.5	806	5	CR405924	Gallus ga	c1257	127.4	4.5	807	6	CQ428748	Sequence
1185	128.4	4.5	816	6	CQ486689	Sequence	1258	127.4	4.5	839	9	BC043574	Homo sapi
1186	128.4	4.5	1065	10	BC049675	Mus muscu	c1259	127.4	4.5	840	8	CNS018QK	Botrytis
1187	128.4	4.5	1889	9	BC073841	Homo sapi	1260	127.4	4.5	1027	9	BC041442	Homo sapi

1261	127.4	4.5	1319	9	BC015490	BC015490 Homo sapi	1334	126.4	4.4	861	10	BC049709	BC049709 Mus muscu
1262	127.4	4.5	1331	6	C0776637	C0776637 Sequence	1335	126.4	4.4	919	5	BC079985	BC079985 Xenopus l
1263	127.4	4.5	1923	9	AB093671	AB093671 Macaca fa	1336	126.4	4.4	1280	5	BC063439	BC063439 Homo sapi
1264	127.4	4.5	3686	10	BC043709	BC043709 Mus muscu	1337	126.4	4.4	1410	5	BC049418	BC049418 Danto rer
1265	127.4	4.5	4298	9	HS0804564	AL833251 Homo sapi	1338	126.4	4.4	2072	9	BC044245	BC044245 Homo sapi
1266	127.4	4.5	4438	10	BC067016	BC067016 Mus muscu	1339	126.4	4.4	2106	5	BC075571	BC075571 Xenopus t
1267	127.4	4.5	4829	10	BC060175	BC060175 Mus muscu	1340	126.4	4.4	2314	5	BC068218	BC068218 Xenopus t
1268	127.4	4.5	5251	10	BC065072	BC065072 Mus muscu	1341	126.4	4.4	2355	9	HS0801346	AL133075 Homo sapi
cl1269	127.4	4.5	13606	6	AX251315	AX251315 Sequence	1342	126.4	4.4	2415	9	BC028002	BC028002 Homo sapi
cl1270	127.4	4.5	13606	6	AX278002	AX278002 Sequence	1343	126.4	4.4	2421	10	BC061106	BC061106 Homo sapi
cl1271	127.4	4.5	13606	6	AX323699	AX323699 Sequence	1344	126.4	4.4	2607	9	BC053734	BC053734 Homo sapi
cl1272	127.4	4.5	13606	6	AX346712	AX346712 Sequence	1345	126.4	4.4	2611	9	BC041438	BC041438 Homo sapi
1273	127.4	4.5	164288	2	AC128949	AC128949 Rattus no	1346	126.4	4.4	3036	9	AF090896	AF090896 Homo sapi
1274	127.4	4.5	284160	2	AC107858	AC107858 Mus muscu	1347	126.4	4.4	3082	10	BC046972	BC046972 Mus muscu
1275	127.2	4.5	466	6	C0522677	C0522677 Sequence	1348	126.4	4.4	3401	9	BC040376	BC040376 Homo sapi
1276	127.2	4.5	1400	9	BC063708	BC063708 Homo sapi	1349	126.4	4.4	3487	10	BC016095	BC016095 Mus muscu
1277	127.2	4.5	3499	10	BC007476	BC007476 Mus muscu	cl1350	126.4	4.4	9963	6	AX345596	AX345596 Sequence
1278	127.2	4.5	3501	5	BC076842	BC076842 Xenopus l	cl1351	126.4	4.4	34980	6	AX344550	AX344550 Sequence
1279	127.2	4.5	4124	3	AK112284	AK112284 Ciona int	cl1352	126.2	4.4	414	6	CQ397915	CQ397915 Sequence
1280	127.2	4.5	31825	2	AC111154	AC111154 Homo sapi	cl1353	126.2	4.4	414	6	CQ404208	CQ404208 Sequence
cl1281	127.2	4.5	61363	2	AC068364	AC068364 Homo sapi	1354	126.2	4.4	452	6	CQ527434	CQ527434 Sequence
cl1282	127.2	4.5	73885	2	AC025307	AC025307 Homo sapi	1355	126.2	4.4	585	6	CQ526237	CQ526237 Sequence
cl1283	127.2	4.5	81358	2	AC023330	AC023330 Homo sapi	1356	126.2	4.4	997	9	BC047943	BC047943 Homo sapi
1284	127.2	4.5	110000	8	CR382131	Continuation (4 of	1357	126.2	4.4	1073	9	BC032697	BC032697 Homo sapi
1285	127.2	4.5	167728	2	AC115889	AC115889 Mus muscu	1358	126.2	4.4	1568	5	BC050177	BC050177 Danto rer
cl1286	127.2	4.5	178802	2	AC140116	AC140116 Rattus no	1359	126.2	4.4	1886	9	AX025084	AX025084 Homo sapi
cl1287	127.2	4.5	22962	2	AC079520	AC079520 Mus muscu	1360	126.2	4.4	2064	10	BC053424	BC053424 Mus muscu
1288	127	4.5	127	6	B0021987	B0021987 Secreted	1361	126.2	4.4	2692	3	AK173351	AK173351 Ciona int
1289	127	4.5	421	6	CQ526039	CQ526039 Sequence	1362	126.2	4.4	2773	6	AX252502	AX252502 Sequence
1290	127	4.5	481	6	CQ525180	CQ525180 Sequence	1363	126.2	4.4	2773	6	AX092302	AX092302 Sequence
1291	127	4.5	885	3	AK174656	AK174656 Ciona int	1364	126.2	4.4	2773	6	AX376082	AX376082 Sequence
1292	127	4.5	1445	9	BC063545	BC063545 Homo sapi	1365	126.2	4.4	2773	6	AX403291	AX403291 Sequence
1293	127	4.5	1805	9	AB070053	AB070053 Macaca fa	1366	126.2	4.4	2773	9	AX358338	AX358338 Homo sapi
1294	127	4.5	1842	9	BC024042	BC024042 Homo sapi	1367	126.2	4.4	2920	3	AK174466	AK174466 Ciona int
1295	127	4.5	1959	9	BC043548	BC043548 Homo sapi	1368	126.2	4.4	3203	5	BC077358	BC077358 Xenopus l
1296	127	4.5	2150	9	BC025715	BC025715 Homo sapi	1369	126.2	4.4	3547	5	BC084146	BC084146 Xenopus t
1297	127	4.5	2178	9	BC046358	BC046358 Homo sapi	1370	126.2	4.4	5599	10	BC049182	BC049182 Mus muscu
1298	127	4.5	2557	9	BC042875	BC042875 Homo sapi	1371	126.2	4.4	227370	2	AC116888	AC116888 Mus muscu
1299	127	4.5	5891	9	HS080449	AL833188 Homo sapi	1372	126.2	4.4	321708	2	AC087142	AC087142 Mus muscu
1300	126.8	4.5	547	6	CQ526009	CQ526009 Sequence	1373	126	4.4	464	6	CQ523466	CQ523466 Sequence
cl1301	126.8	4.5	606	6	CQ503221	CQ503221 Sequence	1374	126	4.4	519	6	CQ522478	CQ522478 Sequence
cl1302	126.8	4.5	606	6	CQ512068	CQ512068 Sequence	1375	126	4.4	528	10	BC049628	BC049628 Mus muscu
cl1303	126.8	4.5	870	6	CQ482086	CQ482086 Sequence	cl1376	126	4.4	644	9	HS0331225	AD331225 Homo sapi
1304	126.8	4.5	948	10	BC031442	BC031442 Mus muscu	1377	126	4.4	1457	6	BD231695	BD231695 31 human
1305	126.8	4.5	1034	9	AX026865	AX026865 Homo sapi	1378	126	4.4	1801	14	SCU78817	U78817 Saccharomyc
1306	126.8	4.5	1286	10	BC062175	BC062175 Mus muscu	1379	126	4.4	2081	10	BC043712	BC043712 Mus muscu
1307	126.8	4.5	2320	10	BC046962	BC046962 Mus muscu	1380	126	4.4	2108	5	BC084490	BC084490 Xenopus t
1308	126.8	4.5	4064	10	BC072632	BC072632 Mus muscu	1381	126	4.4	2406	9	BC017107	BC017107 Homo sapi
cl1309	126.8	4.5	6485	6	AX251313	AX251313 Sequence	1382	126	4.4	2642	5	BC068637	BC068637 Xenopus l
cl1310	126.8	4.5	6485	6	AX346710	AX346710 Sequence	1383	126	4.4	2767	10	BC014695	BC014695 Mus muscu
cl1311	126.8	4.5	123257	2	AC010694	AC010694 Drosophil	1384	126	4.4	2841	10	BC045601	BC045601 Mus muscu
cl1312	126.8	4.5	143585	2	AC013349	AC013349 Homo sapi	1385	125.8	4.4	300	6	BD213699	BD213699 Novel hum
cl1313	126.8	4.5	156550	2	AC015830	AC015830 Homo sapi	1386	125.8	4.4	381	3	AF159974	AF159974 Buthus ma
1314	126.8	4.5	256944	2	AC138343	AC138343 Mus muscu	1387	125.8	4.4	487	10	BC069220	BC069220 Mus muscu
1315	126.6	4.4	323	6	CQ5224910	CQ5224910 Sequence	1388	125.8	4.4	510	6	CQ526266	CQ526266 Sequence
1316	126.6	4.4	488	6	CQ522468	CQ522468 Sequence	1389	125.8	4.4	700	5	BC051617	BC051617 Danto rer
cl1317	126.6	4.4	656	9	HS0337512	AX3737512 Homo sapi	1390	125.8	4.4	793	9	BC018189	BC018189 Homo sapi
cl1318	126.6	4.4	696	6	CQ422213	CQ422213 Sequence	1391	125.8	4.4	847	9	BC053571	BC053571 Homo sapi
1319	126.6	4.4	1591	9	BC050659	BC050659 Homo sapi	1392	125.8	4.4	1319	9	BC003683	BC003683 Homo sapi
1320	126.6	4.4	1690	9	BC011595	BC011595 Homo sapi	1393	125.8	4.4	1331	10	BC030915	BC030915 Mus muscu
1321	126.6	4.4	1781	5	BC064253	BC064253 Xenopus t	1394	125.8	4.4	1650	9	AB047615	AB047615 Macaca fa
1322	126.6	4.4	1993	3	AK112520	AK112520 Ciona int	1395	125.8	4.4	1706	3	AK112205	AK112205 Ciona int
1323	126.6	4.4	2230	5	BC078288	BC078288 Danto rer	1396	125.8	4.4	1719	3	AK116650	AK116650 Ciona int
1324	126.6	4.4	2240	5	BC084150	BC084150 Xenopus t	1397	125.8	4.4	2082	6	AR059958	AR059958 Sequence
1325	126.6	4.4	2360	9	BC063595	BC063595 Homo sapi	1398	125.8	4.4	2190	9	BC063454	BC063454 Homo sapi
1326	126.6	4.4	2578	9	AB049758	AB049758 Homo sapi	1399	125.8	4.4	3498	5	BC065688	BC065688 Danto rer
1327	126.6	4.4	2924	6	AX683129	AX683129 Sequence	cl1400	125.8	4.4	17721	6	AX346631	AX346631 Dictyoste
1328	126.6	4.4	2924	10	S68736	S68736 Rattus sp.	cl1401	125.8	4.4	151802	3	AC114263	AC114263 Dictyoste
1329	126.6	4.4	3669	10	BC038376	BC038376 Mus muscu	1402	125.8	4.4	172105	2	AC021197	AC021197 Homo sapi
cl1330	126.6	4.4	58571	2	AC023309	AC023309 Homo sapi	1403	125.6	4.4	360	6	CQ524586	CQ524586 Sequence
cl1331	126.6	4.4	154314	2	BX901927	BX901927 Danto rer	cl1404	125.6	4.4	384	6	CQ395463	CQ395463 Sequence
1332	126.4	4.4	247	6	CQ524931	CQ524931 Sequence	cl1405	125.6	4.4	384	6	CQ401799	CQ401799 Sequence
1333	126.4	4.4	263	6	CQ663258	CQ663258 Sequence	1406	125.6	4.4	1164	8	BT009497	BT009497 Triticum

1407	125.6	4.4	2223	5	BC067619	BC067619	Danio rer
1408	125.6	4.4	2735	9	BC046366	BC046366	Homo sapi
c1409	125.6	4.4	8234	6	AX346551	AX346551	Sequence
c1410	125.6	4.4	74119	2	AP036177	AP036177	Homo sapi
1411	125.6	4.4	114897	2	AP003624	AP003624	Oryza sat
c1412	125.6	4.4	134867	2	AC013788	AC013788	Homo sapi
1413	125.6	4.4	220752	2	AC129776	AC129776	Mus muscu
1414	125.4	4.4	270	6	CQ655781	CQ655781	Sequence
1415	125.4	4.4	506	6	CQ518031	CQ518031	Sequence
1416	125.4	4.4	791	5	CQ077926	CQ077926	Xenopus 1
1417	125.4	4.4	1894	9	AB063046	AB063046	Macaca fa
1418	125.4	4.4	2430	10	BC067202	BC067202	Mus muscu
1419	125.4	4.4	6251	10	BC050823	BC050823	Mus muscu
1420	125.4	4.4	110000	2	AL954350.4	Continuation (5 of	
c1421	125.4	4.4	202872	2	AC016160	AC016160	Homo sapi
c1422	125.4	4.4	234081	3	PFMALAP2	AL035475	Plasmodiu
c1423	125.2	4.4	237	6	AX284920	AX284920	Sequence
1424	125.2	4.4	328	6	CQ524509	CQ524509	Sequence
1425	125.2	4.4	403	6	CQ527098	CQ527098	Sequence
c1426	125.2	4.4	425	6	CQ398427	CQ398427	Sequence
c1427	125.2	4.4	425	6	CQ404714	CQ404714	Sequence
1428	125.2	4.4	472	6	CQ518059	CQ518059	Sequence
c1429	125.2	4.4	664	9	HSN327335	HSN327335	Homo sapi
1430	125.2	4.4	831	9	AB070038	AB070038	Macaca fa
1431	125.2	4.4	1501	10	BC039998	BC039998	Mus muscu
1432	125.2	4.4	1958	10	BC023841	BC023841	Mus muscu
1433	125.2	4.4	3250	5	BC068779	BC068779	Xenopus 1
1434	125.2	4.4	3997	6	AX086658	AX086658	Sequence
1435	125.2	4.4	4498	10	BC075723	BC075723	Mus muscu
c1436	125.2	4.4	16167	6	AX281418	AX281418	Sequence
c1437	125.2	4.4	16167	6	AX345985	AX345985	Sequence
c1438	125.2	4.4	16167	6	AX348686	AX348686	Sequence
1439	125.2	4.4	50978	2	AC084751	AC084751	Homo sapi
1440	125.2	4.4	198907	2	AC109232	AC109232	Mus muscu
1441	125.2	4.4	289973	2	AC135678	AC135678	Rattus no
c1442	125	4.4	567	6	AX186756	AX186756	Sequence
1443	125	4.4	580	6	CQ526169	CQ526169	Sequence
c1444	125	4.4	622	6	CQ427774	CQ427774	Sequence
1445	125	4.4	1092	10	BC005748	BC005748	Mus muscu
1446	125	4.4	1155	9	BC036792	BC036792	Homo sapi
1447	125	4.4	1517	9	BC016152	BC016152	Homo sapi
1448	125	4.4	1591	10	AB041801	AB041801	Mus muscl
1449	125	4.4	2005	10	BC052682	BC052682	Mus muscu
1450	125	4.4	475	9	BC013372	BC013372	Homo sapi
1451	125	4.4	2012	9	AY125488	AY125488	Homo sapi
1452	125	4.4	2683	10	BC052924	BC052924	Mus muscu
1453	125	4.4	2820	10	BC062390	BC062390	Rattus no
1454	125	4.4	3983	9	HSN803572	HSN803572	Homo sapi
1455	125	4.4	4083	10	BC075708	BC075708	Mus muscu
1456	125	4.4	5325	9	HSN806205	HSN806205	Homo sapi
1457	125	4.4	52359	2	AC010772	AC010772	Homo sapi
1458	125	4.4	174384	2	AC009524	AC009524	Homo sapi
1459	124.8	4.4	221	6	CQ685593	CQ685593	Sequence
c1460	124.8	4.4	436	6	CQ397977	CQ397977	Sequence
c1461	124.8	4.4	436	6	CQ404269	CQ404269	Sequence
1462	124.8	4.4	447	6	CQ526217	CQ526217	Sequence
c1463	124.8	4.4	726	9	HSN327951	HSN327951	Homo sapi
1464	124.8	4.4	942	5	BC049498	BC049498	Danio rer
1465	124.8	4.4	1108	10	BC033259	BC033259	Mus muscu
1466	124.8	4.4	1630	9	BC039130	BC039130	Homo sapi
1467	124.8	4.4	1653	8	BT009403	BT009403	Triticum
1468	124.8	4.4	1930	5	BC066725	BC066725	Danio rer
1469	124.8	4.4	2196	9	HSN805743	HSN805743	Homo sapi
1470	124.8	4.4	2926	9	HSN808549	HSN808549	Homo sapi
1471	124.8	4.4	2968	9	BC060758	BC060758	Homo sapi
1472	124.8	4.4	3485	5	BC084302	BC084302	Xenopus 1
1473	124.8	4.4	3686	10	BC023773	BC023773	Mus muscu
1474	124.8	4.4	4727	5	BC070018	BC070018	Danio rer
c1475	124.8	4.4	131271	2	AC015927	AC015927	Homo sapi
c1476	124.6	4.4	268	6	CQ506876	CQ506876	Sequence
c1477	124.6	4.4	291	6	CQ398062	CQ398062	Sequence
c1478	124.6	4.4	291	6	CQ404353	CQ404353	Sequence
1479	124.6	4.4	299	6	CQ397773	CQ397773	Sequence
c1480	124.6	4.4	299	6	CQ404070	CQ404070	Sequence
c1481	124.6	4.4	503	6	CQ524887	CQ524887	Sequence
c1482	124.6	4.4	534	6	AX284254	AX284254	Sequence
1483	124.6	4.4	743	10	BC034898	BC034898	Mus muscu
1484	124.6	4.4	860	9	BC038839	BC038839	Homo sapi
1485	124.6	4.4	1368	9	AB069989	AB069989	Macaca fa
1486	124.6	4.4	1612	9	BC044235	BC044235	Homo sapi
1487	124.6	4.4	1612	9	BC068406	BC068406	Danio rer
1488	124.6	4.4	3914	5	HSN803724	HSN803724	Sequence
1489	124.6	4.4	8059	5	BC076779	BC076779	Xenopus 1
c1490	124.6	4.4	12669	6	AX252150	AX252150	Sequence
c1491	124.6	4.4	12669	6	AX344518	AX344518	Sequence
c1492	124.6	4.4	12669	6	AX348921	AX348921	Sequence
1493	124.6	4.4	155316	2	AC114646	AC114646	Mus muscu
c1494	124.6	4.4	194180	2	AC069140	AC069140	Homo sapi
c1495	124.6	4.4	217621	2	BX901924	BX901924	Danio rer
c1496	124.4	4.4	367	6	CQ417446	CQ417446	Sequence
1497	124.4	4.4	410	6	CQ522484	CQ522484	Sequence
1498	124.4	4.4	607	6	CQ526845	CQ526845	Sequence
c1499	124.4	4.4	779	8	AJ840713	AJ840713	Arabidops
1500	124.4	4.4	2740	9	BC053595	BC053595	Homo sapi
ALIGNMENTS							
RESULT 1	2846 bp DNA linear PAT 20-DEC-2002						
AR252533	Sequence 230 from patent US 6478825.						
LOCUS	AR252533						
DEFINITION	Sequence 230 from patent US 6478825.						
ACCESSION	AR252533						
VERSION	AR252533.1 GI:27300441						
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 2846)						
AUTHORS	Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.						
TITLE	Implant, method of making same and use of the implant for the						
	treatment of bone defects						
JOURNAL	Patent: US 6478825-A 230 12-NOV-2002;						
FEATURES	Location/Qualifiers						
source	1..2846						
	/organism="unknown"						
	/mol_type="genomic DNA"						
ORIGIN							
Query Match	100.0%; Score 2846; DB 6; Length 2846;						
Best Local Similarity	100.0%; Pred.No. 0;						
Matches 2846; Conservative	0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1	CGCTCGGCACACGCGCGCAAGATGAGCTGGTGTCTGGACGCGAGTTGGGGCTCAC	60				
Db	1	CGCTCGGCACACGCGCGCGCAAGATGAGCTGGTGTCTGGACGCGAGTTGGGGCTCAC	60				
Qy	61	TTTTTCTTCAGCTCTCTTCATCTCGTCTCTGCCAAGAGATACACAGTCATTAATGAAGC	120				
Db	61	TTTTTCTTCAGCTCTCTTCATCTCGTCTCTGCCAAGAGATACACAGTCATTAATGAAGC	120				
Qy	121	CTGCCCTGGACAGATGGAATATCATGTCTGGAGTCTGTGTAATATGATCAGATTGA	180				
Db	121	CTGCCCTGGACAGATGGAATATCATGTCTGGAGTCTGTGTAATATGATCAGATTGA	180				
Qy	191	GTGGCTGTGCCCCGGAAGAGGGAAGTCTGGGTGTATACCATCCCTCTCTGCAGGAATGA	240				
Db	191	GTGGCTGTGCCCCGGAAGAGGGAAGTCTGGGTGTATACCATCCCTCTCTGCAGGAATGA	240				
Qy	241	GGAGAAATGAGTGTGATCTCTGCCTGATCCACCCAGAGTTGTACCAATCTTTGAAAC	300				
Db	241	GGAGAAATGAGTGTGATCTCTGCCTGATCCACCCAGAGTTGTACCAATCTTTGAAAC	300				
Qy	301	GAGCTGCCGAAATGGCTCATCGGGGGGTACCTTGTGATGACTTCTATGTGAGGGGTTCTA	360				
Db	301	GAGCTGCCGAAATGGCTCATCGGGGGGTACCTTGTGATGACTTCTATGTGAGGGGTTCTA	360				


```
QY 2521 GGAAGATCTGGCTTCATGAGGCCCTTTTGGAGGCTCTCAAGTCTTAGAGAGTGCCTG 2580
|||||
Db 2521 GGAAGATCTGGCTTCATGAGGCCCTTTTGGAGGCTCTCAAGTCTTAGAGAGTGCCTG 2580
|||||
QY 2581 TGGGACAGCCAGGCGAGAGCTGGGATGGTGCGATGCGCTTGTGTACATGGCCACA 2640
|||||
Db 2581 TGGGACAGCCAGGCGAGAGCTGGGATGGTGCGATGCGCTTGTGTACATGGCCACA 2640
|||||
QY 2641 GTACAGTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTTAAATAAAGGGTTG 2700
|||||
Db 2641 GTACAGTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTTAAATAAAGGGTTG 2700
|||||
QY 2701 GCTTCTGAACACTACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2760
|||||
Db 2701 GCTTCTGAACACTACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2760
|||||
QY 2761 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2820
|||||
Db 2761 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2820
|||||
QY 2821 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2846
|||||
Db 2821 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2846
|||||

RESULT 2
AX092306 2846 bp DNA linear PAT 21-MAR-2001
LOCUS Sequence 37 from Patent WO0116318.
DEFINITION AX092306
ACCESSION AX092306
VERSION AX092306.1 GI:13444467
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Eaton, D. L., Filvaroff, E., Gerritsen, M. E., Goddard, A.,
Godowski, P. J., Grimaldi, C. J., Gurney, A. L., Watanabe, C. K. and
Wood, W. I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 37 08-MAR-2001;
Genentech, Inc. (US)
FEATURES
source
1..2846
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 2846; DB 6; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCTCGGCGACGAGCGCGCAAGATGGAGTGGGTGCTGGAGCGAGTGGGGCTCAC 60
Db 1 CGCTCGGCGACGAGCGCGCAAGATGGAGTGGGTGCTGGAGCGAGTGGGGCTCAC 60

QY 61 TTTTCTTACAGTCTCTCATCTGCTCTTGGCAAGAGAGTACACAGTCAATTAATGAAGC 120
Db 61 TTTTCTTACAGTCTCTCATCTGCTCTTGGCAAGAGAGTACACAGTCAATTAATGAAGC 120

QY 121 CTGCGCTGGAGCAGAGTGAATATCATGTGTCGGGAGTCTGTGAATGATCAGATTGA 180
Db 121 CTGCGCTGGAGCAGAGTGAATATCATGTGTCGGGAGTCTGTGAATGATCAGATTGA 180

QY 181 GTGCGTCTGCCCGAAGAGGGAAGTCTGTGGGTATACATCCCTTGTCTGAGGAATGA 240
Db 181 GTGCGTCTGCCCGAAGAGGGAAGTCTGTGGGTATACATCCCTTGTCTGAGGAATGA 240

QY 241 GGAGAAATGATGTGACTCTCGCTGATCCACCAGGTTGTACCATCTTTGAAAAATGCAA 300
|||||
```

```
Db 241 GGAGAAATGATGTGACTCTCGCTGATCCACCAGGTTGTACCATCTTTGAAAAATGCAA 300
QY 301 GAGCTGCCGAAATGAGCTCATGGGGGGGTACCTTTGGATGACTTCTATGTGAAGGGTTCTA 360
|||||
Db 301 GAGCTGCCGAAATGAGCTCATGGGGGGGTACCTTTGGATGACTTCTATGTGAAGGGTTCTA 360
|||||
QY 361 CTGTGAGAGTGCAGAGCAGGCTGTACGGAGGAGACTGCGATGCGATGTGGCCAGGTTCT 420
|||||
Db 361 CTGTGAGAGTGCAGAGCAGGCTGTACGGAGGAGACTGCGATGCGATGTGGCCAGGTTCT 420
|||||
QY 421 CGGAGCCCAAGGGTCAAGATTTTCTTGGAAAGCTATCCCTAAATGCTCACTGTGAATG 480
|||||
Db 421 CGGAGCCCAAGGGTCAAGATTTTCTTGGAAAGCTATCCCTAAATGCTCACTGTGAATG 480
|||||
QY 481 GACCAATTCATGCTAAACCTGGGTTTGTTCATCCAACTAAAGATTTGTGATGCTGGA 540
|||||
Db 481 GACCAATTCATGCTAAACCTGGGTTTGTTCATCCAACTAAAGATTTGTGATGCTGGA 540
|||||
QY 541 GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTTGTGATGGAGACACCGCGATGG 600
|||||
Db 541 GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTTGTGATGGAGACACCGCGATGG 600
|||||
QY 601 CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCAGCTCTATCCAGAGCATAGGATC 660
|||||
Db 601 CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCAGCTCTATCCAGAGCATAGGATC 660
|||||
QY 661 CTCACTCCAGCTCTCTTCCACTCCGATGGCTCCAAGAAATTTTGACGGTTTCCATGCCAT 720
|||||
Db 661 CTCACTCCAGCTCTCTTCCACTCCGATGGCTCCAAGAAATTTTGACGGTTTCCATGCCAT 720
|||||
QY 721 TTATGAGGAGATCACAGCATGCTCTCATGCCCTTGTTCATGACGGCAGTCGTGCTCT 780
|||||
Db 721 TTATGAGGAGATCACAGCATGCTCTCATGCCCTTGTTCATGACGGCAGTCGTGCTCT 780
|||||
QY 781 TGCAAGCTCGATCTTACAGTGTGCTGTGGCAGGCTATCTGGCAGGCTATCTGGCAGGCTGTA 840
|||||
Db 781 TGCAAGCTCGATCTTACAGTGTGCTGTGGCAGGCTATCTGGCAGGCTATCTGGCAGGCTGTA 840
|||||
QY 841 AAATCTCTTGAAGAAAGAACTGTCTAGACCTCGGGGGCCCGAGTCAATGGGTACAGAA 900
|||||
Db 841 AAATCTCTTGAAGAAAGAACTGTCTAGACCTCGGGGGCCCGAGTCAATGGGTACAGAA 900
|||||
QY 901 AATAACAGGGGCGCTTGGCTTTTCAACGGAGCCCATGCTAAATTTGGCAGCGTGTGTC 960
|||||
Db 901 AATAACAGGGGCGCTTGGCTTTTCAACGGAGCCCATGCTAAATTTGGCAGCGTGTGTC 960
|||||
QY 961 TTTCTTTTGTAACTCTTATGTTCTTAGTGGCAATGAGAAAGAACTTGGCCAGCAGAA 1020
|||||
Db 961 TTTCTTTTGTAACTCTTATGTTCTTAGTGGCAATGAGAAAGAACTTGGCCAGCAGAA 1020
|||||
QY 1021 TGGAGAGTGGTCAAGGAAACAGCCCATCTGCATAAAGCTCTGCCAGAACCAAGATTTTC 1080
|||||
Db 1021 TGGAGAGTGGTCAAGGAAACAGCCCATCTGCATAAAGCTCTGCCAGAACCAAGATTTTC 1080
|||||
QY 1081 AGACCTGTGAGAAAGAGAGTCTTTCGATGCGAGTTCAGTCAAGGGAGACACCATTA 1140
|||||
Db 1081 AGACCTGTGAGAAAGAGAGTCTTTCGATGCGAGTTCAGTCAAGGGAGACACCATTA 1140
|||||
QY 1141 CCAGCTATATCTCAGCGGCTTTCAGCAACGAGAACTGCGAGAGTGCCTTACCAAGAGCC 1200
|||||
Db 1141 CCAGCTATATCTCAGCGGCTTTCAGCAACGAGAACTGCGAGAGTGCCTTACCAAGAGCC 1200
|||||
QY 1201 AGCCCTCTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATATCCAGCTCCAGTA 1260
|||||
Db 1201 AGCCCTCTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATATCCAGCTCCAGTA 1260
|||||
QY 1261 TGAGTGCATCTACCCCTTCTACCGCGCTTGGGAGCAGCAGGAGACATGTCTGAGGAC 1320
|||||
Db 1261 TGAGTGCATCTACCCCTTCTACCGCGCTTGGGAGCAGCAGGAGACATGTCTGAGGAC 1320
|||||
QY 1321 TGGGAAGTGGAGTGGGCGGCGACCATCTGTCATCCCTATCTGCGGGAAAAATTTGAGACAT 1380
|||||
Db 1321 TGGGAAGTGGAGTGGGCGGCGACCATCTGTCATCCCTATCTGCGGGAAAAATTTGAGACAT 1380
|||||
```


Db 181 GTGCGTCTGCCCGGAAAGAGGAAGTCGTGGGTTATACCATCCCTTGTGTCAGGAATGA 240
Qy 241 GGAGAAATGAGTGTGACTCTGCTCTGATCCACCAGGTTGTACCATCTTTGAAAACTGCAA 300
Db 241 GGAGAAATGAGTGTGACTCTGCTCTGATCCACCAGGTTGTACCATCTTTGAAAACTGCAA 300
Qy 301 GAGCTGCCGAATGAGTCTATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTA 360
Db 301 GAGCTGCCGAATGAGTCTATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTA 360
Qy 361 CTGTGCAGATGCCGAGCAGGCTGTACGGAGGAGCTGCATGCGATGTGGCCAGGTTCT 420
Db 361 CTGTGCAGATGCCGAGCAGGCTGTACGGAGGAGCTGCATGCGATGTGGCCAGGTTCT 420
Qy 421 GCGAGCCCAAGAGGTTCAGATTTTGTGGAAAGCTATCCCTTAAATGTCTCACTGTGAATG 480
Db 421 GCGAGCCCAAGAGGTTCAGATTTTGTGGAAAGCTATCCCTTAAATGTCTCACTGTGAATG 480
Qy 481 GACCAATTCATGCTAAACCTGGGTTGTCTATCCAACTAAGATTTGTGATGTGAGTCTGGA 540
Db 481 GACCAATTCATGCTAAACCTGGGTTGTCTATCCAACTAAGATTTGTGATGTGAGTCTGGA 540
Qy 541 GTTTCGACTACATGTGCCAGTATGACTATGTTGAGGTTGCTGATGGAGACAACCGGATGG 600
Db 541 GTTTCGACTACATGTGCCAGTATGACTATGTTGAGGTTGCTGATGGAGACAACCGGATGG 600
Qy 601 CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATC 660
Db 601 CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATC 660
Qy 661 CTCACCTCAGCTCTTCCACTCCGATGGCTCCAAAGATTTTGACGGTTTCCATGCCAT 720
Db 661 CTCACCTCAGCTCTTCCACTCCGATGGCTCCAAAGATTTTGACGGTTTCCATGCCAT 720
Qy 721 TTATGAGGAGATCACAGCATGCTCTCATCCCTTGTTCATGACGCGACGCTGGTCT 780
Db 721 TTATGAGGAGATCACAGCATGCTCTCATCCCTTGTTCATGACGCGACGCTGGTCT 780
Qy 781 TGACAAGGCTGGATCTTCAAGTGTGCTGTGGCAGGCTATATCTGGGACGCGCTGTA 840
Db 781 TGACAAGGCTGGATCTTCAAGTGTGCTGTGGCAGGCTATATCTGGGACGCGCTGTA 840
Qy 841 AAATCTCTTGAAGAAAGAACTGCTCAGACCCCTGGGGCCAGTCAATGGGTACAGAA 900
Db 841 AAATCTCTTGAAGAAAGAACTGCTCAGACCCCTGGGGCCAGTCAATGGGTACAGAA 900
Qy 901 AATAACGGGGCCCTGGGCTTATCAACGAGCGCATGCTAAATTTGSCACCGTGTGTC 960
Db 901 AATAACGGGGCCCTGGGCTTATCAACGAGCGCATGCTAAATTTGSCACCGTGTGTC 960
Qy 961 TTTCTTTTGTAACTCCTATGTTCTTAGTGGCAATGAGAAAGAACTTGGCAGAGAA 1020
Db 961 TTTCTTTTGTAACTCCTATGTTCTTAGTGGCAATGAGAAAGAACTTGGCAGAGAA 1020
Qy 1021 TGGAGATGGTCAGGAAACAGCCCATCTGCATAAAGCTGCGCCAGAAACCAAGATTTC 1080
Db 1021 TGGAGATGGTCAGGAAACAGCCCATCTGCATAAAGCTGCGCCAGAAACCAAGATTTC 1080
Qy 1081 AGACTGTGTGAGAGAGAGTCTTCCGATGCGGTTCAAGTCAAGGGAGACCAATTACA 1140
Db 1081 AGACTGTGTGAGAGAGAGTCTTCCGATGCGGTTCAAGTCAAGGGAGACCAATTACA 1140
Qy 1141 CCAGCTATATCTCAGCGGCTTCCAGCAAGCAGAAATCTGAGAGTGCCCTTCCAAAGAGCC 1200
Db 1141 CCAGCTATATCTCAGCGGCTTCCAGCAAGCAGAAATCTGAGAGTGCCCTTCCAAAGAGCC 1200
Qy 1201 AGCCCTTCCCTTTGAGATCTGCCCATGGGATACCAACATCTGCATATCCAGCTCCAGTA 1260
Db 1201 AGCCCTTCCCTTTGAGATCTGCCCATGGGATACCAACATCTGCATATCCAGCTCCAGTA 1260
Qy 1261 TGAGTGCATCTCACCTTCTACCGCGCTGGGAGCAGGAGGACATGCTCTGAGGAC 1320
Db 1261 TGAGTGCATCTCACCTTCTACCGCGCTGGGAGCAGGAGGACATGCTCTGAGGAC 1320

Qy 1321 TGGGAAGTGGAGTGGGCGGGCAACATCTCTGATCCCTATCTGCGGAAAAATTTGAAACAT 1380
Db 1321 TGGGAAGTGGAGTGGGCGGGCAACATCTCTGATCCCTATCTGCGGAAAAATTTGAAACAT 1380
Qy 1381 CACTGCTCCAAAGACCCCAAGGTTGCGCTGCGCGTGGCAGGAGCCATCTACAGGAGAC 1440
Db 1381 CACTGCTCCAAAGACCCCAAGGTTGCGCTGCGCGTGGCAGGAGCCATCTACAGGAGAC 1440
Qy 1441 CAGCGGGTGCATGACGCGACCTACACAAGGGAGCGTGGTTCTCTAGTCTGACGCGGTGC 1500
Db 1441 CAGCGGGTGCATGACGCGACCTACACAAGGGAGCGTGGTTCTCTAGTCTGACGCGGTGC 1500
Qy 1501 CTTGTTGAATGAGCGCACTGTGGTGGCTGCGCCACCTGTGTACTGACTGCGGGAAGGT 1560
Db 1501 CTTGTTGAATGAGCGCACTGTGGTGGCTGCGCCACCTGTGTACTGACTGCGGGAAGGT 1560
Qy 1561 CACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGAAAAATCTACCGGGATGATGA 1620
Db 1561 CACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGAAAAATCTACCGGGATGATGA 1620
Qy 1621 CCGGATGAGAAAGACCATCCAGAGCTACAGATTTCTGCTATCATTTCTGCAATCCCACTA 1680
Db 1621 CCGGATGAGAAAGACCATCCAGAGCTACAGATTTCTGCTATCATTTCTGCAATCCCACTA 1680
Qy 1681 TGACCCCATCTGCTTGTATGCTGACATCGCCATCTCTGAAGCTCTTAGACAAGGCCGTAT 1740
Db 1681 TGACCCCATCTGCTTGTATGCTGACATCGCCATCTCTGAAGCTCTTAGACAAGGCCGTAT 1740
Qy 1741 CAGCACCCGAGTCAGAGCCCATCTGCTCGCTGCGAGTCGGGATCTCAGCACTTCTTCCA 1800
Db 1741 CAGCACCCGAGTCAGAGCCCATCTGCTCGCTGCGAGTCGGGATCTCAGCACTTCTTCCA 1800
Qy 1801 GGAGTCCCACTCACTGTGGCTGGCTGGAATGTCTCGCAGACGCTGAGGAGCCCTGGCTT 1860
Db 1801 GGAGTCCCACTCACTGTGGCTGGCTGGAATGTCTCGCAGACGCTGAGGAGCCCTGGCTT 1860
Qy 1861 CAAGAACACACACTGCGCTCTGGGGTGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGA 1920
Db 1861 CAAGAACACACACTGCGCTCTGGGGTGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGA 1920
Qy 1921 GCAGCATGAGACCATGGCATCCAGTCAGTGTCTACTGATTAACATGTTCTGTGCCAGCTG 1980
Db 1921 GCAGCATGAGACCATGGCATCCAGTCAGTGTCTACTGATTAACATGTTCTGTGCCAGCTG 1980
Qy 1981 GGAACCCACTGCCCCCTTCTGATATCTGCACTGCGAGACAGAGGACATCGCGGCTGTGTC 2040
Db 1981 GGAACCCACTGCCCCCTTCTGATATCTGCACTGCGAGACAGAGGACATCGCGGCTGTGTC 2040
Qy 2041 CTTCCCGGAGCAGACATCTCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAG 2100
Db 2041 CTTCCCGGAGCAGACATCTCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAG 2100
Qy 2101 CTATGATAAACAATGCAAGGCTCTCCAGCTCTCCAGCTTCCAGAGTGTGCTGCTTTTAA 2160
Db 2101 CTATGATAAACAATGCAAGGCTCTCCAGCTCTCCAGCTTCCAGAGTGTGCTGCTTTTAA 2160
Qy 2161 AGACTGGATTCGAAGAAATATGAAATGAACATGCTCATGCACTCTTGAAGAGTGTTC 2220
Db 2161 AGACTGGATTCGAAGAAATATGAAATGAACATGCTCATGCACTCTTGAAGAGTGTTC 2220
Qy 2221 TGTATATCCGTCTGTACGTGTCTATTCGCTGAAGCAGTGTGGGCTGAAAGTGTGATTG 2280
Db 2221 TGTATATCCGTCTGTACGTGTCTATTCGCTGAAGCAGTGTGGGCTGAAAGTGTGATTG 2280
Qy 2281 GCCTGTGAACCTTGGCTGTGCCAGGCTTCTGACTTCAGGGAACAACTCAGTGAAGGGTG 2340
Db 2281 GCCTGTGAACCTTGGCTGTGCCAGGCTTCTGACTTCAGGGAACAACTCAGTGAAGGGTG 2340
Qy 2341 AGTAGACCTCCAATGCTGTAGGTGATGCGCGCTGCACTACTAGGACAGCCAAATTTGAA 2400
Db 2341 AGTAGACCTCCAATGCTGTAGGTGATGCGCGCTGCACTACTAGGACAGCCAAATTTGAA 2400

1741 QY CAGCACCCGAGTCCAGCCCATCTGCTCGCTGCCAGTCCGGATCTCAGCAGCTTCTTCCA 1800
1741 Db CAGCACCCGAGTCCAGCCCATCTGCTCGCTGCCAGTCCGGATCTCAGCAGCTTCTTCCA 1800
1801 QY GGAGTCCACATCATCTGTGGCTGGTGAATGTCTGCGAGACGTGAGAGCCCTGGCTT 1860
1801 Db GGAGTCCACATCATCTGTGGCTGGTGAATGTCTGCGAGACGTGAGAGCCCTGGCTT 1860
1861 QY CAAGAACACACACTCGCTCGGGGTGGTCACTGTGGTGGACTCGCTGCTGTGTGAGGA 1920
1861 Db CAAGAACACACACTCGCTCGGGGTGGTCACTGTGGTGGACTCGCTGCTGTGTGAGGA 1920
1921 QY GCAGCATGAGGACCATGCGATCCAGTGGTGTCTGATGATCACTGATCACTGTGTGCCAGCTG 1980
1921 Db GCAGCATGAGGACCATGCGATCCAGTGGTGTCTGATGATCACTGATCACTGTGTGCCAGCTG 1980
1981 QY GGAACCCACTGCCCTTCTGATATCTGACTGAGTGTGATGATCACTGATCACTGTGTGCTC 2040
1981 Db GGAACCCACTGCCCTTCTGATATCTGACTGAGTGTGATGATCACTGATCACTGTGTGCTC 2040
2041 QY CTTCCCGGAGCAGGACATCTCCTGAGCCAGCTGGCATCTGATGGGACTGGTCACTGGAG 2100
2041 Db CTTCCCGGAGCAGGACATCTCCTGAGCCAGCTGGCATCTGATGGGACTGGTCACTGGAG 2100
2101 QY CTATGATAAAAATGACAGCAGGCTCTCCACTGCCCTTCCAGAGGTGCTGCCCTTTTAA 2160
2101 Db CTATGATAAAAATGACAGCAGGCTCTCCACTGCCCTTCCAGAGGTGCTGCCCTTTTAA 2160
2161 QY AGACTGGATTTGAAGAAATATGAATATGAACATGCTCATGCACTCTTGGAGAAGTGTTC 2220
2161 Db AGACTGGATTTGAAGAAATATGAATATGAACATGCTCATGCACTCTTGGAGAAGTGTTC 2220
2221 QY TGTATATCCGCTGTACGTGTGTCTATGCTGAAGCAGTGTGGGCTCAAGTGTGATTTG 2280
2221 Db TGTATATCCGCTGTACGTGTGTCTATGCTGAAGCAGTGTGGGCTCAAGTGTGATTTG 2280
2281 QY GCCTGTGAACCTTGGCTGTGCCAGGCTCTTGTGACTTCCAGGGAACAAACTCAGTGAAGGCTG 2340
2281 Db GCCTGTGAACCTTGGCTGTGCCAGGCTCTTGTGACTTCCAGGGAACAAACTCAGTGAAGGCTG 2340
2341 QY AGTAGACCTCCATTTGCTGGTAGGCTGTGCGCGTCCACTACTAGGACAGCCAAATGGAA 2400
2341 Db AGTAGACCTCCATTTGCTGGTAGGCTGTGCGCGTCCACTACTAGGACAGCCAAATGGAA 2400
2401 QY GATGCCAGGCTTGCAGAGTAAGTCTTCCAAAGAGACCATATACAAACCTCTCCA 2460
2401 Db GATGCCAGGCTTGCAGAGTAAGTCTTCCAAAGAGACCATATACAAACCTCTCCA 2460
2461 QY CTCCACTGACCTGTGTGCTTCCCAACTTTTCAAGTATACGAATGCCATCAGCTTGACCA 2520
2461 Db CTCCACTGACCTGTGTGCTTCCCAACTTTTCAAGTATACGAATGCCATCAGCTTGACCA 2520
2521 QY GGGAAAGATCTGGGCTTTCATGAGGCCCTTTTGAAGCTCTCAAGTCTTAGAGAGCTGCCTG 2580
2521 Db GGGAAAGATCTGGGCTTTCATGAGGCCCTTTTGAAGCTCTCAAGTCTTAGAGAGCTGCCTG 2580
2581 QY TGGGACGCCAGGACGAGCTGGGATGTGGTGTGCTTGTCTACATGCGCCACA 2640
2581 Db TGGGACGCCAGGACGAGCTGGGATGTGGTGTGCTTGTCTACATGCGCCACA 2640
2641 QY GTACAGTCTGTGCTTCTTCCCATCTCTTGTACACATTTTAAATAAGGGTTG 2700
2641 Db GTACAGTCTGTGCTTCTTCCCATCTCTTGTACACATTTTAAATAAGGGTTG 2700
2701 QY GCTTCTGAACACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2760
2701 Db GCTTCTGAACACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2760
2761 QY AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 2820
2761 Db AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 2820

2821 QY AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2846
2821 Db AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2846
RESULT 6
HSM803699 HSM803699 2768 bp mRNA linear PRI 10-JUL-2002
LOCUS Homo sapiens mRNA; cDNA DKFZp667H2312 (from clone DKFZp667H2312).
DEFINITION
ACCESSION AL832391
VERSION AL832391.1 GI:21732954
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Koshner, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp667H2312) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
FEATURES
Location/Qualifiers
1..2768
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="RZPD:DKFZp667H2312"
/db_xref="taxon:9606"
/clone="DKFZp667H2312"
/tissue_type="lymph node"
/clone_lib="667 (synonym: hlno2). Vector pSport1; host DH10B; sites NotI + SalI"
/dev_stage="adult"
polyA_signal 2672..2677
polyA_site 2698
ORIGIN
Query Match 97.0%; Score 2761.6; DB 9; Length 2768;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2764; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
14 GCCGCGGCAAGATGGAGCTGGGTTGCTGGACGAGTGGGCTCATTTCCTCAGCTC 73
1 GCCGCGGCAAGATGGAGCTGGGTTGCTGGACGAGTGGGCTCATTTCCTCAGCTC 60
74 CTTCTCATCTCGTCTTCCCAAGAGATACAGTCATTAATGAAGCTGCCCTGAGCA 133
61 CTTCTCATCTCGTCTTCCCAAGAGATACAGTCATTAATGAAGCTGCCCTGAGCA 120
134 GAGTGGAAATATCATGTGTGCGGAGTGTGTAATATGATCAGATTGAGTGGCTGCCCC 193
121 GAGTGGAAATATCATGTGTGCGGAGTGTGTAATATGATCAGATTGAGTGGCTGCCCC 180
194 GGAAAGAGGGAAGTCTGGGTTTATACCATCCCTGCTGCAGGAATGAGGAATGAGTGT 253
181 GGAAAGAGGGAAGTCTGGGTTTATACCATCCCTGCTGCAGGAATGAGGAATGAGTGT 240
254 GACTCCTGCTGATCCACCCAGGTTGTACCATCTTTTGAATACTGCAAGCTGCCGAAT 313
241 GACTCCTGCTGATCCACCCAGGTTGTACCATCTTTTGAATACTGCAAGCTGCCGAAT 300
314 GGCTCATGGGGGGTACCTTCGATGACCTTCTATGTGAAGGGGTTCTACTGTGCAGAGTC 373
301 GGCTCATGGGGGGTACCTTCGATGACCTTCTATGTGAAGGGGTTCTACTGTGCAGAGTC 360


```

Db      2521 CTTTCATGAGGCCCTTTTGGGCTCTCAAGTTCTAGAGAGTGCCTGTGGGACAGCCCG 2580
Qy      2594 GGCAGCAGAGCTGGGATGTGGTCATGCCCTTTGTGTACATGGCCACAGTACAGTCTGGTC 2653
Db      2581 GGCAGCAGAGCTGGGATGTGGTCATGCCCTTTGTGTACATGGCCACAGTACAGTCTGGTC 2640
Qy      2654 CTTTTCCTCCCATCTCTGTGTACACATTTTAAATAAAGGTTGGCTTCTGAACATAC 2713
Db      2641 CTTTTCCTCCCATCTCTGTGTACACATTTTAAATAAAGGTTGGCTTCTGAACATAC 2700
Qy      2714 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2773
Db      2701 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2760
Qy      2774 AAAAAAAA 2781
Db      2761 AAAAAAAA 2768

RESULT 7
LOCUS   BD157134                      2784 bp    DNA    linear    PAT 17-JAN-2003
DEFINITION
Primer for synthesizing full-length cDNA and use thereof.
ACCESSION
BD157134
VERSION
BD157134.1 GI:27862892
KEYWORDS
JP 2002191363-A/11977.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2784)
AUTHORS
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE
Primer for synthesizing full-length cDNA and use thereof
JOURNAL
Patent: JP 2002191363-A 11977 09-JUL-2002;
COMMENT
HELIX RESEARCH INSTITUTE
OS      Homo sapiens (human)
PN      JP 2002191363-A/11977
PD      09-JUL-2002
PF      28-JUL-2000 JP 2000280990
PI      TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI      SAITO,
PI      JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI      KEIICHI NAGAI, TETSUJI OTSUKI
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
(47)..(2257).
FT      CDS
Location/Qualifiers
1..2784
source
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 92.6%; Score 2636.8; DB 6; Length 2784;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 2710; Conservative 0; Mismatches 2; Indels 52; Gaps 2;

Qy      1 CGCTCGGCACCGCGCGGCAAGATGGAGCTGGGTGCTGGAGCGCAGTTCGGGCTCAC 60
Db      22 CGCTCGGCACCGCGCGGCAAGATGGAGCTGGGTGCTGGAGCGCAGTTCGGGCTCAC 81
Qy      61 TTTTCTTACGCTCTCTCATCTCGTCTTGCACAGAGAGTACACAGTCAATTAATGAAGC 120
Db      82 TTTTCTTACGCTCTCTCATCTCGTCTTGCACAGAGAGTACACAGTCAATTAATGAAGC 141
Qy      121 CTGCGCTGGAGCAGAGTGAATATCATGTGCGGAGTCTGTGAATGATCAGATTGA 180
Db      142 CTGCGCTGGAGCAGAGTGAATATCATGTGCGGAGTCTGTGAATGATCAGATTGA 201

```

```

Qy      181 GTGCGTCTGCCCCGGAAGAGAGGAAAGTCTGTGGTTTATACATCCCTTGTCTGCAGGAATGA 240
Db      202 GTGCGTCTGCCCCGGAAGAGAGGAAAGTCTGTGGTTTATACATCCCTTGTCTGCAGGAATGA 261
Qy      241 GGAGAAATGAGTGTGACTCTCTGCTGATCCACCCAGGTTGTACATCTTTTGAACATGCA 300
Db      262 GGAGAAATGAGTGTGACTCTCTGCTGATCCACCCAGGTTGTACATCTTTTGAACATGCA 321
Qy      301 GAGCTGCCAAATGGCTCATGGGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCTA 360
Db      322 GAGCTGCCAAATGGCTCATGGGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCTA 381
Qy      361 TTGTGCAAGTGCCTGAGCAGGCTGTGACGGAGGAGACTGCATGCGATGTGGCCAGGTTCT 420
Db      382 TTGTGCAAGTGCCTGAGCAGGCTGTGACGGAGGAGACTGCATGCGATGTGGCCAGGTTCT 441
Qy      421 GCGAGCCCCAAGGGTCAAGTTTGTGGGAAGCTATCCCCATAATGCTCACTGTGAATG 480
Db      442 GCGAGCCCCAAGGGTCAAGTTTGTGGGAAGCTATCCCCATAATGCTCACTGTGAATG 501
Qy      481 GACCAATTCATGCTAAACCTGGGTTTGTCTATCCAACTAAGATTGTGATGTCAGTCTGA 540
Db      502 GACCAATTCATGCTAAACCTGGGTTTGTCTATCCAACTAAGATTGTGATGTCAGTCTGA 561
Qy      541 GTTTCACATGATGCCAGATATGACTATGTTGAGGTTCTGTGATGAGACAAACCGGATGG 600
Db      562 GTTTCACATGATGCCAGATATGACTATGTTGAGGTTCTGTGATGAGACAAACCGGATGG 621
Qy      601 CCAGATCATCAAGCGTGTCTGTGGCAACGAGGGGCGAGCTCTATCCAGAGCATAGGATC 660
Db      622 CCAGATCATCAAGCGTGTCTGTGGCAACGAGGGGCGAGCTCTATCCAGAGCATAGGATC 681
Qy      661 CTCACCTCCACGCTCTCTTCCACTCCGATGGGCTCCAAAGAAATTTGACGGTTTCCATGCCAT 720
Db      682 CTCACCTCCACGCTCTCTTCCACTCCGATGGGCTCCAAAGAAATTTGACGGTTTCCATGCCAT 741
Qy      721 TTATGAGGAGATCACAGCATGCTCTCATCCCTTTGTTTCCATGACGGCAGTGGCTCT 780
Db      742 TTATGAGGAGATCACAGCATGCTCTCATCCCTTTGTTTCCATGACGGCAGTGGCTCT 801
Qy      781 TGCAAGGCTGGATCTTCAAGTGTGCTGCTTGGCAGGCTATATCTGGCAGCGCTGTGA 840
Db      802 TGCAAGGCTGGACCTTCAAGTGTGCTGCTTGGCAGGCTATATCTGGCAGCGCTGTGA 861
Qy      841 AAATC-----TCCT 849
Db      862 AAATCTTCTGGAGGCTGGAAAGTCCAAGATCAAGCGCTCAGAAATTCAATTGTCTGTCT 921
Qy      850 TGAAGAAAGAAATCTGCTCAGACCCCTGGGGGCCAGTCAATGGGTACCGAGAAATAACAGG 909
Db      922 TGAAGAAAGAAATCTGCTCAGACCCCTGGGGGCCAGTCAATGGGTACCGAGAAATAACAGG 981
Qy      910 GGGCCCTGGGCTTATCAACGAGCGCATGCTTAAATTTGGCACCGTGGTCTTTCTTTTG 969
Db      982 GGGCCCTGGGCTTATCAACGAGCGCATGCTTAAATTTGGCACCGTGGTCTTTCTTTTG 1041
Qy      970 TAAACACTCTTATGTTCTTAGTGGCAATGAGAAAGAACTTCCAGCAGCAATGGAGAGTG 1029
Db      1042 TAAACACTCTTATGTTCTTAGTGGCAATGAGAAAGAACTTCCAGCAGCAATGGAGAGTG 1101
Qy      1030 GTTCAGGAAACAGCCCATCTGTCATAAAAGCCTGCCGAGAACCAAGATTTTCAGACTGT 1089
Db      1102 GTTCAGGAAACAGCCCATCTGTCATAAAAGCCTGCCGAGAACCAAGATTTTCAGACTGT 1161
Qy      1090 GAGAAGGAGAGTTCTTCCGATGCGAGTTCACTCAAGGGAGACACCATTTACACAGCTATA 1149
Db      1162 GAGAAGGAGAGTTCTTCCGATGCGAGTTCACTCAAGGGAGACACCATTTACACAGCTATA 1221
Qy      1150 CTCAGCGGCTTTCAGCAAGCAGAACTGCAGATGCCCTTACCAAGAGCCAGCCCTTCC 1209
Db      1222 CTCAGCGGCTTTCAGCAAGCAGAACTGCAGATGCCCTTACCAAGAGCCAGCCCTTCC 1281

```

Qy	1210	CTTTGGAGATCTGCCCATGGGATACCAACATCTGTCATACCCAGTCCAGTATCAGTGCAT	1269
Db	1282	CTTTTGGAGATCTGCCCATGGGATACCAACATCTGTCATACCCAGTCCAGTATCAGTGCAT	1341
Qy	1270	CTCACCCTTTACCGCGCGCTGGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTG	1329
Db	1342	CTCACCCTTTCTACCGCGCGCTGGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTG	1401
Qy	1330	GAGTGGCGGGGCACCATCTCTGCATCCCTATCTGCGGAAAAATTGAGAACATCACTGCTCC	1389
Db	1402	GAGTGGCGGGGCACCATCTCTGCATCCCTATCTGCGGAAAAATTGAGAACATCACTGCTCC	1461
Qy	1390	AAAGACCAAGAGGTGTGCGCTGGCGTGGCAGGAGCACCATCTACAGGAGGACGACGGGGT	1449
Db	1462	AAAGACCAAGAGGTGTGCGCTGGCGTGGCAGGAGCACCATCTACAGGAGGACGACGGGGT	1521
Qy	1450	GCATGACGGCAGCCTACACAAGGAGGAGCGTGGTTCCTAGTCTGCAGCGGTGCCCTGGTAA	1509
Db	1522	GCATGACGGCAGCCTACACAAGGAGGAGCGTGGTTCCTAGTCTGCAGCGGTGCCCTGGTAA	1581
Qy	1510	TGAGCGCACTGTGTGTGTGGCTGCCCACTGTGTACTGACCTGGGGAAAGTCCACCATGAT	1569
Db	1582	TGAGCGCACTGTGTGTGTGGCTGCCCACTGTGTACTGACCTGGGGAAAGTCCACCATGAT	1641
Qy	1570	CAAGACAGCAGACCTGTAAAGTTGTTTGGGAAAAATTCTACCGGGATGATGACCGGGATGA	1629
Db	1642	CAAGACAGCAGACCTGTAAAGTTGTTTGGGAAAAATTCTACCGGGATGATGACCGGGATGA	1701
Qy	1630	GAAGACCATCCAGAGCCTACAGATTTCTGCTATCATCTTCGCATCCCACTATCAGCCCAT	1689
Db	1702	GAAGACCATCCAGAGCCTACAGATTTCTGCTATCATCTTCGCATCCCACTATCAGCCCAT	1761
Qy	1690	CCTGCTTGATGCTGACATCGCCATCTCTGAAAGCTCTTAGACAAGGCCCGTATCAGCACCCG	1749
Db	1762	CCTGCTTGATGCTGACATCGCCATCTCTGAAAGCTCTTAGACAAGGCCCGTATCAGCACCCG	1821
Qy	1750	AGTCCAGCCCATCTGCTCGCTGCCAGTGGGATCTCAGCACTTCCTTCAGAGTCCCA	1809
Db	1822	AGTCCAGCCCATCTGCTCGCTGCCAGTGGGATCTCAGCACTTCCTTCAGAGTCCCA	1881
Qy	1810	CATCAGTGTGGCTGGCTGGAAATGTCCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGA	1869
Db	1882	CATCAGTGTGGCTGGCTGGAAATGTCCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGA	1941
Qy	1870	CACACTCGCTCTGGGGTGTGTCAGTGTGTGGACTCGCTGCTGTGTGAGGAGCAGCATGA	1929
Db	1942	CACACTCGCTCTGGGGTGTGTCAGTGTGTGGACTCGCTGCTGTGTGAGGAGCAGCATGA	2001
Qy	1930	GGACCATGGCATCCACGTGAGTGTCACTGATAAACATGTTCTGTGCCAGCTGGGAACCCAC	1989
Db	2002	GGACCATGGCATCCACGTGAGTGTCACTGATAAACATGTTCTGTGCCAGCTGGGAACCCAC	2061
Qy	1990	TGCCCCCTTCTGATATCTGCACTGCAGAGACAGGAGGCATCGCGCTGTGTCTTCCGGG	2049
Db	2062	TGCCCCCTTCTGATATCTGCACTGCAGAGACAGGAGGCATCGCGCTGTGTCTTCCGGG	2121
Qy	2050	ACGAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGCTCAGCTGGAGCTATGATAA	2109
Db	2122	ACGAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGCTCAGCTGGAGCTATGATAA	2181
Qy	2110	AACATGACGCCACAGGCTCTCCACTGCTCTTCAACCAAGGTGCTGCTTTTAAAGACTGGAT	2169
Db	2182	AACATGACGCCACAGGCTCTCCACTGCTCTTCAACCAAGGTGCTGCTTTTAAAGACTGGAT	2241
Qy	2170	TGAAGAAATATGAAATGAAACCATGCTCATGCACTCCTTGAGAGTGTGTTTCTGTATATCC	2229
Db	2242	TGAAGAAATATGAAATGAAACCATGCTCATGCACTCCTTGAGAGTGTGTTTCTGTATATCC	2301
Qy	2230	GTCTGTACGTGTGTCAATTGCTGTAAGCAGTGTGGGCTGAAAGTGTGAAATTTGGGCTGTGAA	2289
Db	2302	GTCTGTACGTGTGTCAATTGCTGTAAGCAGTGTGGGCTGAAAGTGTGAAATTTGGGCTGTGAA	2361
Qy	2290	CTTGGCTGTGCCAGGGCTTCTGACTTTCAGGGAACAAACTCAGTCAAGGGGTGAGTAGACCT	2349

Db	2362	CTTGGCTGTGCCAGGGCTTCTGACTTTCAGGGACAAAACTCAGTGAAGGGTGAGTAGACCT	2421
Qy	2350	CCATTGCTGTAGGCTGATGCCCGCTCCACTACTAGGACAGCCAAATTGGAAGATGCCAGG	2409
Db	2422	CCATTGCTGTAGGCTGATGCCCGCTCCACTACTAGGACAGCCAAATTGGAAGATGCCAGG	2481
Qy	2410	GCTTGCAGAAGTAAGTTTCTTCAAAGAGACCATATACAAAACCTCTCCACTCCACTGA	2469
Db	2482	GCTTGCAGAAGTAAGTTTCTTCAAAGAGACCATATACAAAACCTCTCCACTCCACTGA	2541
Qy	2470	CCTGGTGGTCTTCCCAAACCTTTCAGTTTATACGAATGCATCAGCTTGACACAGGAGATC	2529
Db	2542	CCTGGTGGTCTTCCCAAACCTTTCAGTTTATACGAATGCATCAGC - TGACCAGGAGATC	2600
Qy	2530	TGGGCTTTCATGAGGCCCCCTTTTGGAGGCTCTCAAGTTCTTAGAGAGCTGCCTGTGGGACAGC	2589
Db	2601	TGGGCTTTCATGAGGCCCCCTTTTGGAGGCTCTCAAGTTCTTAGAGAGCTGCCTGTGGGACAGC	2660
Qy	2590	CCAGGGCAGCAGAGCTGGGATGTGGTCATGCGCTTGTGTATACATGGCCACAGTACAGTCT	2649
Db	2661	CCAGGGCAGCAGAGCTGGGATGTGGTCATGCGCTTGTGTATACATGGCCACAGTACAGTCT	2720
Qy	2650	GGTCCCTTTTCTTCCCATCTCTTGTACACATTTTAAATAAGGTTGGCTTCTGAA	2709
Db	2721	GGTCCCTTTTCTTCCCATCTCTTGTACACATTTTAAATAAGGTTGGCTTCTGAA	2780
Qy	2710	CTAC 2713	
Db	2781	CTAC 2784	
RESULT 8			
AX878296			
LOCUS	AX878296	2784 bp	DNA
DEFINITION	Sequence	13201 from Patent EP1074617.	linear
ACCESSION	AX878296		
VERSION	AX878296.1	GI:40033032	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
CDS			

ORIGIN

Query Match	92.6%;	Score 2636.8;	DB 6;	Length 2784;
Best Local Similarity	98.0%;	Prod. No. 0;		
Matches 2710;	Conservative	0;	Mismatches	2; Indels 52; Gaps 2;
1	CGCTCGGCGACAGCGCGGCAAGCATGGAGCTGGGTTGCTGGACGCGATTTGGGGCTCAC	60		
22	CGCTCGGCGACAGCGCGGCAAGGATGAGCTGGGTTGCTGGACGCGATTTGGGGCTCAC	81		
61	TTTTCTTCAGCTCCTTCTCATCTCGTCTCTTGGCCAAAGAGATACACAGTCATTAAATGAAGC	120		
82	TTTTCTTCAGCTCCTTCTCATCTCGTCTCTTGGCCAAAGAGATACACAGTCATTAAATGAAGC	141		
121	CTGCCCTGGAGCAGAGTGAATATCATGTGTGGGAGTGTGTGAATATGATCAATTTGA	180		
142	CTGCCCTGGAGCAGAGTGAATATCATGTGTGGGAGTGTGTGAATATGATCAATTTGA	201		
181	GTGCGTCTGCCCGGAAGAGGGGAGTGTGGGTTATACCATCCCTTCCTGCACAGGATGA	240		
202	GTGCGTCTGCCCGGAAGAGGGGAGTGTGGGTTATACCATCCCTTCCTGCAGGAATGA	261		
241	GGAGAATGAGTGTGACTCTCTGCTCATCCACCAGGTTGTACCATCTTTGAAAACTGCAA	300		
262	GGAGAATGAGTGTGACTCTCTGCTCATCCACCAGGTTGTACCATCTTTGAAAACTGCAA	321		
301	GAGCTGCCGAATGCTCATCTGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTA	360		
322	GAGCTGCCGAATGCTCATCTGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTA	381		
361	CTGTGAGAGTCCGAGCAGGCTGTGTACGGAGGAGATGCGATGCGATGTGGCGAGGTTCT	420		
382	CTGTGAGAGTCCGAGCAGGCTGTGTACGGAGGAGATGCGATGCGATGTGGCGAGGTTCT	441		
421	GCGAGCCCAAGGGTTCAGATTTTGTGTGGAAGCTATCCCTTAAATGCTCACTGTGAATG	480		
442	GCGAGCCCAAGGGTTCAGATTTTGTGTGGAAGCTATCCCTTAAATGCTCACTGTGAATG	501		
481	GACCAATTCATGCTAAACCTGGGTTTGTATCCAACTAAGATTTTGTGATGTTGAGTCTGGA	540		
502	GACCAATTCATGCTAAACCTGGGTTTGTATCCAACTAAGATTTTGTGATGTTGAGTCTGGA	561		
541	GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTTGTGATGGAGACAACCCGGATGG	600		
562	GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTTGTGATGGAGACAACCCGGATGG	621		
601	CCAGATCATCAAGCGTGTCTGTGGCAACAGCGGGCCAGTCTCTATCCAGAGCATAGATC	660		
622	CCAGATCATCAAGCGTGTCTGTGGCAACAGCGGGCCAGTCTCTATCCAGAGCATAGATC	681		
661	CTCACTCCACGTCTCTTTCACATCCGATGGCTCCAAAGAAATTTTGACGGTTTCCATGCCAT	720		
682	CTCACTCCACGTCTCTTTCACATCCGATGGCTCCAAAGAAATTTTGACGGTTTCCATGCCAT	741		
721	TTATGAGGAGATCAAGCATGCTCTCATGCCCTTGTGTTTCAATGACGGCACTGTGGCTCT	780		
742	TTATGAGGAGATCAAGCATGCTCTCATGCCCTTGTGTTTCAATGACGGCACTGTGGCTCT	801		
781	TGACAAGGCTGATCTTACAGTGTGCCCTGTCTTGGCAGGCTATACTGGGCGACGCTGTGA	840		
802	TGACAAGGCTGATCTTACAGTGTGCCCTGTCTTGGCAGGCTATACTGGGCGACGCTGTGA	861		
841	AAATC-----	889		
862	AAATCTTCTGGAGGCTGGGAGTCCAGATCAAGCGCTCAGAGATTCATTGTCTGTCTCT	921		
850	TGAAGAAAGAACTGCTCAGACCTCTGGGGGCCAGTCAATGGGTACCAAGAAATAACAGG	909		
922	TGAAGAAAGAACTGCTCAGACCTCTGGGGGCCAGTCAATGGGTACCAAGAAATAACAGG	981		
910	GGGCCCTGGGCTTATCAACGAGCGCATGCTAAATTTGGCACCGGTGTCTTTCTTTTG	969		
982	GGGCCCTGGGCTTATCAACGAGCGCATGCTAAATTTGGCACCGGTGTCTTTCTTTTG	1041		

QY	970	TAACAAC	TCTCTATGTTCTT	AGTGGCAATGAGAAAAGAACTT	TGCCAGCAGCAAGTGGAGAGTG	1021
DB	1042	TAACAAC	TCTCTATGTTCTT	AGTGGCAATGAGAAAAGAACTT	TGCCAGCAGCAAGTGGAGAGTG	1101
QY	1030	GTCAAGG	AAACACAGCCCATCT	GCATATAAGCCTCGAGAACAAAGATT	TTCAGACCTGGT	1089
DB	1102	GTCAAGG	AAACACAGCCCATCT	GCATATAAGCCTCGCGAAGAACAAAGATT	TTCAGACCTGGT	1161
QY	1090	GAGAAG	GAGAGGTTCTT	CCGATGCAAGTTCAGTCAAGGGAGACACCAATT	TACACCAAGCTATA	1149
DB	1162	GAGAAG	GAGAGGTTCTT	CCGATGCAAGTTCAGTCAAGGGAGACACCAATT	TACACCAAGCTATA	1221
QY	1150	CTCAGC	GGCCTTCAGCAAGCAGAAA	CTGCAGAGTGCCCTTACCAAGAGCCAGCCCTTC		1209
DB	1222	CTCAGC	GGCCTTCAGCAAGCAGAAA	CTGCAGAGTGCCCTTACCAAGAGCCAGCCCTTC		1281
QY	1210	CTTTTGA	GAGATCTGCCCATGGGATACCAACATCT	GCATACCCAGCTCCAGTATCAGATGTCAT		1269
DB	1282	CTTTTGA	GAGATCTGCCCATGGGATACCAACATCT	GCATACCCAGCTCCAGTATCAGATGTCAT		1341
QY	1270	CTCACCC	TTCTTACCGCGCCTTGGGCAGCAGCAGGAGGACATGTCT	GAGGACTGGGAAGTG		1329
DB	1342	CTCACCC	TTCTTACCGCGCCTTGGGCAGCAGCAGGAGGACATGTCT	GAGGACTGGGAAGTG		1401
QY	1330	GAGTGG	GGGGACCACTCTGCATATCCCTATCT	TCTGCGGGAATAATTAGAGAACATCACTGCTCC		1389
DB	1402	GAGTGG	GGGGACCACTCTGCATATCCCTATCT	TCTGCGGGAATAATTAGAGAACATCACTGCTCC		1461
QY	1390	AAAGACC	CAAGGGTTGGCTGGCGTGGCAGGAGGAGCCATCTAC	GAGGAGCAGCAGCGGGT		1449
DB	1462	AAAGACC	CAAGGGTTGGCGTGGCAGGAGGAGCCATCTAC	GAGGAGCAGCAGCGGGT		1521
QY	1450	GCATGAC	CGGCAGCCTACACAAGGAGCGTGGTTCCTAGTCT	GCAGCGGTGCCCTGGTGAA		1509
DB	1522	GCATGAC	CGGCAGCCTACACAAGGAGCGTGGTTCCTAGTCT	GCAGCGGTGCCCTGGTGAA		1581
QY	1510	TGAGCG	CACTGTGGTGTGCTGCCCACTGTGTTTACTGACCT	GGGAGAGTCAACATGAT		1569
DB	1582	TGAGCG	CACTGTGGTGTGCTGCCCACTGTGTTTACTGACCT	GGGAGAGTCAACATGAT		1641
QY	1570	CAAGAC	AGCAGACCTGAAAGTCTGTTTGGGGAATAATTCTAC	CGGGATGATGACCGGGATGA		1629
DB	1642	CAAGAC	AGCAGACCTGAAAGTCTGTTTGGGGAATAATTCTAC	CGGGATGATGACCGGGATGA		1701
QY	1630	GAAGACC	ATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCAT	CCCCCATGACCCCCAT		1689
DB	1702	GAAGACC	ATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCAT	CCCCCATGACCCCCAT		1761
QY	1690	CCTGCT	TGATGCTGACATCCGCCATCTCGAAGCTCTTAGAC	AAGCGCCGTTATCAGCACCCG		1749
DB	1762	CCTGCT	TGATGCTGACATCCGCCATCTCGAAGCTCTTAGAC	AAGCGCCGTTATCAGCACCCG		1821
QY	1750	AGTCCAG	CCCATCTGCTCGCTGCCAGTCCGGATCTCAGCAGCT	TTCTTCCAGGAGTCCCA		1809
DB	1822	AGTCCAG	CCCATCTGCTCGCTGCCAGTCCGGATCTCAGCAGCT	TTCTTCCAGGAGTCCCA		1881
QY	1810	CATCAG	CTGCGCTGGCTGGAATGCTCTGGCAGACGTGAGGAGCCCTGGCTT	CAAGAACGA		1869
DB	1882	CATCAG	CTGCGCTGGCTGGAATGCTCTGGCAGACGTGAGGAGCCCTGGCTT	CAAGAACGA		1941
QY	1870	CACACT	CGCTCTGGGGTGTGAGTGTGGTACTCGCTGCTGTGT	GAGGAGCAGCATGA		1929
DB	1942	CACACT	CGCTCTGGGGTGTGAGTGTGGTACTCGCTGCTGTGT	GAGGAGCAGCATGA		2001
QY	1930	GGACAT	TGGCATCCAGTGTACTGTATACATGTTCTGTG	CCAGCTGGGAACCCAC		1989
DB	2002	GGACAT	TGGCATCCAGTGTACTGTATACATGTTCTGTG	CCAGCTGGGAACCCAC		2061
QY	1990	TGCCCT	TTCTGATATCTGCACCTGCAGAGACAGAGGACATCG	CGCGCTGTGCTTCCCGG		2049
DB	2062	TGCCCT	TTCTGATATCTGCACCTGCAGAGACAGAGGACATCG	CGCGCTGTGCTTCCCGG		2121
QY	2050	ACGAGCA	TCTCTTGAGCCACGCTGGCATCTGATGGGACTGGT	CAGCTGGAGCTATGATAA		2109

Db 2122 ACAGCATCTCTGAGCCACAGCTGGCATGTGAGGAGCTGGTGCAGCTGAGCTATGATAA 2181
Qy 2110 AACATGACGACAGAGCTCTCACTGCGCTTACCAAGGTGCTGCCCTTTAAAGACTGGAT 2169
Db 2182 AACATGACGACAGAGCTCTCACTGCGCTTACCAAGGTGCTGCCCTTTAAAGACTGGAT 2241
Qy 2170 TGAAGAAGAAATATGAATGAACCATCTCATGCACTCTTGTGAAGTGTCTGTATATACC 2229
Db 2242 TGAAGAAGAAATATGAATGAACCATCTCATGCACTCTTGTGAAGTGTCTGTATATACC 2301
Qy 2230 GTCTGTACGTGTGTCATTCGCGTGAAGCAGTGTGGCCCTCAAGTGTGATTTGGCCCTGTGAA 2289
Db 2302 GTCTGTACGTGTGTCATTCGCGTGAAGCAGTGTGGCCCTCAAGTGTGATTTGGCCCTGTGAA 2361
Qy 2290 CTTGCTGTGCCAGGCTCTTGACTTTCAGGACCAAACTCAGTGAAGGTGAGTAGACCT 2349
Db 2362 CTTGCTGTGCCAGGCTCTTGACTTTCAGGACCAAACTCAGTGAAGGTGAGTAGACCT 2421
Qy 2350 CCAATGCTGTAGGTGATGTCGCGCTTCCACTACTAGGACAGCAATTTGGAAGATGCCAGG 2409
Db 2422 CCAATGCTGTAGGTGATGTCGCGCTTCCACTACTAGGACAGCAATTTGGAAGATGCCAGG 2481
Qy 2410 GCTTGCAGAAAGTAAATTTCTTCAAGAGAACCATATACAAACCTCTCCACTCCACTGA 2469
Db 2482 GCTTGCAGAAAGTAAATTTCTTCAAGAGAACCATATACAAACCTCTCCACTCCACTGA 2541
Qy 2470 CTTGCTGTGTCCTCCCACTTTCAGTTATACGAATGCCATCAGCTTGACAGGGAAGATC 2529
Db 2542 CTTGCTGTGTCCTCCCACTTTCAGTTATACGAATGCCATCAGC-TGACCAAGGGAAGATC 2600
Qy 2530 TGGGCTTCATGAGGCCCCCTTTGAGGCTCTCAAGTCTTAGAGAGCTGCTGTGGACAGC 2589
Db 2601 TGGGCTTCATGAGGCCCCCTTTGAGGCTCTCAAGTCTTAGAGAGCTGCTGTGGACAGC 2660
Qy 2590 CCAGGCGACGAGCTGGGATGTGTCATGCTTTGTGTACATGCCACAGTACAGTCT 2649
Db 2661 CCAGGCGACGAGCTGGGATGTGTCATGCTTTGTGTACATGCCACAGTACAGTCT 2720
Qy 2650 GGTCTCTTCTTCCCATCTCTGTACACATTTAAATAAGGTTGGCTTCTGAA 2709
Db 2721 GGTCTCTTCTTCCCATCTCTGTACACATTTAAATAAGGTTGGCTTCTGAA 2780
Qy 2710 CTAC 2713
Db 2781 CTAC 2784

RESULT 9
BD012234
LOCUS
DEFINITION A novel gene encoding a serine protease-like protein.
ACCESSION BD012234
VERSION BD012234.1 GI:22092423
KEYWORDS WO 0109349-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 2784)
Ota.T., Isogai.T., Nishikawa.T., Hayashi.K., Saito.K., Yamamoto.J.,
Ishii.S., Sugiyama.T., Wakamatsu.A., Nagai.K., Otsuki.T., Yano.K.,
Murakami.K., Kanazaki.K., Inoue.Y., Hashimoto.E. and Kashima.A.
A novel gene encoding a serine protease-like protein
Parent: WO 0109349-A 1 08-FEB-2001;
HEILX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA,
SUJI HAYASHI, KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, OMOYASU
KOJI HAYASHI, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI, KAZUHIRO YANO,
OJI MURAKAMI, KOJI KANZAKI, YOSHIHISA INOUE, EMI HASHIMOTO, AKIKO
KASHIMA
OS Homo sapiens (human)
PN WO 0109349-A/1
PD 08-FEB-2001

PF 28-JUL-2000 WO 2000JP005062
PR 29-JUL-1999 JP 99P 248036.27-AUG-1999 JP 99P 300253 PR
11-JAN-2000 JP 00P 118776.02-MAY-2000 JP 00P 183767 PR
18-OCT-1999 US 60/159590.17-FEB-2000 US 60/183322 PI TOSHIO
OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, PI KAORU SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI, KAZUHIRO YANO, KOJI MURAKAMI, PI
KOJI KANZAKI,
PI YOSHIHISA INOUE, EMI HASHIMOTO, AKIKO KASHIMA
PC C12N15/57, C12N9/64, C12N15/63, C12N5/06, C07K16/40, C1201/68, PC
G01N33/573,
PC A61K38/48, A61K31/7052, A61K48/00//C12P21/08, (C12N9/64, C12R1:91)
CC
FH Key Location/Qualifiers
FT CDS (47)..(2257).
FEATURES
source
1..2784
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 92.6%; Score 2636.8; DB 6; Length 2784;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 2710; Conservative 0; Mismatches 2; Indels 52; Gaps 2;
Qy 1 CGCTCGGCGACAGCGCGCAAGATGAGCTGGGTTGCTGGACGAGTTGGGGCTCAC 60
Db 22 CGCTCGGCGACAGCGCGCAAGATGAGCTGGGTTGCTGGACGAGTTGGGGCTCAC 81
Qy 61 TTTTCTTCAGCTCTCTCATCTCGTCTTCCCAAGAGAGTACACAGTCAATTAATGAAGC 120
Db 82 TTTTCTTCAGCTCTCTCATCTCGTCTTCCCAAGAGAGTACACAGTCAATTAATGAAGC 141
Qy 121 CTGCGCTCGGAGAGAGTGGAAATATCATGTGTCGGAGTCTGTGAATGATGATGATGA 180
Db 142 CTGCGCTCGGAGAGAGTGGAAATATCATGTGTCGGAGTCTGTGAATGATGATGATGA 201
Qy 181 GTGGCTCTGCGCGCAAGAGAGAGTCTGGGTTTATACCATCCCTCTCGCAGGAATGA 240
Db 202 GTGGCTCTGCGCGCAAGAGAGAGTCTGGGTTTATACCATCCCTCTCGCAGGAATGA 261
Qy 241 GGAGAAATGAGTGTGATCTCTCTGATCCACCCAGAGTTGTACCATCTTTGAAACCTGCAA 300
Db 262 GGAGAAATGAGTGTGATCTCTCTGATCCACCCAGAGTTGTACCATCTTTGAAACCTGCAA 321
Qy 301 GAGCTGCGGAAATGGCTCATGGGGGTACCTTGGATGACTTCTATGTAAGGGGTTCTA 360
Db 322 GAGCTGCGGAAATGGCTCATGGGGGTACCTTGGATGACTTCTATGTAAGGGGTTCTA 381
Qy 361 CTGTGACAGTGGCGAGCAGGCTGTGTCGGAGGAGCTGTCATGTCGTCAGGTTCT 420
Db 382 CTGTGACAGTGGCGAGCAGGCTGTGTCGGAGGAGCTGTCATGTCGTCAGGTTCT 441
Qy 421 GCGAGCCCAAGGGTCAAGTATTTTGTGGAAAGCTATCCCTTAAATGCTCACTGTGAATG 480
Db 442 GCGAGCCCAAGGGTCAAGTATTTTGTGGAAAGCTATCCCTTAAATGCTCACTGTGAATG 501
Qy 481 GACCAATTCATGCTAAACCTGGGTTTGTTCATCAACATAGATTTGTGTCAGTCTGGA 540
Db 502 GACCAATTCATGCTAAACCTGGGTTTGTTCATCAACATAGATTTGTGTCAGTCTGGA 561
Qy 541 GTTTGACTACATGTCAGGATGATGATGTTGAGGTTGCTGATGAGACCAACCGGATGG 600
Db 562 GTTTGACTACATGTCAGGATGATGATGTTGAGGTTGCTGATGAGACCAACCGGATGG 621
Qy 601 CCAGATCATCAAGGCTGTCTGTGGCAACGAGCGGCGAGCTCCTATCCAGAGCATAGGATC 660
Db 622 CCAGATCATCAAGGCTGTCTGTGGCAACGAGCGGCGAGCTCCTATCCAGAGCATAGGATC 681
Qy 661 CTCACCTCAGCTCTCTTCCACTCCGATGGCTCCAGAAATTTTGAAGGTTTCCATGCCAT 720
Db 682 CTCACCTCAGCTCTCTTCCACTCCGATGGCTCCAGAAATTTTGAAGGTTTCCATGCCAT 741

to LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84) .

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK027841
AK027841.1 GI:14042813
oligo capping, fis (full insert sequence).
Homo sapiens
Homo sapiens

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1
Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
Sekine, M., Ohtsuka, M., Nishii, T., Shibahara, T., Tanaka, T.,
Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
Negahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M.,
Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T.,
Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K.,
Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H.,
Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S.,
Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A.,
Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R.,
Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A.,
Sasaki, N., Aotsuka, S., Yoshioka, Y., Matsunawa, H., Ichihara, T.,
Shichata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S.,
Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H.,
Goto, Y., Shinzui, F., Wakebe, H., Hishigaki, H., Watanabe, T.,
Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,
Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M.,
Tadai, H., Tanigami, A., Fujisawa, T., Ono, T., Yamada, K., Fujii, Y.,
Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N.,
Inagaki, H., Ikema, Y., Okamoto, S., Ohtani, R., Kawakami, K.,
Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K.,
Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T.,
Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J.,
Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R.,
Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs

Nat. Genet. 36 (1), 40-45 (2004)
14702039

JOURNAL
PUBMED
REFERENCE
AUTHORS

2
Isogai, T., Ota, T., Hayaashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H.,
Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K.,
Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K.,
Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,
Nakamura, Y., Nagahara, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.
NEDO human cDNA sequencing project
Unpublished

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

3 (bases 1 to 2784)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology; cDNA library construction;
5'- & 3'-end one pass sequencing and clone selection; Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.

FEATURES
source

Location/Qualifiers
1..2784
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1009992"
/tissue_type="placenta"
/clone_lib="PLACE1"

/note="cloning vector: pME18SFL3"
47..2260
/note="unnamed protein product"
/codon_start=1
/protein_id="BAB55404.1"
/db_xref="GI:14042814"

CDS

ORIGIN
Query Match 92.6%; Score 2636.8; DB 9; Length 2784;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 2710; Conservative 0; Mismatches 2; Indels 52; Gaps 2;
QY 1 CGCTCGGCACAGCCGCGCAAGGATGAGCTGGGTTGCTGGACGCGAGTTGGGGCTCAC 60
DB 22 CGCTCGGCACAGCCGCGCGCAAGGATGAGCTGGGTTGCTGGACGCGAGTTGGGGCTCAC 81
QY 61 TTTTCTTTCAGCTCCTCTCATCTCGTCTTCCCAAGAGAGTACACAGTCATTAATGAAGC 120
DB 82 TTTTCTTTCAGCTCCTCTCATCTCGTCTTCCCAAGAGAGTACACAGTCATTAATGAAGC 141
QY 121 CTGCTCGGCACAGAGTGGAATATCATGTGTCGGAGTGCTGTGATATGATCAGATTGA 180
DB 142 CTGCTCGGCACAGAGTGGAATATCATGTGTCGGAGTGCTGTGATATGATCAGATTGA 201
QY 181 GTGCTGTCGCCCGGAAAGAGGGAAGTCTGGGTTTATACCATCCCTCTGCTGCAGGAATGA 240
DB 202 GTGCTGTCGCCCGGAAAGAGGGAAGTCTGGGTTTATACCATCCCTCTGCTGCAGGAATGA 261
QY 241 GGAGAATGAGTGTGACTCTCTGCTGATCCACCCAGGTTGTACCATCTTTGGAATATGCA 300
DB 262 GGAGAATGAGTGTGACTCTCTGCTGATCCACCCAGGTTGTACCATCTTTGGAATATGCA 321
QY 301 GAGTGCAGAAATGGCTCATGCGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCTA 360
DB 322 GAGTGCAGAAATGGCTCATGCGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCTA 381
QY 361 CTGTGAGAGTGCAGAGCAGGCTGCTGCGAGGAGACTGTCATGCGATGTCGCGAGTTCT 420
DB 382 CTGTGAGAGTGCAGAGCAGGCTGCTGCGAGGAGACTGTCATGCGATGTCGCGAGTTCT 441
QY 421 CGGAGCCCAAGGGTCAAGATTTTGTGGAAAGCTATCCCTTAAATGCTCATGTGAATG 480
DB 442 CGGAGCCCAAGGGTCAAGATTTTGTGGAAAGCTATCCCTTAAATGCTCATGTGAATG 501
QY 481 GACCATTCATGCTAAACCTGGGTTTGTTCATCACTCAAGATTTGTTCATGTTGAGTCTCGA 540
DB 502 GACCATTCATGCTAAACCTGGGTTTGTTCATCACTCAAGATTTGTTCATGTTGAGTCTCGA 561
QY 541 GTTTGACTTACATGTGCCAGTATGACTATGTTGAGGTTCTGATGGAGACCAACCGGATGG 600
DB 562 GTTTGACTTACATGTGCCAGTATGACTATGTTGAGGTTCTGATGGAGACCAACCGGATGG 621
QY 601 CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCGAGCTCCTATCCAGAGCATAGGATC 660
DB 622 CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCGAGCTCCTATCCAGAGCATAGGATC 681
QY 661 CTCACCTCCAGCTCTCTTCCACTCGGATGGCTCCAGGAATTTTGACGGTTTCCATGCCAT 720
DB 682 CTCACCTCCAGCTCTCTTCCACTCGGATGGCTCCAGGAATTTTGACGGTTTCCATGCCAT 741

VERSION AX704692.1 GI:29561394
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Deleane, A.M., Gandhi, A.R., Hafalia, A.J., Lu, D.A., Patterson, C.,
Tribouley, C.M., Das, D., Kallick, D.A., Nguyen, D.B., Lee, E.A.,
Khan, F.A., Yue, H., Au-Yang, J., Griffin, J.A., Policky, J.B.,
Ramkumar, J., Yang, J., Thangavelu, K., Ding, L., Kearney, L.,
Baughn, M.R., Borowsky, M.L., Sanjanwalla, M.S., Yao, M.G., Burford, N.,
Walia, N.K., Lal, P., Lee, S., Todd, S., Lo, T.P., Tang, Y.T.,
Elliott, V.S., Azimzai, Y. and Lu, Y.
TITLE Proteases
JOURNAL Patent: WO 0208396-A 38 31-JAN-2002;
Incyte Genomics, Inc. (US)
FEATURES
source Location/Qualifiers
1..2632
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 7479181CBI"

ORIGIN
Query Match 80.5%; Score 2292.4; DB 6; Length 2632;
Best Local Similarity 92.2%; Pred. No. 0;
Matches 2516; Conservative 0; Mismatches 1; Indels 213; Gaps 1;
1 CGCTCGGCACAGCCGGCGCAAGATGGAGCTGGGTTGCTGGACGACAGTTGGGGCTCAC 60
116 CGCTCGGCACAGCCGGCGCAAGATGGAGCTGGGTTGCTGGACGACAGTTGGGGCTCAC 175
61 TTTTCTTCAGCTCCTTCTCATCTCTGCTCTGCTTGGCAAGAGATGACAGTCAATTAATGAAGC 120
176 TTTTCTTCAGCTCCTTCTCATCTCTGCTCTGCTTGGCAAGAGATGACAGTCAATTAATGAAGC 235
121 CTGCCCTCGAGCAGAGTGAATATCATGTGCGGAGTGCTGTGAATGATGATGATGATGA 180
236 CTGCCCTCGAGCAGAGTGAATATCATGTGCGGAGTGCTGTGAATGATGATGATGATGA 295
181 GTGCGTCTGCCCCGAAAGAGAGAGTGTGCGGTTTATACCATCCCTTGTGCGAGGAATGA 240
296 GTGCGTCTGCCCCGAAAGAGAGAGTGTGCGGTTTATACCATCCCTTGTGCGAGGAATGA 355
241 GGAGAAATGAGTGTGACTCTGCTGCTGATCCAGCCAGGTTGTACCATCTTTGAAACTGCAA 300
356 GGAGAAATGAGTGTGACTCTGCTGCTGATCCAGCCAGGTTGTACCATCTTTGAAACTGCAA 415
301 GAGCTGCCGAATAGTCTCATGCGGGGGTACCTTGGATGACTTCTATGTGAAGGGTCTTA 360
416 GAGCTGCCGAATAGTCTCATGCGGGGGTACCTTGGATGACTTCTATGTGAAGGGTCTTA 475
361 CTGTGCAGAGTCCGAGCAGGCTGTGTACGAGGAGACTGCATGCGATGTGCGCAGGTTCT 420
476 CTGTGCAGAGTCCGAGCAGGCTGTGTACGAGGAGACTGCATGCGATGTGCGCAGGTTCT 535
421 CGAGCCCCAAAGGGTCAAGTTTGTGGAAGCTATCCCTTAATGCTCACTGTGAATG 480
536 CGAGCCCCAAAGGGTCAAGTTTGTGGAAGCTATCCCTTAATGCTCACTGTGAATG 595
481 GACCAATTCATGCTAAACCTGGGTTGTGATCCCACTAAGATTGTGATGTTGAGTCTGGA 540
596 GACCAATTCATGCTAAACCTGGGTTGTGATCCCACTAAGATTGTGATGTTGAGTCTGGA 655
541 GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTCTGTGATGAGACAAACCGCATGG 600
656 GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTCTGTGATGAGACAAACCGCATGG 715
601 CCAGATCATCAAGCGTGTCTGTGGCAACGAGGGCGCAGCTCTATCCAGAGCATAGGATC 660
716 CCAGATCATCAAGCGTGTCTGTGGCAACGAGGGCGCAGCTCTATCCAGAGCATAGGATC 775

QY 661 CTCACTCCACGTCCTCTTTCCACTCCGATGGCTCCAAGAAATTTTGACGGTTTCCATGCCAT 720
DB |||||||
QY 776 CTCACTCCACGTCCTCTTTCCACTCCGATGGCTCCAAGAAATTTTGACGGTTTCCATGCCAT 835
DB |||||||
QY 721 TTATGAGGAGATCAGCATGCTCTCTCATCCCTTTGTTTCCATGACGGCAGCTGGTCTCT 780
DB |||||||
QY 836 TTATGAGGAGATCAGCATGCTCTCTCATCCCTTTGTTTCCATGACGGCAGCTGGTCTCT 895
DB |||||||
QY 781 TGACAAGGCTGGATCTTCAAGAGTGTGCTGCTTGGCAGGCTATATCTGGGCGAGCTGTGA 840
DB |||||||
QY 896 TGACAAGGCTGGATCTTCAAGAGTGTGCTGCTTGGCAGGCTATATCTGGGCGAGCTGTGA 955
DB |||||||
QY 841 AAATCTCTTTGAAGAAAGAAATCTGCTCAGACCTCTGGGGGCCAGTCAATGGGTACAGAA 900
DB |||||||
QY 956 AAATC----- 960
QY 901 AATAACAGGGGGCCCTGGGCTTATCAACGGAGCCCATGCTAAATTTGGACCGCTGGTGTCT 960
DB ----- 960
QY 961 TTTCTTTGTAACTCTCTATGTTCTTAGTGGCAATGAGAAAGAACTTGGCCAGCAGAA 1020
DB ----- 960
QY 1021 TGGAGAGTGGTCAAGGAAACAGCCCATCTGCATAAAGCCTGCCGAGAACCAAGATTTTC 1080
DB |||||||-----CCTGCCGAGAAACCAAGATTTTC 982
QY 1081 AGACTGTGTGAGAGAGAGTCTTCCATGAGAGTTTCAAGTTCAGTCAAGGGAGACACCAATTACA 1140
DB |||||||
QY 983 AGACTGTGTGAGAGAGAGTCTTCCATGATGAGTTCAGTCAAGGGAGACACCAATTACA 1042
DB |||||||
QY 1141 CCAGTATACTCAGGGGCTTTCAGCAAGCAGAAATGCGAGAGTCCCTTCAACCAAGAGCC 1200
DB |||||||
QY 1043 CCAGTATACTCAGGGGCTTTCAGCAAGCAGAAATGCGAGAGTCCCTTCAACCAAGAGCC 1102
DB |||||||
QY 1201 AGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATATCCAGCTCCAGTA 1260
DB |||||||
QY 1103 AGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATATCCAGCTCCAGTA 1162
DB |||||||
QY 1261 TGAGTGCATCTCAACCTTCTACCCGCGCTGGGAGCAGCAGAGGAGCAATGTCTGAGGAC 1320
DB |||||||
QY 1163 TGAGTGCATCTCAACCTTCTACCCGCGCTGGGAGCAGCAGAGGAGCAATGTCTGAGGAC 1222
DB |||||||
QY 1321 TGGGAAGTGGAGTGGGGGCGCACCATCTCTGCATCCCTATCTCGCGGAAATTTGAGAACAT 1380
DB |||||||
QY 1223 TGGGAAGTGGAGTGGGGGCGCACCATCTCTGCATCCCTATCTCGCGGAAATTTGAGAACAT 1282
DB |||||||
QY 1381 CACTGCTCCAAAGACCCCAAGGGTTGCGCTGGCCGCTGGCAGGCGAGCCATCTACAGAGGAC 1440
DB |||||||
QY 1283 CACTGCTCCAAAGACCCCAAGGGTTGCGCTGGCCGCTGGCAGGCGAGCCATCTACAGAGGAC 1342
DB |||||||
QY 1441 CAGCGGGTGCATGACCGGACGCTTACAAAGGAGCGTGGTTCCTAGTCTGCGAGCGGTGC 1500
DB |||||||
QY 1343 CAGCGGGTGCATGACCGGACGCTTACAAAGGAGCGTGGTTCCTAGTCTGCGAGCGGTGC 1402
DB |||||||
QY 1501 CCTGTGTAATCAGCGCACTGTGTGGCTGCCACCTGCTTACTGACTGGGGAAGGT 1560
DB |||||||
QY 1403 CCTGTGTAATCAGCGCACTGTGTGGTGGCTGGCCACCTGTGTACTGACCTGGGGAAGGT 1462
DB |||||||
QY 1561 CACCATGATCAAGACAGCAGACCTCAAAAGTTGTTTGGGGAATTTCTACCGGGATGATGA 1620
DB |||||||
QY 1463 CACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAATTTCTACCGGGATGATGA 1522
DB |||||||
QY 1621 CCGGATGAGAAAGACCATCCAGAGCTTACAGATTTCTGCTATCATTTCTGCAATGCCAATGA 1680
DB |||||||
QY 1523 CCGGATGAGAAAGACCATCCAGAGCTTACAGATTTCTGCTATCATTTCTGCAATGCCAATGA 1582
DB |||||||
QY 1681 TGACCCCATCTGCTTGTGATGCTGATCGCCATCTCTGAAGCTCTTAGAACAGGCCCCGTAT 1740
DB |||||||
QY 1583 TGACCCCATCTGCTTGTGATGCTGATCGCCATCTCTGAAGCTCTTAGAACAGGCCCCGTAT 1642
DB |||||||
QY 1741 CAGCACCCGAGTCCAGCCCATCTGCTGCTGCCAGTGGGATCTCAGACTTCTTCTTCCA 1800

[illegible]

RESULT 12			
AR263926			
LOCUS	AR263926	2886 bp	DNA
DEFINITION	Sequence 104 from patent US 6331427.		linear
ACCESSION	AR263926		PAT 29-JAN-2003

Db 890 CATGCGGACGCTGGCTCCTTGCAAGGCTGGATCTTACAAGTGTGCTGTGGCAGGC 949
QY 821 -TATACTGGGACGCTGTGAAAATCTCTTCAAGAAAGAAACTGCTCAGACCTCTGGGG 879
Db 950 TTATACTGGGACGCTGTGAAAATCTCTTCAAGAAAGAAACTGCTCAGACCTCTGGGG 1009
QY 880 CCCAGTCAATGGGTACCGAAAATTAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGC 939
Db 1010 CCCAGTCAATGGGTACCGAAAATTAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGC 1069
QY 940 TAAATTTGGACCGTGGTGTCTTTCTTTTGTAACTCTTAAGTCTTGTAGTGGCAATGA 999
Db 1070 TAAATTTGGACCGTGGTGTCTTTCTTTTGTAACTCTTAAGTCTTGTAGTGGCAATGA 1129
QY 1000 GAAAGAACTTCCAGCAGAGTGGAGAGTGGTCAGGGAACAGCCATCTGCATAAAAGC 1059
Db 1130 GAAAGAACTTCCAGCAGAGTGGAGAGTGGTCAGGGAACAGCCATCTGCATAAAAGC 1189
QY 1060 CTGCCGAGAACCAAGATTTTCAGACCTGGTGAGAGAGAGTTCCTTCGGATGTCAGGTTCA 1119
Db 1190 CTGCCGAGAACCAAGATTTTCAGACCTGGTGAGAGAGAGTTCCTTCGGATGTCAGGTTCA 1249
QY 1120 GTCAAGGAGACA -CCATTAACACAGCTATATCTAGCGGCTTTCAGAGCAGAAACT-- 1176
Db 1250 GTCAAGGAGACACCCAAATTCACAGCTATATCTAGCGGCTTTCAGAGCAGAAACTTG 1309
QY 1177 GCAGAGTGCCTTACCAAGAACCCAGCCCTTCCCTTTGGAGATC -TGCCCATGGATACC 1235
Db 1310 CAAGAGTGCCTTACCAAGAACCCAGCCCTTCCCTTTGGAGATCTTGCCCATGGATACC 1369
QY 1236 AACATC -TGCCATACCAGCTCCAGTATGAGTGCATCTCACCCCTTCTACCGCGCCTGGGC 1294
Db 1370 AACATCTTGCATACCAGCTCCAGTATGAGTGCATCTCACCCCTTCTACCGCGCCTGGGC 1429
QY 1295 AGCAGCA -GGAGGACATGCTGAGGACCTGGGAAGTGGAGTGGGC -GGGCAACCATCCTGCA 1352
Db 1430 AGCAGCAGGAGGACATGTTTGGAGACTGGGAAGTGGAGTGGGCGGGGCAACCATCCTGCA 1489
QY 1353 TCCCTATCTGGGGAATTTGAGAACATCACTGCTCCAAAGACCCAAAGGTTGGCTGGC 1412
Db 1490 TCCCTATCTGGGGAATTTGAGAACATCACTGCTCCAAAGACCCAAAGGTTGGCTGGC 1549
QY 1413 CTTGCGAGGAGCCATCTACAGGAGGACCCAGCGGGTGCATGACCGGAGCCTTACAAAGG 1472
Db 1550 CTTGCGAGGAGCCATCTACAGGAGGACCCAGCGGGTGCATGACCGGAGCCTTACAAAGG 1609
QY 1473 GAGCGTGTCTAGTCTGCGAG -CGGTGCTGTGTAATGAGCGCAC -TGTGGTGGTGGC 1530
Db 1610 GAGCGTGTCTAGTCTGCGAGCGGCTGCTGTGTAATGAGCGCAC -TGTGGTGGTGGC 1669
QY 1531 TGCCCACTGTGTTACTGACCTGGGGAAGTGCATGATCAAGACAGCAGACCTGAAAGT 1590
Db 1670 TGCCCACTGTGTTACTGACCTGGGGAAGTGCATGATCAAGACAGCAGACCTGAAAGT 1729
QY 1591 TGTGTTGGGAAATTTCTACCGGATGATGACC -GGGATGAGAAACCATCCAGAGCCTTAC 1649
Db 1730 TGTGTTGGGAAATTTCTACCGGATGATGACC -GGGATGAGAAACCATCCAGAGCCTTAC 1789
QY 1650 AGATTTCTGCTATCATCTTCGATCCCAACTATGACCCCATCTGCTGTGATGCTGACATCG 1709
Db 1790 AGATTTCTGCTATCATCTTCGATCCCAACTATGACCCCATCTGCTGTGATGCTGACATCG 1849
QY 1710 CCATCTCAAGCTCTACAGAGGCGCTTATCAGACCCGAGTCCAGGCCCATCTGCGCTCG 1769
Db 1850 CCATCTCAAGCTCTACAGAGGCGCTTATCAGACCCGAGTCCAGGCCCATCTGCGCTCG 1909
QY 1770 CTGCCAGTCTGGGATCTCAGCACTTCTTCCAGGAGTCCCAATC -ACTGTGGCTGGCTGG 1828
Db 1910 CTGCCAGTCTGGGATCTCAGCACTTCTTCCAGGAGTCCCAATCAGCATGCTGGCTGG 1969
QY 1829 AATGTCCTGGCAGAGCTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTG 1888
Db 1970 AATGTCCTGGCAGAGCTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTG 2029

QY 1889 GTCAGTGTGGTGGACTCGCTGCTGTGTGAGG -AGCAGCATGA -GGACCATGGCATCCCCAG 1946
Db 2030 GTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAACATGAGGAGCAATGGCATCCCCAG 2089
QY 1947 T -GAGTGTCACTGATPAACATGTTCTGTGCCAGCTGGGAACCACTGCCCCCTTCTGATATC 2005
Db 2090 TGGAGTGTCACTGATPAACATGTTCTGTGCCAGCTGGGAACCACTGCCCCCTTCTGATATC 2149
QY 2006 TGCACTGAGAGACAGGAGGCATCGCGCTGTGTCTTCCCGGAGCAGCATCTCTGTAG 2065
Db 2150 TGCACTGAGAGACAGGAGGCATCGCGCTGTGTCTTCCCGGAGCAGCATCTCTGTAG 2209
QY 2066 CCAGCTCTGGCATCTGATGGGACTGTC - -AGCTGGAGC -TATGATAAAACATGCGAGCCAC 2122
Db 2210 CCAGCTCTGGCATCTGATGGGACTGTCAGCTGAGCTTATGATAAAACATGCGAGCCAC 2269
QY 2123 AGGCTCTCCACTGCTTCCACCAAGGTGCTGCTTTT - AAAGA CTGGATTTGAAAGAAATAT 2181
Db 2270 AGGCTCTCCACTGCTTCCACCAAGGTGCTGCTTTTAAAGACTGGAATTGAAAGAAATAT 2329
QY 2182 GAAATGAACCATGCTCATGCACTCCTTGAG -AAGTGTCTTCTGTATATCGCTGTGACGTG 2240
Db 2330 GAAATGAACCATGCTCATGCACTCCTTGAGAAAGTGTCTGTATATCCGCTGTGACGTG 2389
QY 2241 TGTCAATTGCGTGAAGCAGTGTGGGCTCGAAGTGTGATTGGCTCTGTAACCTTGGCTGTGC 2300
Db 2390 TGTCAATTGCGTGAAGCAGTGTGGGCTCGAAGTGTGATTGGCTGTGTAACCTTGGCTGTGC 2449
QY 2301 CAGGCTCTTCACTTTACGGGACAAACTCAGTGAAGGTGAGTAGACCTCCATTCCTGCTGGT 2360
Db 2450 CAGGCTCTTCACTTTACGGGACAAACTCAGTGAAGGTGAGTAGACCTCCATTCCTGCTGGT 2509
QY 2361 AGGCTGATGCGCGCTCCACTACTAGGACAGCCAAATTTGGAAGATGCGAGGCTTGCAGAA 2420
Db 2510 AGGCTGATGCGCGCTCCACTACTAGGACAGCCAAATTTGGAAGATGCGAGGCTTGCAGAA 2569
QY 2421 GTAAGTTTC -TTCAAAGAAAGCAATATACAAACCTCTCCACTCCACTGACCTGCTGGTGC 2479
Db 2570 GTAAGTTTCGTTCAAAGAAAGCAATATACAAACCTCTCCACTCCACTGACCTGCTGGTGC 2629
QY 2480 TTCCCCAACTTTCAGTTATACGAATGCGCATCAGCTTGACAGGGAAGATCTGGGCTTCAT 2539
Db 2630 TTCCCCAACTTTCAGTTATACGAATGCGCATCAGCTTGACAGGGAAGATCTGGGCTTCAT 2689
QY 2540 GAGGCCCCCTTTGAGGCTCTCAAGTCTTAGAGA -GCTGCGCTGTGGACAGCCAGGCGAG 2598
Db 2690 GAGGCCCCCTTTGAGGCTCTCAAGTCTTAGAGACGCTGCTGTGGGACAGCCAGGCGAG 2749
QY 2599 CAGAGCTGGGA - -TGTGCTGATGCTTGTGTATACATGGCCACAGTAC -AGTCTGCTGCT 2655
Db 2750 CAGAGCTGGGAATGCTGCTGATGCTTGTGTATGCTGCTTGTGATGCTGCTGCT 2809
QY 2656 TTTCCTTCCCATCTCTTGTGACATTTAATAAAGGTTGGCTTCTGAACTACAA 2715
Db 2810 TTTCCTTCCCATCTCTTGTGACATTTAATAAAGGTTGGCTTCTGAACTACAA 2869
QY 2716 AAAAAAAAAAAAAA 2730
Db 2870 AAAAAAAAAAAAAA 2884

RESULT 13

BC038457

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BC038457 2350 bp mRNA linear PRI 26-JUN-2004
Homo sapiens regeneration associated muscle protease, mRNA (cdna
clone IMAGE:4526572), partial cds.

BC038457

BC038457.1 GI:23620401

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 2350)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, P.S., Wagner, K.H., Shenmen, C.M., Schuler, G.D.,
 Alschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Wotley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huiyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
 Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL PUBMED 12477932

2 (bases 1 to 2350)
 Strausberg, R.

Direct Submission

Submitted (04-OCT-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgaps-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc.mgc@nri.nih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Scantripop, S., Thomas, P.J., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAP Plate: 78 Row: b Column: 7.

Location/Qualifiers

1. 2350

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4526572"

/tissue_type="Bladder, transitional cell papilloma"

/clone_lib="NIH MGC_93"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

FEATURES

source

ORIGIN

Query Match 78.1%; Score 2223.8; DB 9; Length 2350;

Best Local Similarity 97.7%; Pred. No. 0;

Matches 2286; Conservative 2; Mismatches 2; Indels 51; Gaps 1;

QY 515 CTAAGATTGTCATGTCGAGTTCGAGTTTGACTACATGTCGAGTTCGAGTTCGAG 574

DB 12 CTAAGATTGTCATGTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAG 71

QY 575 GTTCGTGATGAGACAACCGCGATGCGCAGATCATCAAGCGTGTCTGTGGCAACGAGCG 634
 DB 72 GTTCGTGATGAGACAACCGCGATGCGCAGATCATCAAGCGTGTCTGTGGCAACGAGCG 131
 QY 635 CCAGTCTCTATCCAGAGCATAGGATCTCTCACTCCAGCTGCTCTTCCACTCCGATGCTCC 694
 DB 132 CCAGTCTCTATCCAGAGCATAGGATCTCTCACTCCAGCTGCTCTTCCACTCCGATGCTCC 191
 QY 695 AAGAAATTTGACGGTTTCATGCCATTTATGAGGAGATCACAGCATGTCTCTCATCCCT 754
 DB 192 AAGAAATTTGACGGTTTCATGCCATTTATGAGGAGATCACAGCATGTCTCTCATCCCT 251
 QY 755 TGTTCATGACGGCACTGCGTCTTCAAGGCTGGATTTACAAGTGTGCTGCTG 814
 DB 252 TGTTCATGACGGCACTGCGTCTTCAAGGCTGGATTTACAAGTGTGCTGCTG 311
 QY 815 GCAGCTATACCTGGCAGCGCTGTGAANAATC----- 845
 DB 312 GCAGCTATACCTGGCAGCGCTGTGAANAATCTTCTGGAGGCTGGGAAGTCCAAGATCAAG 371
 QY 846 -----TCCTTGAAGAAAGAAACTGCTCAGACCTCGGGGGCCCA 883
 DB 372 CGGTGAGAAATTCATGCTGCTCTTGAAGAAAGAAACTGCTCAGACCTCGGGGGCCCA 431
 QY 884 GTCAATGGGTACAGAAATAACAGGGGCGCTTGGGCTTATCAACGAGCGCATGCTAAA 943
 DB 432 GTCAATGGGTACAGAAATAACAGGGGCGCTTGGGCTTATCAACGAGCGCATGCTAAA 491
 QY 944 ATTGGACACGCTGCTGCTCTTTTGTAACTCTATGTTCTTAGTGGCAATGAGAAA 1003
 DB 492 ATTGGACACGCTGCTGCTCTTTTGTAACTCTATGTTCTTAGTGGCAATGAGAAA 551
 QY 1004 AGAAGCTTCCAGCAGATGAGAGTGTGTCAGGAAACAGCCATCTGCATAAAGCCTGC 1063
 DB 552 AGAAGCTTCCAGCAGATGAGAGTGTGTCAGGAAACAGCCATCTGCATAAAGCCTGC 611
 QY 1064 CGAGAACCAAGATTTTCAGACCTGCTGAGAGGAGAGTTCCTCCGATGAGTTCAGTCA 1123
 DB 612 CGAGAACCAAGATTTTCAGACCTGCTGAGAGGAGAGTTCCTCCGATGAGTTCAGTCA 671
 QY 1124 AGGAGACACATTTACACAGCTATACCTAGGCGCTTTCAGCAAGCAGAACTGAGAT 1183
 DB 672 AGGAGACACATTTACACAGCTATACCTAGGCGCTTTCAGCAAGCAGAACTGAGAT 731
 QY 1184 GCCCTTACCAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGGATACCAACATCTG 1243
 DB 732 GCCCTTACCAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGGATACCAACATCTG 791
 QY 1244 CATACCCAGCTCCAGTATGATGTCATCTCACCTTTCTACCGCGCTTGGGAGCAGCAGG 1303
 DB 792 CATACCCAGCTCCAGTATGATGTCATCTCACCTTTCTACCGCGCTTGGGAGCAGCAGG 851
 QY 1304 AGGACATGTCGAGGACCTGGGAAGTGGAGTGGGGGGGAGCCATCTCTGATCCCTATGTC 1363
 DB 852 AGGACATGTCGAGGACCTGGGAAGTGGAGTGGGGGGGAGCCATCTCTGATCCCTATGTC 911
 QY 1364 GGGAAATTTGAGAACATCACTGCTTCCAAAGACCCAAAGGTTTGGCTGGCGTGGCAGGCA 1423
 DB 912 GGGAAATTTGAGAACATCACTGCTTCCAAAGACCCAAAGGTTTGGCTGGCGTGGCAGGCA 971
 QY 1424 GCCATCTACAGGAGGACCCAGCGGGTGCATGACGGCAGCTTACACAGGGAGCGTGGTTC 1483
 DB 972 GCCATCTACAGGAGGACCCAGCGGGTGCATGACGGCAGCTTACACAGGGAGCGTGGTTC 1031
 QY 1484 CTAGTCTCAGCGTGCCTGCTGTAATGAGCGCATGTGGTGGCTGGCTGCCACCTGTGTT 1543
 DB 1032 CTAGTCTCAGCGTGCCTGCTGTAATGAGCGCATGTGGTGGCTGGCTGCCACCTGTGTT 1091
 QY 1544 ACTGACCTGGGAGGTCACCATGATCAAGACAGCAGACCTGGAAGTGTGTTTGGGAAA 1603
 DB 1092 ACTGACCTGGGAGGTCACCATGATCAAGACAGCAGACCTGGAAGTGTGTTTGGGAAA 1151

QY 301 GAGTGCAGAAATGGCTCATGGGGGGTACCTTGGATGACTCTATGTGAAGGGTTCTTA 360
DB 403 GAGTGCAGAAATGGCTCATGGGGGGTACCTTGGATGACTCTATGTGAAGGGTTCTTA 462
QY 361 CTGTGCAGATGCGCAGCAGGCTGTGACGAGGAGACTGCATGCGATGTGCGCAGGTTCT 420
DB 463 CTGTGCAGATGCGCAGCAGGCTGTGACGAGGAGACTGCATGCGATGTGCGCAGGTTCT 522
QY 421 CGAGCCCCAAAGGGTCAGATTTTGTGTGAAGCTATCCCTTAATGCTCACTGTGAATG 480
DB 523 CGAGCCCCAAAGGGTCAGATTTTGTGTGAAGCTATCCCTTAATGCTCACTGTGAATG 582
QY 481 GACCAATCATGCTAAACCTGGTGTGTCATCCAACTAAAGATTTGTCATGTTGAGTCTGGA 540
DB 583 GACCAATCATGCTAAACCTGGTGTGTCATCCAACTAAAGATTTGTCATGTTGAGCTGGA 642
QY 541 GTTTGACTACATGTCGCCAGTATGACTATGTTGAGGTTGCTGATGGAGACAACCGCATGG 600
DB 643 GTTTGACTACATGTCGCCAGTATGACTATGTTGAGGTTGCTGATGGAGACAACCGCATGG 702
QY 601 CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATC 660
DB 703 CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATC 762
QY 661 CTCACTCCAGCTCTCTTCCACTCCGATGGCTCCAAAGATTTTGAACGGTTTCCATGCCAT 720
DB 763 CTCACTCCAGCTCTCTTCCACTCCGATGGCTCCAAAGATTTTGAACGGTTTCCATGCCAT 822
QY 721 TTATGAGGAGATCACAGCATGCTCTCATCCCTGTTTCCATGACGCGCATGGTCTCT 780
DB 823 TTATGAGGAGATCACAGCATGCTCTCATCCCTGTTTCCATGACGCGCATGGTCTCT 882
QY 781 TGACAAGGCTGGATCTTCAAGTGTGCTCTTGGCAGGCTATATCTGGCAGCGCTGTGA 840
DB 883 TGACAAGGCTGGATCTTCAAGTGTGCTCTTGGCAGGCTATATCTGGCAGCGCTGTGA 942
QY 841 AAATCTCTTGAAGAAAGAACTGTCTAGACCTGGGGGCCAGTCAATGGGTACAGAA 900
DB 943 AAATCTCTTGAAGAAAGAACTGTCTAGACCTGGGGGCCAGTCAATGGGTACAGAA 1002
QY 901 AATAACAGGGGGCCCTGGGCTTATCAACGAGCGCATGCTTAAATTTGCCACCGTGTCTC 960
DB 1003 AATAACAGGGGGCCCTGGGCTTATCAACGAGCGCATGCTTAAATTTGCCACCGTGTCTC 1062
QY 961 TTTCTTTTGTAACTACTCTATGTTCTTAGTGGCAATGAGAAAGAACTTGGCAGCAGAA 1020
DB 1063 TTTCTTTTGTAACTACTCTATGTTCTTAGTGGCAATGAGAAAGAACTTGGCAGCAGAA 1122
QY 1021 TGGAGATGGTTCAGGGAACAGCCCATCTGCATAAAGCCTGCCAGAAACCAAGATTTTC 1080
DB 1123 TGGAGATGGTTCAGGGAACAGCCCATCTGCATAAAGCCTGCCAGAAACCAAGATTTTC 1182
QY 1081 AGACCTGTGAGAGGAGTCTTCCGATGCGAGTTGCTCAAGGGAGACACCAATTACA 1140
DB 1183 AGACCTGTGAGAGGAGTCTTCCGATGCGAGTTGCTCAAGGGAGACACCAATTACA 1242
QY 1141 CCAGCTATACTCAGCGGCTTTCAGCAAGCAGAACTGCAGAGTGCCCTTACCAAGAAGCC 1200
DB 1243 CCAGCTATACTCAGCGGCTTTCAGCAAGCAGAACTGCAGAGTGCCCTTACCAAGAAGCC 1302
QY 1201 AGCCCTTCCCTTTGGAGATCTGCCCATACCAACATCTGCATATCCAGCTCCAGTA 1260
DB 1303 AGCCCTTCCCTTTGGAGATCTGCCCATACCAACATCTGCATATCCAGCTCCAGTA 1362
QY 1261 TGAGTGCATCTCACCTTCTACCGCGCTTGGGAGCAGCAGGAGGACATGCTCAGGAC 1320
DB 1363 TGAGTGCATCTCACCTTCTACCGCGCTTGGGAGCAGCAGGAGGACATGCTCAGGAC 1422
QY 1321 TGGGAAGTGGAGTGGGGGGCAGCATCTGTCATCCCTTCTGCGGGAATTTGAGAACAT 1380
DB 1423 TGGGAAGTGGAGTGGGGGGCAGCATCTGTCATCCCTTCTGCGGGAATTTGAGAACAT 1482
QY 1381 CACTGCTCCAAAGACCCAAAGGGTTGCGTGGCGGTGGCAGGCGCATCTACAGGAGGAC 1440

DB 1483 CACTGCTCCAAAGACCCCAAGGGTTGCGTGGCCGTGGCAGGAGCATCTACAGGAGGAC 1542
QY 1441 CAGCGGGTGCATGACGCGCAGCTACCAAGGAGCGTGGTTCCTAGTCTCTGAGCGGTGC 1500
DB 1543 CAGCGGGTGCATGACGCGCAGCTACCAAGGAGCGTGGTTCCTAGTCTCTGAGCGGTGC 1602
QY 1501 CCTGGTGAATGAGCGCACTGTGGTGGCTGGCCACCTGTGTACTGACCTGGGGAAGGT 1560
DB 1603 CCTGGTGAATGAGCGCACTGTGGTGGCTGGCCACCTGTGTACTGACCTGGGGAAGGT 1662
QY 1561 CACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAATTTCTACCGGATGATGA 1620
DB 1663 CACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAATTTCTACCGGATGATGA 1722
QY 1621 CCGGATGAGAAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCAATCCCACTA 1680
DB 1723 CCGGATGAGAAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCAATCCCACTA 1782
QY 1681 TGACCCCATCTGTTGATGTGACATCGCCATCTCTGAAGTCTCTAGACAAGGCCGTAT 1740
DB 1783 TGACCCCATCTGTTGATGTGACATCGCCATCTCTGAAGTCTCTAGACAAGGCCGTAT 1842
QY 1741 CAGCACCCGAGTCCAGCCCATCTGCTCGCTGCCAGTCCGGATCTCAGCACTTCTTCCA 1800
DB 1843 CAGCACCCGAGTCCAGCCCATCTGCTCGCTGCCAGTCCGGATCTCAGCACTTCTTCCA 1902
QY 1801 GGAGTCCCAATCACTGTTGGTGGCTGGAATGTCTGCGCAGACGCTGAGGAGCCCTGGCTT 1860
DB 1903 GGAGTCCCAATCACTGTTGGTGGCTGGAATGTCTGCGCAGACGCTGAGGAGCCCTGGCTT 1962
QY 1861 CAAGAACACACACTGCGCTCTGGGGTGGTCAAGTGTGTGAGACTCGCTGTGTGAGAA 1920
DB 1963 CAAGAACACACACTGCGCTCTGGGGTGGTCAAGTGTGTGAGACTCGCTGTGTGAGAA 2022
QY 1921 GCAGCATGAGAACCATGGCATCCCAAGTGTGCTCACTGATTAACATGTTCTGTGCCAGTGT 1980
DB 2023 GCAGCATGAGAACCATGGCATCCCAAGTGTGCTCACTGATTAACATGTTCTGTGCCAGTGT 2082
QY 1981 GGAAACCACTCCCTTCTGATATCTGACCTGCGCAGACAGAGGACATCGCGGCTGTCTC 2040
DB 2083 GGAAACCACTCCCTTCTGATATCTGACCTGCGCAGACAGAGGACATCGCGGCTGTCTC 2142
QY 2041 CTTCCCGGAGCAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGGTCACTGGAG 2100
DB 2143 CTTCCCGGAGCAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGGTCACTGGAG 2202
QY 2101 CTATGATAAATGACATGACGCTCTCAGCTCCCTTCCAGAGGTTGCTGCTTTTAA 2160
DB 2203 CTATGATAAATGACATGACGCTCTCAGCTCCCTTCCAGAGGTTGCTGCTTTTAA 2262
QY 2161 AGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACT 2204
DB 2263 AGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACT 2306

RESULT 15
AX133839
LOCUS AX133839 2306 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 25 from Patent WO0119856.
ACCESSION AX133839
VERSION AX133839.1 GI:14139791
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets, R.A., Fernandes, E., Herrmann, J.L., Liu, X., Yang, M. and Boldog, F.L.
TITLE Secreted human proteins, polynucleotides encoding them and methods of using the same
JOURNAL Patent: WO 0119856-A 25 22-MAR-2001;

FEATURES		Curagen Corporation (US)
source	1..2306	Location/Qualifiers
	/organism="Homo sapiens"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:9606"	
CDS	128..2290	
	/note="unnamed protein product"	
	/codon_start=1	
	/protein_id="CAC38970.1"	
	/db_xref="GI:14139792"	
	/translation="MELGCVTQLGLTFLQLLLISLPREYTVINEACPAEWNIMCRE CCEYDQIEVCPGKEVVGVTIPCCRNENECDCLIPHGCTIIFENCKSRGWSGGT LDDFVFGYCAECREAGWYGDCKRGVLRAPKQIILLESYPLNAHCWTHAKPGF VIQIRFVMSLFEFYMCQDYVEVDGDNRDGQIILKRVGNERPAPIQISGLHLVLF HSDGSKNFDGFAHYEITACSSSPCFHDGTCVLDKAGSYKACLAGYTGRCENILLE ERNDCDPPGVNGYQKITGGPGLNGHAKIGTVVSPFCNNYSYVLSGNEKRTCCQNGE WSGQPICIKARPEKISDLVRLRPMQVSRRETPHQLYSAAFQKQLQSAATKPK ALPFDLPMGQHLHLTQYBICISPFYRLGSRKTLCTKQWGRAPSCVPICKIE NITAPKTGLRWQAAIYVRTSGVHSLKGAFLVCSGALVNERPVVAAHCVTD LGKVTMIKTADLVVLGKRYRDDRDDEXTIOSLOISAIILHPNVDPIILLADIALLKL LDKARISIRVQPICLAASRDLSFQESHITVAGNNVLADVRSFGFNDTIRSGVSVR VDSLCEQHEHDGIPVSDTNMFCAWSPEPTAPSDICTAETGAGIAAVSFPRASPEPR WHLMLVSWSYDKTCSHRLSTAFTKVLPPFKDWIERNMK"	
ORIGIN		
Query Match		77.2%; Score 2197.6; DB 6; Length 2306;
Best Local Similarity		99.8%; Pred. No. 0;
Matches 2200; Conservative		0; Mismatches 4; Indels 0; Gaps 0;
Qy	1	CGCTCGGACACAGCGCGGAAGAGTGGAGTGGGTTGCTGGAGCGCAGTTGGGGCTCAC 60
Db	103	CGCTCGGACACAGCGCGGAAGAGTGGAGTGGGTTGCTGGAGCGCAGTTGGGGCTCAC 162
Qy	61	TTTTCTTCAGTCTCTTCATCTCGTCTTGGCAAGAGAGTACACAGTCATTAATGAAGC 120
Db	163	TTTTCTTCAGTCTCTTCATCTCGTCTTGGCAAGAGAGTACACAGTCATTAATGAAGC 222
Qy	121	CTGCCCTCGAGCAGAGTGGAAATATCATGTGCGGAGTGCTGTGAATATGATCAGATTGA 180
Db	223	CTGCCCTCGAGCAGAGTGGAAATATCATGTGCGGAGTGCTGTGAATATGATCAGATTGA 282
Qy	181	GTGCGTCTGCCCCGAAAGAGGAAAGTCTGGGTTTATACCATCCCTTGTCTGCAGGAATGA 240
Db	283	GTGCGTCTGCCCCGAAAGAGGAAAGTCTGGGTTTATACCATCCCTTGTCTGCAGGAATGA 342
Qy	241	GGAGAAATGAGTGTGATCTCGTCTGATCCACCCAGGTTGTACCATCTTTGAAACTGCAA 300
Db	343	GGAGAAATGAGTGTGATCTCGTCTGATCCACCCAGGTTGTACCATCTTTGAAACTGCAA 402
Qy	301	GAGCTGCCGAAATGGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTA 360
Db	403	GAGCTGCCGAAATGGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTA 462
Qy	361	CTGTGCAGAGTGGCCGAGCAGGCTGGTACGAGGAGACTGCATGCGATGTGGCCAGGTTCT 420
Db	463	CTGTGCAGAGTGGCCGAGCAGGCTGGTACGAGGAGACTGCATGCGATGTGGCCAGGTTCT 522
Qy	421	CGGAGCCCAAGGGGTGAGATTTTGTGGAAAGCTATCCCTTAATGCTCATGTGGAATG 480
Db	523	CGGAGCCCAAGGGGTGAGATTTTGTGGAAAGCTATCCCTTAATGCTCATGTGGAATG 582
Qy	481	GACCATTCATGTAACCTGGGTTTGTTCATCCAACTAAGATTGTTCATGTTGAGTCTGGA 540
Db	583	GACCATTCATGTAACCTGGGTTTGTTCATCCAACTAAGATTGTTCATGTTGAGCCTGGA 642
Qy	541	GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTGCTGATGGAGACAAACCGGATGG 600
Db	643	GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTGCTGATGGAGACAAACCGGATGG 702
Qy	601	CCAGATCATCAAGCGTGTCTGTGGCAACGAGGGCGCAGCTCTTATCCAGAGCATAGGATC 660
Db	703	CCAGATCATCAAGCGTGTCTGTGGCAACGAGGGCGCAGCTCTTATCCAGAGCATAGGATC 762

Qy	661	CTCACTCCACGTCCTCTTCCACTCCGATGGCTCCAGAAATTTTGACGGTTTCCATGCCAT 720
Db	763	CTCACTCCACGTCCTCTTCCACTCCGATGGCTCCAGAAATTTTGACGGTTTCCATGCCAT 822
Qy	721	TTATGAGGAGATCACAGCATGCTCCTCATCCCCCTTTGTTTCCATGACGCGCATGTCGCT 780
Db	823	TTATGAGGAGATCACAGCATGCTCCTCATCCCCCTTTGTTTCCATGACGCGCATGTCGCT 882
Qy	781	TGACNAGGCTGGATCTTCAAGTGTGCTGCTTGGCAGGCTATATCTGGGACGCGCTGTGA 840
Db	883	TGACNAGGCTGGATCTTCAAGTGTGCTGCTTGGCAGGCTATATCTGGGACGCGCTGTGA 942
Qy	841	AAATCTCTTCAAGAAAGAAACTGCTCAGACCCCTGGGGGCCAGTCAATGGGTACAGAA 900
Db	943	AAATCTCTTCAAGAAAGAAACTGCTCAGACCCCTGGGGGCCAGTCAATGGGTACAGAA 1002
Qy	901	AATAACAGGGGGCCTTGGGCTTATCAACGAGCGCCATGCTAAAAATTGGCACCGTGGTGC 960
Db	1003	AATAACAGGGGGCCTTGGGCTTATCAACGAGCGCCATGCTAAAAATTGGCACCGTGGTGC 1062
Qy	961	TTTTCTTTGTAACTCTTATGTTCTTAGTGGCAATGAGAAAGAACTTGGCAGCAGAA 1020
Db	1063	TTTTCTTTGTAACTCTTATGTTCTTAGTGGCAATGAGAAAGAACTTGGCAGCAGAA 1122
Qy	1021	TGGAGAGTGGTCAGGAAACAGCCCATCTGCATAAAAAGCTGCCGAGAACCAAGATTTC 1080
Db	1123	TGGAGAGTGGTCAGGAAACAGCCCATCTGCATAAAAAGCTGCCGAGAACCAAGATTTC 1182
Qy	1081	AGACTGTGTGAGAGGAGGAGTTCTTCCGATCGAGTTTCAGTCAAGGGGAGACACCAATTACA 1140
Db	1183	AGACTGTGTGAGAGGAGGAGTTCTTCCGATCGAGTTTCAGTCAAGGGGAGACACCAATTACA 1242
Qy	1141	CCAGCTATACTCAGGGGCTTTCAGAAAGCAGAAATCTGAGATGCCCCCTACCAAGAGCC 1200
Db	1243	CCAGCTATACTCAGGGGCTTTCAGAAAGCAGAAATCTGAGATGCCCCCTACCAAGAGCC 1302
Qy	1201	AGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATATCCAGCTCCAGTA 1260
Db	1303	AGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATATCCAGCTCCAGTA 1362
Qy	1261	TGAGTGCATCTCAACCTTCTACCGCGCTGGGAGCAGCAGCAGGAGGACATGTCTGAGGAC 1320
Db	1363	TGAGTGCATCTCAACCTTCTACCGCGCTGGGAGCAGCAGCAGGAGGACATGTCTGAGGAC 1422
Qy	1321	TGGGAAAGTGGAGTGGGGGGGCAACCATCTGCATCCCTATCTGCGGGAATTTGAGAACAT 1380
Db	1423	TGGGAAAGTGGAGTGGGGGGGCAACCATCTGCATCCCTATCTGCGGGAATTTGAGAACAT 1482
Qy	1381	CACCTGCTCCAAAGACCCAAAGGTTGCGCTGGCCGCTGGCAGCAGCCATCTACAGGAGGAC 1440
Db	1483	CACCTGCTCCAAAGACCCAAAGGTTGCGCTGGCCGCTGGCAGCAGCCATCTACAGGAGGAC 1542
Qy	1441	CAGCGGGGTGCATGACGCGCAGCTTACAAAGGAGCGTGGTTCCTAGTCTGACGCGGTGC 1500
Db	1543	CAGCGGGGTGCATGACGCGCAGCTTACAAAGGAGCGTGGTTCCTAGTCTGACGCGGTGC 1602
Qy	1501	CCTGTGAAATGAGCGCACTGTGTGGTGGCTGCCACTGTCTTACTGACCTGGGGGAAGGT 1560
Db	1603	CCTGTGAAATGAGCGCACTGTGTGGTGGCTGCCACTGTCTTACTGACCTGGGGGAAGGT 1662
Qy	1561	CACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGGAAATTTCTACCGGGGATGATGA 1620
Db	1663	CACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGGAAATTTCTACCGGGGATGATGA 1722
Qy	1621	CCGGGATGAGAAAGCCATCCAGAGCTACAGATTTCTGCTATCATTTCTGCAATCCCACTA 1680
Db	1723	CCGGGATGAGAAAGCCATCCAGAGCTACAGATTTCTGCTATCATTTCTGCAATCCCACTA 1782
Qy	1681	TGACCCCATCTGCTTGTGATGCTGATCGCCATCTGAGCTCTTAGACAGGCCCGGTAT 1740
Db	1783	TGACCCCATCTGCTTGTGATGCTGATCGCCATCTGAGCTCTTAGACAGGCCCGGTAT 1842

```
Qy 1741 CAGCACCCGAGTCAGCCCATCTGCTCGCTGCCAGTCGGGATCTCAGCACTTCTCTTCCA 1800
Db |||||||
Qy 1843 CAGCACCCGAGTCAGCCCATCTGCTCGCTGCCAGTCGGGATCTCAGCACTTCTCTTCCA 1902
Db |||||||
Qy 1801 GGAGTCCCAATCACTGTGGCTGGCTGGAATGTCTCGCAGACGTGAGGAGCCCTGGCTT 1860
Db |||||||
Qy 1903 GGAGTCCCAATCACTGTGGCTGGCTGGAATGTCTCGCAGACGTGAGGAGCCCTGGCTT 1962
Db |||||||
Qy 1861 CAAGAACGACACACTGCGCTCTGGGGTGGTCAGTGTGGTGGACTCGCTGTGTGTGAGGA 1920
Db |||||||
Qy 1963 CAAGAACGACACACTGCGCTCTGGGGTGGTCAGTGTGGTGGACTCGCTGTGTGTGAGGA 2022
Db |||||||
Qy 1921 GCAGCATGAGGACCATGCGCATCCCACTGAGTGTCACTGATTAACATGTTCTGTGCCAGCTG 1980
Db |||||||
Qy 2023 GCAGCATGAGGACCATGCGCATCCCACTGAGTGTCACTGATTAACATGTTCTGTGCCAGCTG 2082
Db |||||||
Qy 1981 GGAACCCACTGCCCTTCTGATATCTGCATCTGCAGACAGAGGCATCGCGGCTGTGTC 2040
Db |||||||
Qy 2083 GGAACCCACTGCCCTTCTGATATCTGCATCTGCAGACAGAGGCATCGCGGCTGTGTC 2142
Db |||||||
Qy 2041 CTTCCCGGGACGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAG 2100
Db |||||||
Qy 2143 CTTCCCGGGACGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAG 2202
Db |||||||
Qy 2101 CTATGATAAAACATGACGCCACAGGCTCTCCACTGCTTCAACCAAGGTGCTGCCCTTTTAA 2160
Db |||||||
Qy 2203 CTATGATAAAACATGACGCCACAGGCTCTCCACTGCTTCAACCAAGGTGCTGCCCTTTTAA 2262
Db |||||||
Qy 2161 AGACTGGATTGAAGAAATATGAATGAACCATGCTCATGCACT 2204
Db |||||||
Qy 2263 AGACTGGATTGAAGAAATATGAATGAACCATGCTCATGCACT 2306
Db |||||||
```

Search completed: May 6, 2005, 17:15:37
Job time : 8165 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2005, 11:25:17 ; Search time 5968 Seconds
(without alignments)
18151.962 Million cell updates/sec

Title: US-10-063-692-37

Perfect score: 2846
Sequence: 1 cgcctggcaccagccggc.....aaaaaaaaaaaaaaaaaaaaa 2846

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsl1:*

9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2734.4	96.1	3165	3 HGM806734	BX640676 Homo sapi
2	2630.6	92.4	2650	3 AF370388	AF370388 Homo sapi
3	1893	66.5	2214	9 AY406074	AY406074 Homo sapi
4	1788.2	62.8	2746	3 AK088017	AK088017 Mus muscu
5	1466.6	51.5	2214	9 AY406076	AY406076 Mus muscu
6	1437.2	50.5	2214	9 AY406075	AY406075 Pan trogl
7	965.8	33.9	1100	5 BX337780	BX337780 BX337780
8	942	33.1	1008	5 BX399904	BX399904 BX399904
9	885.8	31.1	897	5 BX434191	BX434191 BX434191
10	821.6	28.9	1049	5 BX399905	BX399905 BX399905
11	815.2	28.6	952	5 BX439313	BX439313 BX439313
12	809.8	28.5	879	6 CD514783	CD514783 AGENCOURT
13	809.4	28.4	886	5 BX337781	BX337781 BX337781
14	797.6	28.0	2184	3 AK031254	AK031254 Mus muscu
15	742.2	26.1	795	6 CD655367	CD655367 AGENCOURT
16	736.8	25.9	740	5 BQ009840	BQ009840 UI-H-ED1-
17	721.4	25.3	723	5 BQ014545	BQ014545 UI-H-ED1-
18	709.4	24.9	722	5 BQ014522	BQ014522 UI-H-ED1-
19	708.4	24.9	722	5 BQ014522	BQ014522 UI-H-ED1-
20	676.2	23.8	718	7 CF125161	CF125161 UI-HF-BLO
21	656.6	23.1	851	7 CO394970	CO394970 AGENCOURT
22	656.4	23.1	742	5 BX350293	BX350293 BX350293
23	640	22.5	1158	4 BM461342	BM461342 AGENCOURT
24	640	22.5	645	4 BM728083	BM728083 UI-E-EJO-

25	640	22.5	645	5	BM930545	UI-E-EJ1-
26	639	22.5	645	5	BM929554	UI-E-EJ1-
27	636.2	22.4	650	4	BM684138	UI-E-EJ1-
28	636	22.3	645	4	BM683392	UI-E-EJ1-
29	634.2	22.3	649	4	BM680642	UI-E-EJO-
30	625	22.0	633	2	AW957662	EST369732
31	621.8	21.8	626	5	BP381335	BP381335
32	604.4	21.2	630	4	BM724013	UI-E-EJO-
33	587.2	20.6	715	7	CO397557	AGENCOURT
34	585.4	20.6	785	7	AL048495	DKFZP586L
35	581.8	20.4	586	5	BM998737	UI-H-DT1-
36	581.4	20.4	584	5	BP205877	BP205877
37	566	19.9	566	5	BP289572	BP289572
38	561.4	19.7	574	1	AI671186	6014404.X
39	558.4	19.6	773	4	BG403264	6214919
40	557	19.6	557	1	AI954161	wx80603.X
41	544.4	19.1	557	1	AA460698	zx69c08.X
42	544.2	19.1	693	7	CO880461	BovGen.08
43	533.2	18.7	660	7	CK959441	4100177.B
44	514	18.1	697	2	BB620582	BB620582
45	511.6	18.0	545	1	AA045104	zk63508.B
46	511	18.0	711	7	CO733882	S1LH03C07
47	505.4	17.8	830	7	CK474785	AGENCOURT
48	486.2	17.1	595	4	BI346571	375792.MA
49	476	16.7	476	5	EX282717	EX282717
50	475.6	16.7	795	1	AL048496	DKFZP586L
51	474.2	16.7	846	7	CO387203	AGENCOURT
52	467.2	16.4	472	2	AW340294	hc95d04.X
53	466.8	16.4	891	6	CB204666	AGENCOURT
54	458	16.1	635	2	BB632336	BB632336
55	455.4	16.0	491	1	AA460872	zx69c08.X
56	455	16.0	593	2	AW918019	EST349323
57	453.4	15.9	492	7	CN296855	170004250
58	453.4	15.9	711	5	BU253929	603747035
59	452	15.9	452	2	BE048236	tz48g03.Y
60	451.6	15.9	546	4	BM254217	515580.MA
61	447.4	15.7	449	1	AI990243	w620c03.X
62	446.4	15.7	449	1	AI088620	q614f03.X
63	443.8	15.6	447	2	AW028008	wv61b05.X
64	441.2	15.5	507	1	AA043793	zk59g10.X
65	441.2	15.5	584	5	BP312143	BP312143
66	437.2	15.4	442	1	AI823626	wi85e01.X
67	433	15.2	774	1	AU067539	AU067539
68	431.4	15.2	433	1	AI432522	th38b12.X
69	430.6	15.1	832	5	BP464936	BP464936
70	428	15.0	557	4	BM106593	510508.MA
71	427.8	15.0	547	2	BE231795	136621.MA
72	426.4	15.0	428	2	BF197805	7p92f09.X
73	421.2	14.8	522	4	BI346989	376376.MA
74	415.8	14.6	419	1	AA708420	2157a04.B
75	413.4	14.5	415	1	AI624892	t672f03.X
76	412.4	14.5	436	1	AA430705	zw52f06.X
77	410.4	14.4	583	5	BP216550	BP216550
78	410	14.4	500	6	CB712029	AMGNNUC.N
79	401.2	14.1	519	2	BE683792	183732.MA
80	398.8	14.0	404	2	AW206753	UI-H-B11-
81	397	13.9	397	1	AA812954	ai77a01.B
82	396	13.9	660	6	BY745962	BY745962
83	394.6	13.9	590	7	CK622160	mi01d03.Y
84	392.8	13.8	400	5	BM929450	UI-E-EJ1-
85	391.8	13.8	401	5	BU742789	UI-E-EJ1-
86	389.4	13.7	687	4	BI526460	602925034
87	385	13.5	938	5	BU383403	603582549
88	383.4	13.5	468	2	AW484384	60496.MAR
89	368.6	13.0	405	2	AW511691	xu51b03.X
90	367	12.9	367	1	AI057206	cz11a09.X
91	364.2	12.8	482	5	BX515589	BX515589
92	360.6	12.7	375	2	AW069518	cr48b11.X
93	360.6	12.7	463	1	AA444868	ve75f07.X
94	360.2	12.7	483	1	BM088773	502313.MA
95	356.4	12.5	382	6	CD707019	EST32546
96	349.6	12.3	520	2	BE653376	UI-M-ALI-
97	348	12.2	348	7	CN334668	170005999

C 98	339.2	11.9	356	7	N94393	N94393 zb76e06.s1	171	186	6.5	188	6	C21546	C21546 HUMS001054
C 99	338	11.9	359	2	AW340199	AW340199 hc94d04.x	C 172	185.8	6.5	731	9	AG511653	AG511653 Mus muscu
C 100	337.8	11.9	521	2	BE910833	BE910833 601661905	C 173	185	6.5	188	5	BO694586	BO694586 1000729 H
C 101	337	11.8	337	1	AA433935	AA433935 zw52f05.s	C 174	184.4	6.5	438	1	AI972676	AI972676 wr41b06.x
C 102	335.2	11.8	458	1	AA549757	AA549757 ve5f07.y	C 175	181.8	6.4	539	9	CG991118	CG991118 CH240.449
C 103	329.4	11.6	338	1	AA375185	AA375185 EST87423	C 176	181.8	6.4	633	5	BU252479	BU252479 603746867
C 104	329	11.6	373	1	AA126930	AA126930 z123a01.x	C 177	177	6.2	185	2	BF366351	BF366351 IL2-NT009
C 105	327.4	11.5	456	7	C0260289	C0260289 z131981.B	C 178	175.2	6.2	399	1	AJ696577	AJ696577 AJ696577
C 106	326.8	11.5	330	1	AI583699	AI583699 tc01h09.x	C 179	175.2	6.2	776	9	CC530365	CC530365 CH240.406
C 107	326.6	11.5	320	1	AI536361	AI536361 ma97ell.y	C 180	173.4	6.1	409	5	BY264071	BY264071 BY264071
C 108	325	11.4	325	1	AI420902	AI420902 tf03g11.x	C 181	172.4	6.1	270	6	CD371468	CD371468 UI-R-DX0-
C 109	319.8	11.2	410	5	BA473159	BA473159 DKF2p686f1	C 182	172	6.0	445	5	BY289536	BY289536 BY289536
C 110	319.8	11.2	419	4	BA484683	BA484683 S38615.MA	C 183	171	6.0	611	5	BU477941	BU477941 603847283
C 111	316.4	11.1	422	2	AW223842	AW223842 uo77d04.y	C 184	170.6	6.0	389	4	BM876043	BM876043 if86h06.y
C 112	315	11.1	315	1	AI579963	AI579963 tq35905.x	C 185	168.6	5.9	714	7	CF525168	CF525168 AGENCOURT
C 113	314.8	11.1	378	2	AW426139	AW426139 59708.MAR	C 186	166.6	5.9	688	8	AZ794032	AZ794032 2M0047D11
C 114	314	11.0	817	7	CK775452	CK775452 966578.MA	C 187	163	5.7	163	7	CN334667	CN334667 170005319
C 115	312.4	11.0	411	7	CK296856	CK296856 170005326	C 188	162.6	5.7	752	5	EX879710	EX879710 BX067747
C 116	311	10.9	664	7	CN059249	CN059249 Salamande	C 189	161.4	5.7	902	1	AU067747	AU067747 AU067747
C 117	298.2	10.5	489	5	BY243636	BY243636	C 190	159.2	5.6	620	6	BY761773	BY761773 BY761773
C 118	290.8	10.2	310	7	CN122781	CN122781 TgESTy12	C 191	157.6	5.5	256	6	CD371132	CD371132 UI-R-DY0-
C 119	284.2	10.0	814	5	BM006384	BM006384 603951279	C 192	157	5.5	569	7	CO631899	CO631899 DG9-66k1
C 120	284	10.0	378	4	BM090462	BM090462 505887.MA	C 193	157	5.5	157	5	BU929055	BU929055 AGENCOURT
C 121	283.4	10.0	756	7	CN334669	CN334669 170006000	C 194	156.2	5.5	352	5	BY310228	BY310228 BY310228
C 122	280.4	9.9	482	5	BY243643	BY243643	C 195	155.2	5.5	241	5	BU788909	BU788909 il192e10.y
C 123	275	9.7	482	4	BM105355	BM105355 508793.MA	C 196	152.4	5.4	949	5	BU938597	BU938597 AGENCOURT
C 124	268.6	9.4	395	2	AW416537	AW416537 51984.MAR	C 197	151.4	5.3	489	2	AN528858	AN528858 UI-R-BT1-
C 125	268	9.4	385	5	BY275139	BY275139	C 198	151.2	5.3	489	2	AN528858	AN528858 UI-R-BT1-
C 126	267.6	9.4	504	1	CN061039	CN061039 Ag20_p42	C 199	151	5.3	975	6	CO517925	CO517925 AGENCOURT
C 127	267	9.4	504	1	AA199196	AA199196 mv43503.f	C 200	150.6	5.3	304	6	CB341161	CB341161 CA23E1011
C 128	265	9.3	435	6	CB793009	CB793009 AMGNNUC.N	C 201	150.6	5.3	995	5	BU559882	BU559882 AGENCOURT
C 129	264.4	9.3	343	2	AW307893	AW307893 1225.MARC	C 202	149.2	5.2	935	5	BU842252	BU842252 AGENCOURT
C 130	263.6	9.3	381	7	CR772910	CR772910 DKF2p458N	C 203	148.8	5.2	375	6	CB088705	CB088705 if04e03.b
C 131	259.6	9.1	465	5	BY244862	BY244862	C 204	148.8	5.2	412	7	CR765787	CR765787 DKF2p468f1
C 132	258	9.1	959	1	AU051031	AU051031	C 205	148.8	5.2	615	7	CR958946	CR958946 4093793.B
C 133	257	9.0	271	1	AI824672	AI824672 wc48c08.x	C 206	148.8	5.2	1067	5	BU942149	BU942149 AGENCOURT
C 134	252.2	8.9	374	5	BY131558	BY131558	C 207	148.8	5.2	748	5	CF782696	CF782696 AGENCOURT
C 135	252	8.9	258	1	AL701986	AL701986 DKF2p686N	C 208	148.4	5.2	327	6	CB073971	CB073971 taa22h05.
C 136	250.4	8.8	662	5	BU218794	BU218794	C 209	148.2	5.2	901	5	BU531218	BU531218 AGENCOURT
C 137	249.6	8.8	421	5	BY295210	BY295210	C 210	148	5.2	345	4	BM534831	BM534831 fx71h06.y
C 138	247.4	8.7	325	2	AW957673	AW957673 EST369743	C 211	148	5.2	374	4	BM154585	BM154585 fv86h02.y
C 139	243.4	8.6	416	6	CB768218	CB768218 AMGNNUC.N	C 212	148	5.2	478	7	CO722515	CO722515 Mdf13017c
C 140	241	8.5	333	7	TS2085	TS2085 yb10g01.r1	C 213	148	5.2	886	5	BU555623	BU555623 AGENCOURT
C 141	240.8	8.5	410	2	BF920134	BF920134 MR1-NT017	C 214	147.8	5.2	642	9	AG144714	AG144714 Pan trogl
C 142	237.8	8.4	416	5	BY238364	BY238364	C 215	147.6	5.2	339	1	AL731319	AL731319 AGENCOURT
C 143	237	8.3	237	1	AA989716	AA989716 am65h09.s	C 216	147.6	5.2	857	5	BU534369	BU534369 AGENCOURT
C 144	234.6	8.2	425	5	BY266233	BY266233	C 217	147.4	5.2	354	4	BM154696	BM154696 fv86c03.y
C 145	234	8.2	494	2	BE374037	BE374037 601228074	C 218	147.4	5.2	356	4	BM155084	BM155084 fv93c11.y
C 146	232.2	8.2	907	5	BU358450	BU358450 603477265	C 219	147.2	5.2	305	6	CA391105	CA391105 cs11e08.y
C 147	232	8.2	651	5	BQ205135	BQ205135 UI-R-D21-	C 220	147.2	5.2	406	5	BQ526114	BQ526114 NISC no14
C 148	230.6	8.1	427	5	BY273129	BY273129	C 221	147.2	5.2	479	7	CN833789	CN833789 AGENCOURT
C 149	230.2	8.1	414	5	BY282746	BY282746	C 222	147	5.2	273	7	CO416891	CO416891 Mdf+3011i
C 150	228.8	8.1	404	5	BY271161	BY271161	C 223	147	5.2	454	7	CF315576	CF315576 HD-04-12
C 151	228.8	8.0	708	7	CO039157	CO039157 UI-M-AL1-	C 224	147	5.2	829	6	CD357006	CD357006 AGENCOURT
C 152	226.4	8.0	643	8	BZ245624	BZ245624 CH230-314	C 225	146.8	5.2	5949	3	HSM804512	HSM804512
C 153	224.6	7.9	506	1	AA266124	AA266124 mza49a06.x	C 226	146.8	5.2	257	5	BM476287	BM476287 DKF2p686f
C 154	221.8	7.8	348	7	R47049	R47049 Y436.Rat.in	C 227	146.8	5.2	270	4	BJ696724	BJ696724 BJ696724
C 155	221.2	7.8	808	5	BU359706	BU359706 603478496	C 228	146.8	5.2	282	6	CD641456	CD641456 AGENCOURT
C 156	217.2	7.6	386	2	BF451877	BF451877 uz80g03.y	C 229	146.8	5.2	408	7	CR770942	CR770942 DKF2p4696
C 157	215.6	7.6	425	5	BY295062	BY295062	C 230	146.6	5.2	255	4	CB879342	CB879342 lb62905.y
C 158	214.4	7.5	791	5	BU316123	BU316123 603850187	C 231	146.6	5.2	247	6	CB723709	CB723709 UI-M-GK0-
C 159	213.6	7.5	369	1	AA833310	AA833310 ud03b01.x	C 232	146.6	5.2	509	6	CB080062	CB080062 hp80f10.b
C 160	212.8	7.5	410	5	BY287911	BY287911	C 233	146.4	5.1	340	1	A1436456	A1436456 ti09c12.x
C 161	211	7.4	297	2	AW483167	AW483167 52006.MAR	C 234	146.4	5.1	395	6	CB044960	CB044960 NISC gc07
C 162	205.6	7.2	327	2	AW353000	AW353000 35212.MAR	C 235	146.4	5.1	573	5	BQ395751	BQ395751 NISC ng16
C 163	204.4	7.2	262	2	AW431829	AW431829 73099.MAR	C 236	146.4	5.1	1130	4	BM480137	BM480137 AGENCOURT
C 164	198.2	7.0	427	5	BY265763	BY265763	C 237	146.2	5.1	302	5	BU760983	BU760983 sas61c10.
C 165	196	6.9	749	5	BU298865	BU298865 603736330	C 238	146.2	5.1	871	5	BU587772	BU587772 AGENCOURT
C 166	195.8	6.9	423	5	BY259943	BY259943	C 239	146.2	5.1	992	7	CK798269	CK798269 AGENCOURT
C 167	192	6.7	358	5	BY128083	BY128083	C 240	146.2	5.1	974	9	CN001TT	CN001TT
C 168	189.6	6.7	359	6	BY783505	BY783505	C 241	146	5.1	390	6	CA379181	CA379181 658209.NC
C 169	188.6	6.6	359	5	BY341239	BY341239	C 242	146	5.1	415	7	CF546043	CF546043 lad89c05.
C 170	186.8	6.6	357	5	BY339892	BY339892	C 243	146	5.1	1000	5	BQ721431	BQ721431 AGENCOURT

244	145.8	5.1	313	6	CB709542	CB709542	AMGNNUC.N	1086	4	BM802531	BM802531	AGENCOURT
245	145.8	5.1	393	5	BX507033	BX507033	DKF2p779B	1334	4	BM555708	BM555708	AGENCOURT
246	145.8	5.1	919	5	BUS29432	BUS29432	AGENCOURT	3028	3	HSM801560	HSM801560	Homo sapi
247	145.6	5.1	316	5	BQ523462	BQ523462	NISC n122	182	6	CB101650	CB101650	Y
248	145.6	5.1	320	1	AL706784	AL706784	DKF2p686F	222	1	AL696218	AL696218	KLF2p686C
249	145.6	5.1	332	7	CO185234	CO185234	EC29979.5	272	5	BX507023	BX507023	DKF2p779A
250	145.6	5.1	386	6	CB044394	CB044394	NISC_gco4	283	5	BX644833	BX644833	DKF2p781M
251	145.6	5.1	450	7	CR763214	CR763214	DKF2p470M	340	5	BM155408	BM155408	fwo4e06.Y
252	145.6	5.1	409	6	CB094467	CB094467	h270d02.b	378	5	BU763909	BU763909	saa849f12.Y
253	145.6	5.1	609	5	BQ391639	BQ391639	NISC mg19	459	6	CA356573	CA356573	628793.NC
254	145.6	5.1	785	5	BU842680	BU842680	AGENCOURT	459	6	CB523798	CB523798	UI-M-GK0-
255	145.6	5.1	1200	5	BQ39624	BQ39624	AGENCOURT	462	6	CB410573	CB410573	NISC_ncl12
256	145.4	5.1	314	2	BE047863	BE047863	tz43c10.Y	497	5	BQ522457	BQ522457	NISC_ncl16
257	145.4	5.1	318	7	CF621703	CF621703	lae55a08.	567	5	BQ521934	BQ521934	NISC_nl13
258	145.4	5.1	387	5	BX552476	BX552476	lae55a08.	629	5	BQ522332	BQ522332	NISC_nl16
259	145.4	5.1	439	6	CB945953	CB945953	AGENCOURT	683	1	AV682672	AV682672	AV682672
260	145.4	5.1	487	6	CD238190	CD238190	FNPAXA08	693	1	CD640412	CD640412	AGENCOURT
261	145.4	5.1	503	6	CB350381	CB350381	ACHG165.H	718	7	CB8339409	CB8339409	AGENCOURT
262	145.2	5.1	252	7	CR771899	CR771899	DKF2p468C	806	7	CF783082	CF783082	AGENCOURT
263	145.2	5.1	275	7	CF612845	CF612845	lae11h04.	809	5	BU958264	BU958264	AGENCOURT
264	145.2	5.1	448	7	CF127350	CF127350	UI-HF-ES0	826	7	CV483860	CV483860	AGENCOURT
265	145.2	5.1	582	5	BP306922	BP306922	BP306922	861	5	BU851081	BU851081	AGENCOURT
266	145.2	5.1	770	7	CK399259	CK399259	AGENCOURT	866	5	BU962475	BU962475	AGENCOURT
267	145.2	5.1	957	5	BU563253	BU563253	AGENCOURT	870	8	BR157873	BR157873	ENTR411FR
268	145.2	5.1	1213	5	BQ718626	BQ718626	AGENCOURT	875	5	BU529558	BU529558	AGENCOURT
269	145	5.1	222	6	CA935086	CA935086	sau64b10.	888	5	BU955497	BU955497	AGENCOURT
270	145	5.1	668	6	CD72534	CD72534	AGENCOURT	892	7	CF289361	CF289361	AGENCOURT
271	145	5.1	895	5	BU852045	BU852045	AGENCOURT	931	5	BU960826	BU960826	AGENCOURT
272	145	5.1	965	5	BQ428205	BQ428205	AGENCOURT	1261	5	BQ427870	BQ427870	AGENCOURT
273	144.8	5.1	1025	3	BC027804	BC027804	Mus muscu	1492	4	BM555359	BM555359	AGENCOURT
274	144.8	5.1	259	1	AL697721	AL697721	DKF2p686E	283	3	CB288125	CB288125	CMD74_E02
275	144.8	5.1	381	6	CA736353	CA736353	wpi11s.pK0	334	2	AW100809	AW100809	sd61e08.Y
276	144.8	5.1	442	1	AV681872	AV681872	AGENCOURT	535	1	AV757455	AV757455	CAV757455
277	144.8	5.1	591	7	CK426420	CK426420	rx15b10.Y	741	6	CB339355	CB339355	CA23E1031
278	144.8	5.1	637	7	CK005551	CK005551	AGENCOURT	832	5	BU540250	BU540250	AGENCOURT
279	144.8	5.1	661	1	AV710508	AV710508	AGENCOURT	833	5	CK793654	CK793654	AGENCOURT
280	144.8	5.1	821	3	BC015144	BC015144	Homo sapi	840	5	BU567115	BU567115	AGENCOURT
281	144.6	5.1	280	7	CK975391	CK975391	4106215.B	840	5	BU935967	BU935967	AGENCOURT
282	144.6	5.1	215	7	CK975391	CK975391	4106215.B	906	5	BU943644	BU943644	AGENCOURT
283	144.6	5.1	397	1	AL723541	AL723541	AGENCOURT	918	6	CA455250	CA455250	AGENCOURT
284	144.6	5.1	398	3	AF116644	AF116644	Homo sapi	956	5	BU563381	BU563381	AGENCOURT
285	144.6	5.1	415	7	CK193529	CK193529	rg88c02.Y	1073	5	BQ230841	BQ230841	AGENCOURT
286	144.6	5.1	421	1	AV682249	AV682249	AGENCOURT	1235	4	BM470058	BM470058	AGENCOURT
287	144.6	5.1	791	1	AV755207	AV755207	AGENCOURT	1379	6	CD049761	CD049761	AGENCOURT
288	144.6	5.1	871	5	BU589926	BU589926	AGENCOURT	1379	6	CD384991	CD384991	AGENCOURT
289	144.6	5.1	891	4	BM449741	BM449741	AGENCOURT	261	4	BJ469921	BJ469921	BJ469921
290	144.6	5.1	965	5	BQ921874	BQ921874	AGENCOURT	310	4	BJ703028	BJ703028	DKF2p686H
291	144.4	5.1	305	7	CO168362	CO168362	DKF2p686L	328	5	BX476122	BX476122	DKF2p686H
292	144.4	5.1	308	5	CK384228	CK384228	lah06h09.	425	7	CF279639	CF279639	14ETL--06
293	144.4	5.1	437	7	CK384228	CK384228	lah06h09.	430	5	BQ395458	BQ395458	NISC ng15
294	144.4	5.1	510	7	CV057219	CV057219	BNEL25c9	684	1	AV706164	AV706164	AV706164
295	144.4	5.1	656	7	CV064567	CV064567	WNE112e4	713	7	CK655902	CK655902	AGENCOURT
296	144.4	5.1	884	7	CK385218	CK385218	LE2TR03A0	714	7	CV064496	CV064496	WNE111f11
297	144.4	5.1	891	5	BU531156	BU531156	AGENCOURT	842	5	BU563468	BU563468	AGENCOURT
298	144.4	5.1	1026	3	HSM803537	HSM803537	Homo sapi	856	5	BU940785	BU940785	AGENCOURT
299	144.2	5.1	230	4	BJ697384	BJ697384	AGENCOURT	865	5	BU555370	BU555370	AGENCOURT
300	144.2	5.1	278	7	CF123167	CF123167	UI-HF-CH0	870	6	CB566939	CB566939	AGENCOURT
301	144.2	5.1	285	6	CD521457	CD521457	AGENCOURT	885	5	BU850517	BU850517	AGENCOURT
302	144.2	5.1	296	7	CK353572	CK353572	AGENCOURT	947	5	BQ921561	BQ921561	AGENCOURT
303	144.2	5.1	314	7	CF123198	CF123198	UI-HF-CH0	1057	6	CB561919	CB561919	AGENCOURT
304	144.2	5.1	332	7	CV122318	CV122318	Mdlv4003e	239	6	CA802785	CA802785	AGENCOURT
305	144.2	5.1	371	7	CK377132	CK377132	lah98g02.	252	7	CD415260	CD415260	sau42b04.
306	144.2	5.1	371	7	CK377132	CK377132	lah98g02.	295	6	CD641171	CD641171	AGENCOURT
307	144.2	5.1	415	7	CO192413	CO192413	EC33671.5	302	7	CB833978	CB833978	AGENCOURT
308	144.2	5.1	421	5	BQ396582	BQ396582	NISC_ng21	353	6	CD639674	CD639674	AGENCOURT
309	144.2	5.1	424	1	AV682809	AV682809	AGENCOURT	364	7	CK430797	CK430797	oj54a08.Y
310	144.2	5.1	488	6	CD721930	CD721930	oj03c10.Y	510	1	AV755613	AV755613	AGENCOURT
311	144.2	5.1	485	7	CF755040	CF755040	lae51903.	559	5	BQ520502	BQ520502	NISC nl105
312	144.2	5.1	536	6	CN194226	CN194226	rg91b06.Y	820	5	BU555053	BU555053	AGENCOURT
313	144.2	5.1	635	6	CD638395	CD638395	AGENCOURT	840	7	CF578759	CF578759	AGENCOURT
314	144.2	5.1	664	7	CO072107	CO072107	GR_Ea31B	930	6	CA977162	CA977162	AGENCOURT
315	144.2	5.1	866	5	BU589860	BU589860	WPAEHux15	971	9	CL120194	CL120194	ISB1-78J1
316	144.2	5.1	1066	5	BU589860	BU589860	AGENCOURT					

390	143.4	5.0	1009	5	BUS40024	BUS540024	AGENCOURT	463	142.6	5.0	506	7	CO394068	CO394068	AGENCOURT
391	143.4	5.0	2007	3	HSMB07665	BX647519	Homo sapi	464	142.6	5.0	510	1	AV755290	AV755290	AGENCOURT
392	143.2	5.0	197	7	CO538540	CO538540	tah73a03.	465	142.6	5.0	808	5	BUS30709	BUS30709	AGENCOURT
393	143.2	5.0	286	7	CK385496	CK385496	lah40c02.	466	142.6	5.0	819	5	BUS44250	BUS44250	AGENCOURT
394	143.2	5.0	283	7	CR765052	CR765052	DKF2p470P	467	142.6	5.0	856	7	CO796836	CO796836	AGENCOURT
395	143.2	5.0	286	1	AL589270	AL589270	DKF2p451D	468	142.6	5.0	961	8	AZ691838	AZ691838	ENTW156TF
396	143.2	5.0	361	7	CF370119	CF370119	rg48d07.Y	469	142.6	5.0	1041	6	CD051043	CD051043	AGENCOURT
397	143.2	5.0	404	7	CF358374	CF358374	rm89g07.Y	470	142.6	5.0	1534	3	CR749559	CR749559	Homo sapi
398	143.2	5.0	494	7	CF544979	CF544979	lad85g10.Y	471	142.6	5.0	8296	3	CR749511	CR749511	Homo sapi
399	143.2	5.0	590	6	CB053229	CB053229	NISC_g113	472	142.6	5.0	242	1	AL697724	AL697724	DKF2p686I
400	143.2	5.0	603	5	BQ397550	BQ397550	NISC_rg28	473	142.4	5.0	259	7	CO159753	CO159753	FLDI_15.D
401	143.2	5.0	806	5	BUS81562	BUS81562	AGENCOURT	474	142.4	5.0	265	5	BX480600	BX480600	DKF2p686G
402	143.2	5.0	870	5	BUS89706	BUS89706	AGENCOURT	475	142.4	5.0	325	6	CB079273	CB079273	hp69a01.b
403	143.2	5.0	942	5	BUS32709	BUS32709	AGENCOURT	476	142.4	5.0	367	5	BQ525045	BQ525045	NISC_n008
404	143.2	5.0	963	5	BUS02691	BUS02691	AGENCOURT	477	142.4	5.0	376	5	BX486637	BX486637	DKF2p686M
405	143.2	5.0	996	5	BUS43390	BUS43390	AGENCOURT	478	142.4	5.0	398	5	EX499601	EX499601	DKF2p779M
406	143	5.0	197	4	BG179993	BG179993	602329538	479	142.4	5.0	378	5	CK375940	CK375940	lah76h05.
407	143	5.0	249	7	CK004667	CK004667	ip21e07.g	480	142.4	5.0	402	7	CN161832	CN161832	951158.MA
408	143	5.0	255	6	CA802891	CA802891	sau43g09.	481	142.4	5.0	426	6	CD678845	CD678845	hq01b11.x
409	143	5.0	326	7	CK384989	CK384989	lah57a09.	482	142.4	5.0	443	7	CF743770	CF743770	UI-M-G10-
410	143	5.0	347	4	BM534581	BM534581	fx69b06.Y	483	142.4	5.0	443	7	CK000623	CK000623	AGENCOURT
411	143	5.0	384	7	CF321906	CF321906	HD--13-F0	484	142.4	5.0	494	7	CK371886	CK371886	lai20d05.
412	143	5.0	408	7	CK004614	CK004614	AGENCOURT	485	142.4	5.0	519	7	CK431148	CK431148	oJ58e08.Y
413	143	5.0	585	7	CO403863	CO403863	AGENCOURT	486	142.4	5.0	555	5	BQ397268	BQ397268	NISC_rg26
414	143	5.0	651	6	CD433621	CD433621	EL01N0313	487	142.4	5.0	519	7	CK431148	CK431148	oJ58e08.Y
415	143	5.0	667	6	CD770733	CD770733	AGENCOURT	488	142.4	5.0	555	5	BX555180	BX555180	AGENCOURT
416	143	5.0	730	7	CV484196	CV484196	AGENCOURT	489	142.4	5.0	556	7	CK791071	CK791071	AGENCOURT
417	143	5.0	747	7	CV068710	CV068710	f2_new_ch	490	142.4	5.0	624	7	CK468331	CK468331	939713.MA
418	143	5.0	876	5	BUS40331	BUS40331	AGENCOURT	491	142.4	5.0	678	6	CD639699	CD639699	AGENCOURT
419	143	5.0	888	5	BUS95707	BUS95707	AGENCOURT	492	142.4	5.0	770	1	AV756342	AV756342	AV756342
420	143	5.0	1076	4	BM803989	BM803989	AGENCOURT	493	142.4	5.0	786	5	BUS42092	BUS42092	AGENCOURT
421	143	5.0	4807	3	CR749565	CR749565	Homo sapi	494	142.4	5.0	801	7	CF289632	CF289632	AGENCOURT
422	142.8	5.0	178	6	CA334893	CA334893	NISC_l1c02	495	142.4	5.0	813	5	BUS42692	BUS42692	AGENCOURT
423	142.8	5.0	197	7	CF208356	CF208356	CAB20003	496	142.4	5.0	862	5	BUS61053	BUS61053	AGENCOURT
424	142.8	5.0	207	7	CK119802	CK119802	210107.P1	497	142.4	5.0	885	3	BC022402	BC022402	Homo sapi
425	142.8	5.0	219	7	CF214757	CF214757	CGF100082	498	142.4	5.0	891	7	CN384691	CN384691	LE2TR01J2
426	142.8	5.0	229	6	CB970600	CB970600	CAB10004	499	142.4	5.0	928	5	BUS54720	BUS54720	AGENCOURT
427	142.8	5.0	245	5	BX476550	BX476550	DKF2p686O	500	142.4	5.0	969	6	CB205499	CB205499	AGENCOURT
428	142.8	5.0	252	7	CF212181	CF212181	CGF100066	501	142.4	5.0	979	4	BM415625	BM415625	OP20703.M
429	142.8	5.0	326	5	BS504841	BS504841	DKF2p686M	502	142.4	5.0	1047	5	BQ948873	BQ948873	AGENCOURT
430	142.8	5.0	334	7	CR544048	CR544048	DKF2p470J	503	142.4	5.0	1244	5	BUS08460	BUS08460	AGENCOURT
431	142.8	5.0	362	5	BQ521990	BQ521990	NISC_n114	504	142.4	5.0	1261	4	BM474477	BM474477	AGENCOURT
432	142.8	5.0	380	2	BF449584	BF449584	maa45b06.	505	142.4	5.0	1790	3	HSMB04571	HSMB04571	AGENCOURT
433	142.8	5.0	385	6	CB702425	CB702425	AMGNNUC.N	506	142.4	5.0	2500	3	BC026293	BC026293	Homo sapi
434	142.8	5.0	427	7	CK049668	CK049668	V4_P2_G5	507	142.2	5.0	178	5	BM965687	BM965687	ko15f05.Y
435	142.8	5.0	430	1	AV682289	AV682289	AV682289	508	142.2	5.0	189	5	BQ909669	BQ909669	ku18e11.Y
436	142.8	5.0	463	7	CO866181	CO866181	Mdfr32020m	509	142.2	5.0	260	7	CR772316	CR772316	DKF2p468L
437	142.8	5.0	513	1	AV757158	AV757158	AV757158	510	142.2	5.0	261	7	CV280938	CV280938	WS0138.B2
438	142.8	5.0	514	6	CB051745	CB051745	NISC_g102	511	142.2	5.0	298	5	BX953231	BX953231	DKF2p781D
439	142.8	5.0	569	5	BP306287	BP306287	BP306287	512	142.2	5.0	307	6	CD722153	CD722153	oJ06b12.Y
440	142.8	5.0	607	7	CV490737	CV490737	AGENCOURT	513	142.2	5.0	325	2	AW101005	AW101005	sd64d10.Y
441	142.8	5.0	747	2	B6202334	B6202334	601483329	514	142.2	5.0	346	7	CF380767	CF380767	lac78d04.
442	142.8	5.0	778	7	CN161630	CN161630	950941.MA	515	142.2	5.0	359	6	CA372266	CA372266	652974.NC
443	142.8	5.0	795	5	BUS963666	BUS963666	AGENCOURT	516	142.2	5.0	424	6	CB796123	CB796123	AMGNNUC:S
444	142.8	5.0	820	5	BUS03056	BUS03056	AGENCOURT	517	142.2	5.0	448	6	CA391870	CA391870	cs19g10.x
445	142.8	5.0	821	5	BUS960727	BUS960727	AGENCOURT	518	142.2	5.0	504	6	CA379465	CA379465	658553.NC
446	142.8	5.0	841	5	BUS61035	BUS61035	AGENCOURT	519	142.2	5.0	562	7	CN786219	CN786219	4120178.B
447	142.8	5.0	853	5	BUS27591	BUS27591	AGENCOURT	520	142.2	5.0	623	6	CD770235	CD770235	AGENCOURT
448	142.8	5.0	871	5	BUS29398	BUS29398	AGENCOURT	521	142.2	5.0	808	6	CD520988	CD520988	AGENCOURT
449	142.8	5.0	944	5	BUS904705	BUS904705	AGENCOURT	522	142.2	5.0	819	5	BUS31148	BUS31148	AGENCOURT
450	142.8	5.0	967	6	CB204352	CB204352	AGENCOURT	523	142.2	5.0	827	6	CB317350	CB317350	AGENCOURT
451	142.8	5.0	1251	4	BM453439	BM453439	AGENCOURT	524	142.2	5.0	845	7	CK193161	CK193161	FGAS000157
452	142.6	5.0	216	6	CA935095	CA935095	sau64d09.	525	142.2	5.0	857	5	BUS43015	BUS43015	AGENCOURT
453	142.6	5.0	219	4	BI791181	BI791181	ld05g09.Y	526	142.2	5.0	863	2	BE964633	BE964633	601658560
454	142.6	5.0	293	2	BE023554	BE023554	sm82a07.Y	527	142.2	5.0	864	5	BUS34869	BUS34869	AGENCOURT
455	142.6	5.0	370	7	CK593922	CK593922	tad29h07.	528	142.2	5.0	866	5	BUS87173	BUS87173	AGENCOURT
456	142.6	5.0	407	2	BF022275	BF022275	uy55c06.Y	529	142.2	5.0	876	6	CA988174	CA988174	AGENCOURT
457	142.6	5.0	452	3	BC050981	BC050981	Mus_muscu	530	142.2	5.0	885	5	BUS957927	BUS957927	AGENCOURT
458	142.6	5.0	458	1	AV682521	AV682521	AV682521	531	142.2	5.0	888	6	CB590474	CB590474	AGENCOURT
459	142.6	5.0	464	1	AV708119	AV708119	AV708119	532	142.2	5.0	891	9	CNS009JU	CNS009JU	Drosophi1
460	142.6	5.0	471	1	A1404883	A1404883	GH24733.5	533	142.2	5.0	893	6	CD251249	CD251249	AGENCOURT
461	142.6	5.0	471	7	CF307986	CF307986	ABF--01-J	534	142.2	5.0	900	5	BUS89675	BUS89675	AGENCOURT
462	142.6	5.0	482	7	CV122300	CV122300	Md1v4003a	535	142.2	5.0	904	5	BUS42136	BUS42136	AGENCOURT

536	142.2	5.0	913	5	BUS54763	AGENCOURT	609	141.8	5.0	613	7	CK787090
537	142.2	5.0	932	4	BG033403	602301577	610	141.8	5.0	664	2	BF144889
538	142.2	5.0	935	6	CB193258	AGENCOURT	611	141.8	5.0	721	2	CN845011
539	142.2	5.0	1066	5	BUS40067	AGENCOURT	612	141.8	5.0	775	6	CB319351
540	142.2	5.0	1297	5	BUS40145	AGENCOURT	613	141.8	5.0	784	7	CV487253
541	142.2	5.0	1531	9	AG381853	MUS muscu	614	141.8	5.0	785	7	CK790726
542	142	5.0	222	4	B1863321	r103d06.y	c	615	5.0	796	9	CNS0118D
543	142	5.0	240	4	BG156528	sab10g01.	616	141.8	5.0	875	5	BUS28010
544	142	5.0	286	7	CO067491	Mdfx3014e	617	141.8	5.0	902	3	AF116631
545	142	5.0	294	2	AW101221	ed75f11.y	618	141.8	5.0	908	7	CK797283
546	142	5.0	313	5	BQ523667	NISC n123	619	141.8	5.0	920	5	BUS29185
547	142	5.0	319	5	BX489110	DKP2p686j	620	141.8	5.0	921	5	BQ960309
548	142	5.0	331	4	BG155453	sab4d04.	621	141.8	5.0	942	7	CK406898
549	142	5.0	374	5	CR5953635	DKF2p781M	622	141.8	5.0	943	5	BUS23839
550	142	5.0	374	7	CR549911	DKF2p4690	623	141.8	5.0	966	5	BUS34727
551	142	5.0	407	6	CB570896	AGENCOURT	624	141.8	5.0	1005	9	CL077409
552	142	5.0	403	1	AV682162	AV682162	625	141.8	5.0	2157	3	BC050969
553	142	5.0	405	4	BF970162	BF970162	626	141.8	5.0	5940	3	CR627133
554	142	5.0	429	1	AV681857	AV681857	627	141.6	5.0	198	5	BQ667440
555	142	5.0	431	6	CB044460	NISC gc04	628	141.6	5.0	201	6	CA802122
556	142	5.0	433	5	BX565773	AGENCOURT	629	141.6	5.0	201	6	CB045621
557	142	5.0	453	7	CK005374	AGENCOURT	630	141.6	5.0	213	6	CA935478
558	142	5.0	462	6	CD363777	UI-M-GL0-	631	141.6	5.0	233	7	CV525079
559	142	5.0	466	7	CF369737	IG55ell.y	632	141.6	5.0	243	7	CO752945
560	142	5.0	476	5	BQ391140	NISC mq17	633	141.6	5.0	249	2	BE059724
561	142	5.0	515	7	CN049660	V4_P2_G11	634	141.6	5.0	282	7	CR750600
562	142	5.0	568	5	BQ396954	NISC rg24	635	141.6	5.0	283	4	BI324331
563	142	5.0	613	7	CV121985	Mdlv4002b	636	141.6	5.0	307	5	BX503626
564	142	5.0	615	4	BG435835	602508457	637	141.6	5.0	381	7	CF369462
565	142	5.0	687	6	CD639714	AGENCOURT	638	141.6	5.0	302	2	AW100887
566	142	5.0	689	7	CN832074	AGENCOURT	639	141.6	5.0	314	1	AL715133
567	142	5.0	824	5	BUS81157	AGENCOURT	640	141.6	5.0	314	1	AL715133
568	142	5.0	830	5	BUS65577	AGENCOURT	641	141.6	5.0	316	7	CF653832
569	142	5.0	833	6	CB945951	AGENCOURT	642	141.6	5.0	331	5	AX501327
570	142	5.0	842	7	CK409658	170005999	643	141.6	5.0	341	7	CF369462
571	142	5.0	849	2	BF792099	602252540	644	141.6	5.0	368	4	BM573701
572	142	5.0	911	5	BUS55479	AGENCOURT	645	141.6	5.0	401	5	BQ524783
573	142	5.0	914	5	BUS81349	AGENCOURT	646	141.6	5.0	411	1	AL120854
574	142	5.0	926	7	CK415124	AUF Ip8it	647	141.6	5.0	418	7	CF370486
575	142	5.0	939	7	CK421563	IP8pn	648	141.6	5.0	429	5	BQ454029
576	142	5.0	939	7	CN310359	170005999	649	141.6	5.0	514	5	BQ389814
577	142	5.0	941	6	CD050342	AGENCOURT	650	141.6	5.0	574	7	CO092611
578	142	5.0	944	5	BUI78666	AGENCOURT	651	141.6	5.0	613	7	CK005475
579	142	5.0	979	5	BUI76137	AGENCOURT	652	141.6	5.0	624	7	CO891923
580	142	5.0	984	6	CD513662	AGENCOURT	653	141.6	5.0	642	4	BI870677
581	142	5.0	992	5	BUS81327	AGENCOURT	654	141.6	5.0	745	7	CN175619
582	142	5.0	1018	5	BUS29315	AGENCOURT	655	141.6	5.0	772	1	AV733397
583	142	5.0	1023	5	BUS29766	AGENCOURT	656	141.6	5.0	826	5	BUS30680
584	142	5.0	1034	2	BE964486	601658194	657	141.6	5.0	839	5	BUS34549
585	142	5.0	1050	5	BUS02650	AGENCOURT	658	141.6	5.0	847	5	BUS851147
586	142	5.0	1079	6	CD516973	AGENCOURT	659	141.6	5.0	852	7	CK195112
587	142	5.0	1646	4	BM550636	AGENCOURT	660	141.6	5.0	856	5	BUS65327
588	142	5.0	2080	3	CR749502	Homo sapi	661	141.6	5.0	864	5	BUS30880
589	142	5.0	2735	3	HSN806723	AGENCOURT	662	141.6	5.0	871	5	BUS29359
590	142	5.0	5058	3	BC054079	MUS muscu	663	141.6	5.0	877	5	BUS55691
591	142	5.0	5527	3	CR627393	Homo sapi	664	141.6	5.0	893	5	BUS29816
592	142	5.0	5856	3	HSN803500	AGENCOURT	665	141.6	5.0	896	7	CK197478
593	142	5.0	6082	3	CR749803	Homo sapi	666	141.6	5.0	957	4	BM472626
594	141.8	5.0	195	4	BM186912	fy79e10.y	667	141.6	5.0	1009	5	BUS59877
595	141.8	5.0	206	7	CO938248	UNC-pd14c	668	141.6	5.0	1012	5	BQ954248
596	141.8	5.0	212	7	COL95530	EC40529.5	669	141.6	5.0	1027	6	CB205525
597	141.8	5.0	234	6	CD722269	oj07e09.y	670	141.6	5.0	1034	6	BUS22201
598	141.8	5.0	245	5	BX951835	DKF2p781A	671	141.6	5.0	1180	6	CD384928
599	141.8	5.0	272	2	AW071349	xa65a08.x	672	141.6	5.0	1214	5	BUI67807
600	141.8	5.0	281	4	BM261286	da146d01.	673	141.6	5.0	1241	3	BC050978
601	141.8	5.0	315	7	CV2800973	WS0138.B2	674	141.6	5.0	3775	3	CR627381
602	141.8	5.0	360	7	CK430943	oj55h07.y	675	141.4	5.0	226	4	BM186096
603	141.8	5.0	408	4	BM154430	fv85a07.y	676	141.4	5.0	225	4	BM533163
604	141.8	5.0	431	4	BG363877	dc71h01.y	677	141.4	5.0	234	1	BM154438
605	141.8	5.0	465	6	CD237889	FNPARA08	678	141.4	5.0	235	1	AI443075
606	141.8	5.0	478	5	BQ394696	NISC ng10	679	141.4	5.0	239	7	CK376983
607	141.8	5.0	507	1	AV755614	AV755614	680	141.4	5.0	245	2	AW100988
608	141.8	5.0	589	5	BQ525311	NISC no10	681	141.4	5.0	247	4	BM187242

682	141.4	5.0	254	4	BI705355	fr57g11.y	755	141.2	5.0	1106	4	BM553776	AGENCOURT
683	141.4	5.0	286	7	CF640321	D26_A01.F	756	141.2	5.0	1141	5	BM905793	AGENCOURT
684	141.4	5.0	296	7	CF640227	D25_A01.F	757	141.2	5.0	1268	4	BM804120	AGENCOURT
685	141.4	5.0	303	7	CO752990	MdfF302ze	758	141.2	5.0	1550	3	EC049704	Mus_muscu
686	141.4	5.0	341	6	CB523177	UI-M-GK0	759	141.2	5.0	183	5	BX508387	DKF2p686E
687	141.4	5.0	346	7	UI199646	km17g09.y	760	141	5.0	190	6	CA802078	sau29g04
688	141.4	5.0	351	7	CO417094	MdfF3011p	761	141	5.0	216	2	BE048071	tz47f01.y
689	141.4	5.0	358	7	CO181059	EC13411.5	762	141	5.0	228	6	CA819677	sau74c10.y
690	141.4	5.0	370	4	BG610096	324577.MA	763	141	5.0	231	2	AW733931	sk85c03.y
691	141.4	5.0	398	5	BX503633	DKF2p686I	764	141	5.0	237	7	CK616649	ou23d05.y
692	141.4	5.0	402	1	AJ799457	AJ799457	765	141	5.0	240	7	CR774358	DKF2p459P
693	141.4	5.0	405	7	CB079957	hp79c04.b	766	141	5.0	243	7	CO180411	EC01519.5
694	141.4	5.0	410	6	CB079957	hp79c04.b	767	141	5.0	248	1	AL712394	DKF2p686M
695	141.4	5.0	414	6	CA336104	CA336104	768	141	5.0	265	4	BI674494	sah96g05
696	141.4	5.0	420	6	CB640131	AGENCOURT	769	141	5.0	280	4	BJ019482	BJ019482
697	141.4	5.0	421	2	BE048319	tz49h10.y	770	141	5.0	310	7	CR752937	DKF2p468P
698	141.4	5.0	432	6	CD638524	AGENCOURT	771	141	5.0	335	4	BM534829	ix71h04.y
699	141.4	5.0	462	5	BQ393864	AGENCOURT	772	141	5.0	340	2	BF021460	uy35c02.y
700	141.4	5.0	486	7	CF369647	CF369647	773	141	5.0	345	5	BQ085914	il11f11.y
701	141.4	5.0	503	7	CO417413	MdfF30121	774	141	5.0	349	4	BM574077	fx58g05.y
702	141.4	5.0	512	7	CM994160	MdfF30029	775	141	5.0	450	7	CO065850	MdfF3016a
703	141.4	5.0	530	4	BM573742	fy03b10.y	776	141	5.0	473	6	CD251358	AGENCOURT
704	141.4	5.0	664	1	AV705644	AV705644	777	141	5.0	482	4	BI858408	603383996
705	141.4	5.0	728	5	BH030396	CV064887	778	141	5.0	525	6	CF409572	NISC.nc02
706	141.4	5.0	735	7	CV064887	WNE16e12	779	141	5.0	529	7	CF520953	AGENCOURT
707	141.4	5.0	806	7	CK790380	AGENCOURT	780	141	5.0	535	7	CK427445	xl76b12.y
708	141.4	5.0	822	6	CD520787	AGENCOURT	781	141	5.0	623	1	AI969567	wz68g06.x
709	141.4	5.0	834	5	BH534913	AGENCOURT	782	141	5.0	659	6	CD640691	AGENCOURT
710	141.4	5.0	872	9	CL466757	SAIL_1260	783	141	5.0	681	6	CD768296	AGENCOURT
711	141.4	5.0	893	6	CD243740	AGENCOURT	784	141	5.0	687	6	CD772154	AGENCOURT
712	141.4	5.0	979	5	BH531500	AGENCOURT	785	141	5.0	819	5	BU168192	AGENCOURT
713	141.4	5.0	1010	6	CD389001	AGENCOURT	786	141	5.0	824	5	BU936038	AGENCOURT
714	141.4	5.0	2105	3	HM803705	AGENCOURT	787	141	5.0	826	5	BU529199	AGENCOURT
715	141.2	5.0	228	5	BM888956	kb03b11.y	788	141	5.0	829	5	BU843782	AGENCOURT
716	141.2	5.0	228	7	CF216003	CAST0002	789	141	5.0	830	5	BU843607	AGENCOURT
717	141.2	5.0	240	4	BM521849	sak76g12	790	141	5.0	836	5	BU927827	AGENCOURT
718	141.2	5.0	250	7	CK429184	o33c07.y	791	141	5.0	840	5	BU927827	AGENCOURT
719	141.2	5.0	256	7	CO195335	EC40072.5	792	141	5.0	853	5	BU588997	AGENCOURT
720	141.2	5.0	302	7	CF253048	mdv004_e0	793	141	5.0	864	5	BU851178	AGENCOURT
721	141.2	5.0	302	7	CF546452	DKF2p470A	794	141	5.0	876	7	CK398238	AGENCOURT
722	141.2	5.0	343	6	CB084676	hq19g11.b	795	141	5.0	885	5	BU554652	AGENCOURT
723	141.2	5.0	353	4	BI744697	rk91c06.y	796	141	5.0	951	7	CK425505	AUF_lpt68
724	141.2	5.0	362	1	AI106593	GH06644.5	797	141	5.0	956	5	BU540401	AGENCOURT
725	141.2	5.0	362	1	CK594208	lab42h11	798	141	5.0	960	5	BU860843	AGENCOURT
726	141.2	5.0	371	7	CA269273	170005999	799	141	5.0	987	9	BQ430188	AGENCOURT
727	141.2	5.0	376	6	CB094547	hz71d07.b	800	141	5.0	1059	5	CNS00228	AGENCOURT
728	141.2	5.0	389	4	BF970446	602272785	801	141	5.0	1073	5	BQ930284	AGENCOURT
729	141.2	5.0	431	7	CO191531	EC31328.5	802	141	5.0	1309	4	BM463041	AGENCOURT
730	141.2	5.0	439	1	AL727204	AL727204	803	141	5.0	1321	7	CF579295	AGENCOURT
731	141.2	5.0	462	6	CA394496	cs52b12.y	804	141	5.0	1679	3	BC017752	Homo_sapi
732	141.2	5.0	494	5	BQ391155	NISC_mq17	805	141	5.0	1999	3	BC027914	Homo_sapi
733	141.2	5.0	495	6	CD236950	FNPAG11	806	141	5.0	2700	3	EC036824	Homo_sapi
734	141.2	5.0	501	5	BQ524016	NISC_no02	807	141	5.0	4793	3	CR749666	Homo_sapi
735	141.2	5.0	561	7	CV198844	km31g03.y	808	140.8	4.9	181	5	BM897277	ph39b09.y
736	141.2	5.0	578	2	AW733627	sk83a06.y	809	140.8	4.9	187	7	CO191674	EC31648.5
737	141.2	5.0	604	1	AV756703	AV756703	810	140.8	4.9	198	5	BQ392333	NISC_mq23
738	141.2	5.0	640	6	CB522981	UI-M-GK0	811	140.8	4.9	209	7	CO417475	MdfF30121
739	141.2	5.0	644	7	CO9898186	MdfF3021c	812	140.8	4.9	229	5	CO417475	fz06g08.y
740	141.2	5.0	681	1	AV703695	AV703695	813	140.8	4.9	263	6	CF040070	QCH8409.y
741	141.2	5.0	696	4	BF970731	602273732	814	140.8	4.9	270	2	AW101788	ku05g08.y
742	141.2	5.0	752	8	AZ531014	ENTBD19Ff	815	140.8	4.9	272	5	BM802221	ed70d09.y
743	141.2	5.0	805	9	CNS009F8	AL053500	816	140.8	4.9	273	6	CD520705	AGENCOURT
744	141.2	5.0	812	5	BH534591	AGENCOURT	817	140.8	4.9	277	7	CK266183	170004250
745	141.2	5.0	858	5	BH534591	AGENCOURT	818	140.8	4.9	280	6	CA802930	sau44d08
746	141.2	5.0	872	5	BH588646	AGENCOURT	819	140.8	4.9	281	5	BQ392472	NISC_mq4
747	141.2	5.0	909	5	BH587993	AGENCOURT	820	140.8	4.9	289	7	CK429678	o339g11.y
748	141.2	5.0	922	7	CV069684	WPAEHux15	821	140.8	4.9	290	5	BX501576	DKF2p779M
749	141.2	5.0	927	6	CA455489	AGENCOURT	822	140.8	4.9	340	7	CN836173	AGENCOURT
750	141.2	5.0	929	5	BH588911	AGENCOURT	823	140.8	4.9	342	7	CV1933274	SnEstb2
751	141.2	5.0	943	5	BH504604	AGENCOURT	824	140.8	4.9	351	7	CK378884	lai27f04
752	141.2	5.0	953	5	BH59214	AGENCOURT	825	140.8	4.9	353	6	CB973642	CAB30003
753	141.2	5.0	954	5	BQ220010	AGENCOURT	826	140.8	4.9	360	5	BQ400218	NISC_mq08
754	141.2	5.0	963	5	BQ221886	AGENCOURT	827	140.8	4.9	361	7	CK004628	AGENCOURT

828	140.8	4.9	364	7	CV5224008	CV524008	Mdlv2_401	901	140.6	4.9	848	6	CB236020	CB236020	CB236020	AGENCOURT
829	140.8	4.9	373	7	CK429577	CK429577	oJ38e03.y	902	140.6	4.9	853	6	CA455655	CA455655	CA455655	AGENCOURT
830	140.8	4.9	412	6	CA386106	CA386106	667646 NC	903	140.6	4.9	867	5	BU530924	BU530924	BU530924	AGENCOURT
831	140.8	4.9	419	6	CB079306	CB079306	hp69d02.b	904	140.6	4.9	869	5	BU563713	BU563713	BU563713	AGENCOURT
832	140.8	4.9	435	7	CK373916	CK373916	lai65g04.	905	140.6	4.9	879	5	BU851061	BU851061	BU851061	AGENCOURT
833	140.8	4.9	440	5	BQ522645	BQ522645	NISC nl17	906	140.6	4.9	882	5	BU960445	BU960445	BU960445	AGENCOURT
834	140.8	4.9	445	7	CN838051	CN838051	AGENCOURT	907	140.6	4.9	885	5	BU848031	BU848031	BU848031	AGENCOURT
835	140.8	4.9	448	7	CV514719	CV514719	taJ69g12.	908	140.6	4.9	893	5	BU842336	BU842336	BU842336	AGENCOURT
836	140.8	4.9	454	5	BX500915	BX500915	DKF2p779D	909	140.6	4.9	905	5	BU959672	BU959672	BU959672	AGENCOURT
837	140.8	4.9	469	7	CK429230	CK429230	oJ33h02.y	910	140.6	4.9	955	2	BE890041	BE890041	601512310	BE890041
838	140.8	4.9	478	6	CF030791	CF030791	QCD26e06.	911	140.6	4.9	960	7	CK421571	CK421571	AUF Ipspn	CK421571
839	140.8	4.9	503	5	BX561337	BX561337	EX561337	912	140.6	4.9	977	7	BU858387	BU858387	AGENCOURT	BU858387
840	140.8	4.9	561	5	BQ395163	BQ395163	NISC_nrg13	913	140.6	4.9	980	5	BU844064	BU844064	AGENCOURT	BU844064
841	140.8	4.9	639	1	AI969601	AI969601	wz69b11.x	c	914	140.6	1101	9	CNS00AYO	AL05506	Drosophi	AL05506
842	140.8	4.9	674	7	CK462872	CK462872	933697 MA	915	140.6	4.9	1356	3	CR749814	CR749814	Homo sapi	CR749814
843	140.8	4.9	704	1	AV681630	AV681630	AV681630	916	140.6	4.9	1521	3	AF118070	AF118070	Homo sapi	AF118070
844	140.8	4.9	707	1	AV681647	AV681647	AV681647	917	140.4	4.9	169	5	BM898046	BM898046	ph46f05.y	BM898046
845	140.8	4.9	709	7	CN835711	CN835711	AGENCOURT	918	140.4	4.9	189	4	BM178937	BM178937	saJ61c09.	BM178937
846	140.8	4.9	724	6	CD639470	CD639470	AGENCOURT	919	140.4	4.9	202	4	BM154309	BM154309	fv83e04.y	BM154309
847	140.8	4.9	729	7	CV4866140	CV4866140	AGENCOURT	920	140.4	4.9	205	6	CD723715	CD723715	oJ25f03.y	CD723715
848	140.8	4.9	744	1	AV682252	AV682252	AGENCOURT	921	140.4	4.9	210	6	CA935503	CA935503	saS55a10.	CA935503
849	140.8	4.9	748	7	CO815521	CO815521	AGENCOURT	922	140.4	4.9	213	5	BU927115	BU927115	saS55g09.	BU927115
850	140.8	4.9	779	7	CV482560	CV482560	AGENCOURT	923	140.4	4.9	221	4	BM532327	BM532327	fy06e11.y	BM532327
851	140.8	4.9	786	1	AV682266	AV682266	AGENCOURT	924	140.4	4.9	229	6	CA802763	CA802763	saJ4506.	CA802763
852	140.8	4.9	824	5	BU565362	BU565362	AGENCOURT	925	140.4	4.9	244	4	BM154314	BM154314	fv83e11.y	BM154314
853	140.8	4.9	835	5	BU529221	BU529221	AGENCOURT	926	140.4	4.9	254	2	BE057342	BE057342	sn01h03.y	BE057342
854	140.8	4.9	839	5	BU843334	BU843334	AGENCOURT	927	140.4	4.9	256	6	CB088964	CB088964	1f08a08.b	CB088964
855	140.8	4.9	841	5	BU555504	BU555504	AGENCOURT	928	140.4	4.9	257	7	CO065740	CO065740	Mdf3015j	CO065740
856	140.8	4.9	843	5	BU532179	BU532179	AGENCOURT	929	140.4	4.9	274	5	BM897348	BM897348	ph40h12.y	BM897348
857	140.8	4.9	854	5	BU555510	BU555510	AGENCOURT	c	930	140.4	277	4	BM644186	BM644186	170006873	BM644186
858	140.8	4.9	868	5	BU587825	BU587825	AGENCOURT	931	140.4	4.9	290	5	BM476522	BM476522	DKF2p686K	BM476522
859	140.8	4.9	874	7	CK426264	CK426264	AUF IpTeb	932	140.4	4.9	294	6	CA802699	CA802699	saU0g02.	CA802699
860	140.8	4.9	898	3	BC017007	BC017007	Homo sapi	933	140.4	4.9	297	7	CV525614	CV525614	Mdlv4012o	CV525614
861	140.8	4.9	913	5	BU563702	BU563702	AGENCOURT	934	140.4	4.9	307	7	CV525614	CV525614	Mdlv4012o	CV525614
862	140.8	4.9	920	8	AZ691914	AZ691914	ENTWU26TR	935	140.4	4.9	314	5	BU761114	BU761114	saS63c06.	BU761114
863	140.8	4.9	1022	3	CD050966	CD050966	Mus muscu	936	140.4	4.9	319	5	AN101789	AN101789	sd70d10.y	AN101789
864	140.8	4.9	1027	6	CD389435	CD389435	AGENCOURT	937	140.4	4.9	326	5	BQ128910	BQ128910	1124e02.y	BQ128910
865	140.8	4.9	1055	4	BM562625	BM562625	AGENCOURT	938	140.4	4.9	328	7	CK377760	CK377760	lai08b12.	CK377760
866	140.8	4.9	1106	9	CL103937	CL103937	ISB1-42D1	939	140.4	4.9	329	4	BM774043	BM774043	ra88g10.y	BM774043
867	140.8	4.9	1322	5	BQ223518	BQ223518	AGENCOURT	940	140.4	4.9	342	6	CB566569	CB566569	AGENCOURT	CB566569
868	140.8	4.9	1869	3	BC032469	BC032469	Homo sapi	941	140.4	4.9	342	7	CV546441	CV546441	lae73f10.	CV546441
869	140.8	4.9	2090	3	AF130105	AF130105	Homo sapi	942	140.4	4.9	343	7	CV525143	CV525143	Mdlv4010m	CV525143
870	140.8	4.9	3226	3	CR627326	CR627326	Homo sapi	943	140.4	4.9	348	6	CB704554	CB704554	AMGNNUC:S	CB704554
871	140.8	4.9	3611	3	CR627025	CR627025	Homo sapi	944	140.4	4.9	362	7	CK350334	CK350334	hggtfha23D	CK350334
872	140.6	4.9	195	6	CB817512	CB817512	d3k21p2.f	945	140.4	4.9	373	7	CK431025	CK431025	oJ57a05.y	CK431025
873	140.6	4.9	220	7	CR630411	CR630411	DKF2p469D	946	140.4	4.9	379	7	CF425735	CF425735	lad43e11.	CF425735
874	140.6	4.9	233	7	CF533625	CF533625	UI-M-GHO-	947	140.4	4.9	388	7	CV524829	CV524829	Mdlv2_402	CV524829
875	140.6	4.9	236	6	CB948928	CB948928	AGENCOURT	948	140.4	4.9	396	2	BE806949	BE806949	saS09a08.y	BE806949
876	140.6	4.9	239	5	BX503636	BX503636	DKF2p686J	949	140.4	4.9	399	7	CF369492	CF369492	fv60e02.y	CF369492
877	140.6	4.9	246	1	AL696192	AL696192	DKF2p686B	950	140.4	4.9	410	6	CB567405	CB567405	AGENCOURT	CB567405
878	140.6	4.9	248	1	AJ768204	AJ768204	AJ768204	951	140.4	4.9	410	7	CF425879	CF425879	lad45f06.	CF425879
879	140.6	4.9	257	4	BM582842	BM582842	170006872	952	140.4	4.9	418	4	CK625494	CK625494	mj10a08.y	CK625494
880	140.6	4.9	270	1	AV836739	AV836739	AGENCOURT	953	140.4	4.9	418	4	BF981774	BF981774	602305439	BF981774
881	140.6	4.9	273	6	CB945895	CB945895	AGENCOURT	954	140.4	4.9	430	7	CO415525	CO415525	Mdf33007C	CO415525
882	140.6	4.9	275	7	CR767523	CR767523	DKF2p468K	955	140.4	4.9	431	1	AV682351	AV682351	AGENCOURT	AV682351
883	140.6	4.9	314	1	AL598254	AL598254	DKF2p313N	956	140.4	4.9	448	7	CK597630	CK597630	AGENCOURT	CK597630
884	140.6	4.9	318	5	BX500893	BX500893	DKF2p779B	957	140.4	4.9	476	6	CD802812	CD802812	ui-M-GVO-	CD802812
885	140.6	4.9	346	6	CA337022	CA337022	NISC_1v08	958	140.4	4.9	477	6	CD677843	CD677843	hoi23b03.y	CD677843
886	140.6	4.9	398	7	CO066729	CO066729	Mdf330059	959	140.4	4.9	490	7	CK430328	CK430328	oj48a08.y	CK430328
887	140.6	4.9	424	7	CR23393											

974	140.4	4.9	716	6	CD641621	AGENCOURT	1047	140.2	4.9	893	5	BUS51134	BUS51134	AGENCOURT
975	140.4	4.9	766	5	BUS34557	AGENCOURT	1048	140.2	4.9	901	5	BUS181433	BUS181433	AGENCOURT
976	140.4	4.9	808	6	CD520111	AGENCOURT	1049	140.2	4.9	914	5	BQ718907	BQ718907	AGENCOURT
977	140.4	4.9	843	5	BUS33556	AGENCOURT	1050	140.2	4.9	921	5	BQ222825	BQ222825	AGENCOURT
978	140.4	4.9	855	5	BUS55022	AGENCOURT	1051	140.2	4.9	926	5	BQ222825	BQ222825	AGENCOURT
979	140.4	4.9	864	5	BUS42866	AGENCOURT	1052	140.2	4.9	927	5	BQ222633	BQ222633	AGENCOURT
980	140.4	4.9	872	5	BUS29249	AGENCOURT	1053	140.2	4.9	942	5	BUS08292	BUS08292	AGENCOURT
981	140.4	4.9	872	7	CK022958	AGENCOURT	1054	140.2	4.9	1002	6	CD389396	CD389396	AGENCOURT
982	140.4	4.9	908	5	BUS45120	AGENCOURT	1055	140.2	4.9	1040	5	BQ944642	BQ944642	AGENCOURT
983	140.4	4.9	914	5	BUS87541	AGENCOURT	1056	140.2	4.9	1109	5	BUS30365	BUS30365	AGENCOURT
984	140.4	4.9	920	5	CNS0062R	AL061710 Drosophil	1057	140.2	4.9	1158	4	BMS56158	BMS56158	AGENCOURT
985	140.4	4.9	927	7	CV068663 f2_new_ch	AGENCOURT	1058	140.2	4.9	1699	3	HSM801509	AL133640 Homo sapi	
986	140.4	4.9	946	5	BQ374422	AGENCOURT	1059	140.2	4.9	1926	3	HSM802868	AL133640 Homo sapi	
987	140.4	4.9	951	6	CA792153	AGENCOURT	1060	140.2	4.9	189	7	CO182475	CO182475	AGENCOURT
988	140.4	4.9	954	5	BQ278347	AGENCOURT	1061	140.2	4.9	203	1	AA624239	AA624239	AGENCOURT
989	140.4	4.9	956	9	CL495518	AGENCOURT	1062	140.2	4.9	205	5	BX504787	BX504787	AGENCOURT
990	140.4	4.9	960	5	BUS12150	AGENCOURT	1063	140.2	4.9	208	6	CA802715	CA802715	AGENCOURT
991	140.4	4.9	966	4	BM415421	OP20495 M	1064	140.2	4.9	218	7	CK377805	CK377805	AGENCOURT
992	140.4	4.9	991	6	CD050059	AGENCOURT	1065	140.2	4.9	233	2	BE030380	BE030380	AGENCOURT
993	140.4	4.9	1005	5	BUS29990	AGENCOURT	1066	140.2	4.9	238	7	CO184969	CO184969	AGENCOURT
994	140.4	4.9	1036	9	CNS031MJ	AL250012 Tetraodon	1067	140.2	4.9	277	7	CO185085	CO185085	AGENCOURT
995	140.4	4.9	1040	6	CD047873	AGENCOURT	1068	140.2	4.9	294	1	AL725181	AL725181	AGENCOURT
996	140.4	4.9	1040	6	CD356857	AGENCOURT	1069	140.2	4.9	294	7	CF328198	CF328198	AGENCOURT
997	140.4	4.9	1253	5	BQ230949	AGENCOURT	1070	140.2	4.9	298	7	CN654687	CN654687	AGENCOURT
998	140.4	4.9	1258	4	BM476721	AGENCOURT	1071	140.2	4.9	302	5	BQ740768	BQ740768	AGENCOURT
999	140.4	4.9	2596	3	BC053452	Mus muscu	1072	140.2	4.9	330	4	CK378960	CK378960	AGENCOURT
1000	140.4	4.9	2623	3	HSM808057	AGENCOURT	1073	140.2	4.9	333	7	CK378960	CK378960	AGENCOURT
1001	140.4	4.9	5201	3	BC063852	AGENCOURT	1074	140.2	4.9	346	6	CA380966	CA380966	AGENCOURT
1002	140.2	4.9	175	4	BM187396	fw17b01.Y	1075	140.2	4.9	350	6	CB045394	CB045394	AGENCOURT
1003	140.2	4.9	193	5	BX955696	DKF2p781C	1076	140.2	4.9	371	7	CO736053	CO736053	AGENCOURT
1004	140.2	4.9	196	6	CA819430	sau78c12	1077	140.2	4.9	381	8	CA802337	CA802337	AGENCOURT
1005	140.2	4.9	217	4	BX251664	AGENCOURT	1078	140.2	4.9	391	6	BH294432	BH294432	AGENCOURT
1006	140.2	4.9	222	4	BQ047503	AGENCOURT	1079	140.2	4.9	411	7	CO193835	CO193835	AGENCOURT
1007	140.2	4.9	229	5	BQ085944	AGENCOURT	1080	140.2	4.9	418	4	B1323943	B1323943	AGENCOURT
1008	140.2	4.9	229	5	BQ087771	rt08f06.Y	1081	140.2	4.9	418	5	BX569452	BX569452	AGENCOURT
1009	140.2	4.9	264	6	CB570894	AGENCOURT	1082	140.2	4.9	442	6	CD679816	CD679816	AGENCOURT
1010	140.2	4.9	282	7	CO417188	Mdf+3012a	1083	140.2	4.9	467	6	CB722109	CB722109	AGENCOURT
1011	140.2	4.9	298	7	CO184759	EC28526.5	1084	140.2	4.9	512	5	BQ266641	BQ266641	AGENCOURT
1012	140.2	4.9	332	7	CO194028	EC37288.5	1085	140.2	4.9	554	7	CK384476	CK384476	AGENCOURT
1013	140.2	4.9	333	6	CB422505	595617.MA	1086	140.2	4.9	627	1	AV723953	AV723953	AGENCOURT
1014	140.2	4.9	339	7	CF512490	Cabud0003	1087	140.2	4.9	629	1	AV723953	AV723953	AGENCOURT
1015	140.2	4.9	361	7	CK005157	AGENCOURT	1088	140.2	4.9	640	6	CD766813	CD766813	AGENCOURT
1016	140.2	4.9	369	6	CD638357	AGENCOURT	1089	140.2	4.9	680	7	CO074617	CO074617	AGENCOURT
1017	140.2	4.9	375	7	CK371897	lai20e07	1090	140.2	4.9	688	7	CO074646	CO074646	AGENCOURT
1018	140.2	4.9	378	1	AV762488	AGENCOURT	1091	140.2	4.9	693	6	CD641480	CD641480	AGENCOURT
1019	140.2	4.9	405	1	AJ790913	AJ790913	1092	140.2	4.9	699	6	CD641614	CD641614	AGENCOURT
1020	140.2	4.9	433	1	AV681987	AGENCOURT	1093	140.2	4.9	722	6	CD237110	CD237110	AGENCOURT
1021	140.2	4.9	457	5	BQ527792	NISC no24	1094	140.2	4.9	738	6	CD641072	CD641072	AGENCOURT
1022	140.2	4.9	490	7	CK400599	AGENCOURT	1095	140.2	4.9	776	5	BUS54919	BUS54919	AGENCOURT
1023	140.2	4.9	491	1	AV757797	AV757797	1096	140.2	4.9	799	5	BUS53312	BUS53312	AGENCOURT
1024	140.2	4.9	495	7	CO752765	Mdf+3025b	1097	140.2	4.9	814	5	BUS64423	BUS64423	AGENCOURT
1025	140.2	4.9	498	7	CK428252	AGENCOURT	1098	140.2	4.9	828	5	BUS51224	BUS51224	AGENCOURT
1026	140.2	4.9	516	1	AV757012	AGENCOURT	1099	140.2	4.9	833	5	BUS56151	BUS56151	AGENCOURT
1027	140.2	4.9	519	5	BQ523357	NISC nl21	1100	140.2	4.9	840	5	BM985977	BM985977	AGENCOURT
1028	140.2	4.9	545	7	CV223275	taj59h05	1101	140.2	4.9	842	9	CNS010QN	CNS010QN	AGENCOURT
1029	140.2	4.9	558	4	BG110283	602279148	1102	140.2	4.9	843	5	BUS55415	BUS55415	AGENCOURT
1030	140.2	4.9	583	5	BP209684	BP209684	1103	140.2	4.9	849	5	BUS94129	BUS94129	AGENCOURT
1031	140.2	4.9	583	5	BP341772	BP341772	1104	140.2	4.9	850	5	BUS89468	BUS89468	AGENCOURT
1032	140.2	4.9	583	5	BQ525020	NISC no08	1105	140.2	4.9	854	4	BG286670	BG286670	AGENCOURT
1033	140.2	4.9	608	1	AI731270	BNLGH1903	1106	140.2	4.9	877	5	BUS50612	BUS50612	AGENCOURT
1034	140.2	4.9	661	6	CD640938	AGENCOURT	1107	140.2	4.9	877	5	BUS51483	BUS51483	AGENCOURT
1035	140.2	4.9	663	7	CV481556	AGENCOURT	1108	140.2	4.9	889	5	BUS56131	BUS56131	AGENCOURT
1036	140.2	4.9	686	1	AV682222	AGENCOURT	1109	140.2	4.9	889	5	BUS50913	BUS50913	AGENCOURT
1037	140.2	4.9	802	7	CF153371	AGENCOURT	1110	140.2	4.9	895	7	CF595897	CF595897	AGENCOURT
1038	140.2	4.9	803	5	BUS30984	AGENCOURT	1111	140.2	4.9	904	7	CF580123	CF580123	AGENCOURT
1039	140.2	4.9	820	7	CO403732	AGENCOURT	1112	140.2	4.9	905	5	BUS946070	BUS946070	AGENCOURT
1040	140.2	4.9	843	5	BUS55489	AGENCOURT	1113	140.2	4.9	942	5	BUI70642	BUI70642	AGENCOURT
1041	140.2	4.9	849	7	CK791811	AGENCOURT	1114	140.2	4.9	940	5	BUS87989	BUS87989	AGENCOURT
1042	140.2	4.9	850	6	CA465239	AGENCOURT	1115	140.2	4.9	988	7	CK419790	CK419790	AGENCOURT
1043	140.2	4.9	852	7	CK196873	FGAS00533	1116	140.2	4.9	993	5	BUS36971	BUS36971	AGENCOURT
1044	140.2	4.9	854	7	CK200376	FGAS00889	1117	140.2	4.9	1001	5	BUI72943	BUI72943	AGENCOURT
1045	140.2	4.9	858	5	BUS959480	AGENCOURT	1118	140.2	4.9	1006	7	CK425508	CK425508	AGENCOURT
1046	140.2	4.9	870	5	BUS58052	AGENCOURT	1119	140.2	4.9	1068	5	BUS908068	BUS908068	AGENCOURT

1266	139.6	4.9	571	3	BC049598	Mus muscu	1339	139.4	4.9	426	7	CF545613
1267	139.6	4.9	582	3	BC061127	Mus muscu	c1340	139.4	4.9	440	7	CF301049
1268	139.6	4.9	590	6	CB937830	IpocGjX13_	1341	139.4	4.9	454	5	BX500114
1269	139.6	4.9	594	6	CV199728	kml19b10.y	1342	139.4	4.9	461	1	AV681668
1270	139.6	4.9	607	1	AA522011	vh78c09.r	1343	139.4	4.9	475	1	AJ791816
1271	139.6	4.9	661	6	CD641297	AGENCOURT	1344	139.4	4.9	473	7	CN843209
1272	139.6	4.9	667	6	CD638527	AGENCOURT	1345	139.4	4.9	486	4	BI743903
1273	139.6	4.9	697	4	BC928969	HC22-1-F	1346	139.4	4.9	550	7	CN164657
1274	139.6	4.9	702	7	CV065824	WNEI27b1	1347	139.4	4.9	589	1	AI207510
1275	139.6	4.9	729	4	BF982046	602305336	1348	139.4	4.9	601	7	CF369687
1276	139.6	4.9	730	2	BE613622	601504411	1349	139.4	4.9	608	6	CD766630
1277	139.6	4.9	730	6	CD638709	AGENCOURT	1350	139.4	4.9	619	7	CF357352
1278	139.6	4.9	796	9	CNS011GK	Drosophil	1351	139.4	4.9	623	7	CN051788
1279	139.6	4.9	821	5	BU960356	AGENCOURT	1352	139.4	4.9	734	5	BU535289
1280	139.6	4.9	823	5	BU844017	AGENCOURT	1353	139.4	4.9	739	1	AV706777
1281	139.6	4.9	833	8	AZ667852	ENTWN74TR	1354	139.4	4.9	779	7	CV482931
1282	139.6	4.9	868	7	CO797683	AGENCOURT	1355	139.4	4.9	792	7	CV162353
1283	139.6	4.9	873	5	BU852003	AGENCOURT	1356	139.4	4.9	796	7	CV489012
1284	139.6	4.9	878	5	BU844333	AGENCOURT	1357	139.4	4.9	803	5	BU536633
1285	139.6	4.9	905	5	BU589645	AGENCOURT	1358	139.4	4.9	805	5	BU578444
1286	139.6	4.9	906	5	BU531084	AGENCOURT	1359	139.4	4.9	811	3	BC050987
1287	139.6	4.9	913	6	CH588741	AGENCOURT	1360	139.4	4.9	813	7	CV487986
1288	139.6	4.9	923	5	BU943690	AGENCOURT	1361	139.4	4.9	815	7	CK396579
c1289	139.6	4.9	925	4	BM416279	OP21369 M	1362	139.4	4.9	822	5	BU534594
1290	139.6	4.9	929	5	BU590108	AGENCOURT	1363	139.4	4.9	840	5	BU843224
c1291	139.6	4.9	930	7	CV068616	f2_new_ch	1364	139.4	4.9	848	5	BU529378
1292	139.6	4.9	959	6	CD050373	AGENCOURT	1365	139.4	4.9	848	5	BU558202
1293	139.6	4.9	977	2	BE777769	601463009	1366	139.4	4.9	853	5	BU847233
1294	139.6	4.9	1011	5	BQ928127	AGENCOURT	1367	139.4	4.9	857	7	CO913882
1295	139.6	4.9	1116	6	CA475599	AGENCOURT	1368	139.4	4.9	858	5	BU530595
1296	139.6	4.9	1126	6	CD505160	CDA72-B09	1369	139.4	4.9	859	7	CO808031
1297	139.6	4.9	1842	3	BC036564	Mus muscu	1370	139.4	4.9	867	5	BU595981
1298	139.6	4.9	3250	3	BC035530	Mus muscu	1371	139.4	4.9	871	5	BU587807
1299	139.6	4.9	4366	3	HS807687	BM896912	1372	139.4	4.9	872	7	CN168212
1300	139.6	4.9	160	5	BM896912	ph49f06.y	1373	139.4	4.9	878	5	BU598840
1301	139.4	4.9	166	5	BM97310	ph39e12.y	1374	139.4	4.9	882	5	BU588070
1302	139.4	4.9	170	5	BM97310	ph39e12.y	1375	139.4	4.9	884	5	BU531363
1303	139.4	4.9	172	6	CB075586	h247b03.b	1376	139.4	4.9	890	5	BU603755
1304	139.4	4.9	193	4	BG156523	sab10e12.	1377	139.4	4.9	892	6	CA792742
1305	139.4	4.9	197	6	CA802643	sau39h03.	1378	139.4	4.9	939	5	BQ434577
1306	139.4	4.9	202	5	BM965808	kol7e03.y	1379	139.4	4.9	964	5	BU953880
1307	139.4	4.9	210	4	BM873785	laa03a07.	1380	139.4	4.9	969	5	BQ937042
1308	139.4	4.9	220	4	BM573836	fy04f07.y	1381	139.4	4.9	972	5	BU904623
1309	139.4	4.9	221	7	CO415408	Mdf43006j	1382	139.4	4.9	1012	5	BU904623
1310	139.4	4.9	224	6	CA935085	sau44b08.	1383	139.4	4.9	1020	5	BQ218454
1311	139.4	4.9	236	4	CB679266	BU679266	1384	139.4	4.9	1052	5	BU560001
1312	139.4	4.9	257	6	CB191298	py30e08.y	1385	139.4	4.9	1069	6	CD387126
c1313	139.4	4.9	258	7	CO735938	SILL05b13	1386	139.4	4.9	1074	6	CD051138
1314	139.4	4.9	269	6	CD638413	AGENCOURT	1387	139.4	4.9	1108	5	BU843272
1315	139.4	4.9	271	6	CA802549	sau38b03.	1388	139.4	4.9	1145	3	BC027896
1316	139.4	4.9	276	4	BM341777	fw52f11.y	1389	139.4	4.9	3645	3	HS807326
1317	139.4	4.9	278	7	CO192919	EC34778.5	1390	139.2	4.9	191	1	AL696149
1318	139.4	4.9	279	7	CF805341	lad67a03.	1391	139.2	4.9	203	5	BX470454
1319	139.4	4.9	297	7	CO180424	EC01537.5	c1392	139.2	4.9	204	7	CR545056
1320	139.4	4.9	302	4	BI863806	kx49f04.y	1393	139.2	4.9	208	1	AL697778
1321	139.4	4.9	314	5	BI863806	NKLV107.E	1394	139.2	4.9	216	6	CB073167
1322	139.4	4.9	316	6	CB570335	CAB10003	c1395	139.2	4.9	248	5	BQ265006
1323	139.4	4.9	317	2	AW102509	AMGNNUC:5	1396	139.2	4.9	249	6	CF935136
1324	139.4	4.9	321	6	CB708528	sd60b08.y	c1397	139.2	4.9	250	7	CF208314
1325	139.4	4.9	323	4	BI709353	FE63e06.y	1398	139.2	4.9	251	6	CB045262
1326	139.4	4.9	334	7	CO184694	EC28424.5	c1399	139.2	4.9	252	6	CB043981
c1327	139.4	4.9	338	5	BQ392456	NISC_mq24	1400	139.2	4.9	257	7	CV193143
c1328	139.4	4.9	345	5	BQ526035	NISC_no14	1401	139.2	4.9	269	5	BX474011
1329	139.4	4.9	350	6	CB332172	py68e09.y	1402	139.2	4.9	272	6	CA935343
1330	139.4	4.9	354	6	CB077235	h51d03.g	1403	139.2	4.9	297	5	BQ128810
1331	139.4	4.9	359	6	CB956435	AGENCOURT	1404	139.2	4.9	311	6	CD678330
1332	139.4	4.9	364	7	CK375041	lai44b01.	1405	139.2	4.9	312	7	CK906888
c1333	139.4	4.9	367	1	AI863014	vm45c09.x	c1406	139.2	4.9	313	5	BQ391420
1334	139.4	4.9	390	6	CF008212	QBI8c10.x	1407	139.2	4.9	316	4	BM651303
1335	139.4	4.9	390	7	CR767294	DKF2p468D	c1408	139.2	4.9	317	7	CV248497
c1336	139.4	4.9	409	9	CNS02V5X	Tetraodon	1409	139.2	4.9	317	7	CV248497
1337	139.4	4.9	412	6	CB080314	hp84d12.b	1410	139.2	4.9	318	7	CV467476
c1338	139.4	4.9	417	5	BQ3999330	NISC_mp03	1411	139.2	4.9	333	7	CF571969

CF545613 lad98b09.
CF301049 7LEAF--05
BX500114 DKF2p779J
AV681668 AV681668
AJ791816 AJ791816
CN843209 AGENCOURT
BI743903 kx42d07.y
CN164657 995018 MA
AI207510 HA2865 Hu
CF369687 IG54h07.y
CD766630 AGENCOURT
CF357352 rm84c10.y
CN051788 v7_p96_b3
BU535289 AGENCOURT
AV706777 AV706777
CV482931 AGENCOURT
CN162353 951733 MA
CV489012 AGENCOURT
BU536633 AGENCOURT
BU957844 AGENCOURT
BC050987 Mus muscu
CK396579 AGENCOURT
BU534594 AGENCOURT
BU843224 AGENCOURT
BU529378 AGENCOURT
BU958202 AGENCOURT
BU847233 AGENCOURT
CO913882 AGENCOURT
BU530595 AGENCOURT
CO808031 AGENCOURT
BU959812 AGENCOURT
BU587807 AGENCOURT
CN168212 AGENCOURT
BU598840 AGENCOURT
BU588070 AGENCOURT
BU531363 AGENCOURT
BU603755 AGENCOURT
CA792742 AGENCOURT
BQ434577 AGENCOURT
BU953880 AGENCOURT
BQ937042 AGENCOURT
BU531322 AGENCOURT
BU904623 AGENCOURT
BQ218454 AGENCOURT
BU560001 AGENCOURT
CD387126 AGENCOURT
CD051138 AGENCOURT
BU843272 AGENCOURT
BC027896 Homo sapi
BX647182 Homo sapi
AL696149 DKF2p686B
EX470454 DKF2p686A
CR545056 DKF2p470L
AL697778 DKF2p686P
CB073167 taa29c09.
BQ265006 NISC_ff02
CA935136 sau49b05
CF208314 CAB20003
CB045262 NISC_gc09
CB043981 NISC_gc01
CV193143 SNESTb2
BX474011 DKF2p686L
CA935343 sau52d02
BQ128810 ii23d03.y
CD678330 hp05n10.y
CK906888 TSL9 Tail
BQ391420 NISC_mq18
CO950943 UMC-Pd12c
BM651303 170006873
CV248497 WS01120.B
CV467476 Md1v4005H
CF571969 MCSA031C0

1412	139.2	4.9	347	2	BE785905	BE785905	601477905	1485	139	4.9	209	1	AA638753	AA638753	vm93e12.r
1413	139.2	4.9	356	6	CB722234	CB722234	jnm609B07	1486	139	4.9	217	7	CR524654	CR524654	DKFZp4701
1414	139.2	4.9	357	9	AL054509	AL054509	Drosophila	C1487	139	4.9	219	4	BM587451	BM587451	170006873
1415	139.2	4.9	372	6	CA7011594	CA7011594	tao05d03	1488	139	4.9	225	6	CA819034	CA819034	sau67h08
1416	139.2	4.9	383	7	CR791094	CR791094	DKFZp469C	1489	139	4.9	237	7	CR543081	CR543081	DKFZp470G
1417	139.2	4.9	384	4	BG107847	BG107847	602278030	1490	139	4.9	237	7	CR791203	CR791203	DKFZp468F
1418	139.2	4.9	391	5	BQ398550	BQ398550	NISC_m008	1491	139	4.9	261	6	CA802834	CA802834	sau39g05
1419	139.2	4.9	397	1	AI920968	AI920968	wol16g05.x	1492	139	4.9	272	7	CO184738	CO184738	EC28495.5
1420	139.2	4.9	418	2	BM534662	BM534662	tx70a04.y	1493	139	4.9	291	4	BJ697356	BJ697356	BJ697356
1421	139.2	4.9	418	2	BE048026	BE048026	tz45g12.y	1494	139	4.9	296	7	CO488925	CO488925	GQ0255.B3
1422	139.2	4.9	425	7	CR831880	CR831880	AGENCOURT	1495	139	4.9	301	6	CA802821	CA802821	sau42g02
1423	139.2	4.9	430	7	CF545863	CF545863	lae81g01	1496	139	4.9	320	6	CD640148	CD640148	AGENCOURT
1424	139.2	4.9	431	4	BM815920	BM815920	JCXPO170	1497	139	4.9	323	7	CR763446	CR763446	DKFZp470G
1425	139.2	4.9	435	7	CR7533204	CR7533204	DKFZp4680	1498	139	4.9	348	7	CO191264	CO191264	EC30590.5
1426	139.2	4.9	439	7	CR834293	CR834293	AGENCOURT	1499	139	4.9	364	7	CO183382	CO183382	EC25619.5
1427	139.2	4.9	444	1	AV681785	AV681785	AV681785	1500	139	4.9	366	7	CV525316	CV525316	MDLV4011c
1428	139.2	4.9	461	1	AV682074	AV682074	AV682074								
1429	139.2	4.9	463	6	CB445238	CB445238	696490.MA								
1430	139.2	4.9	477	5	BQ390789	BQ390789	NISC_mq15								
1431	139.2	4.9	489	5	BX490733	BX490733	DKFZp686B								
1432	139.2	4.9	507	7	CF805203	CF805203	lad64c10								
1433	139.2	4.9	522	1	AL665661	AL665661	AL665661								
1434	139.2	4.9	524	7	CK593392	CK593392	tad36g06								
1435	139.2	4.9	538	7	CO752656	CO752656	Mdf-3025c								
1436	139.2	4.9	569	7	CV2222905	CV2222905	taj34d03								
1437	139.2	4.9	582	7	CV2222884	CV2222884	taj54b02								
1438	139.2	4.9	594	5	BQ586905	BQ586905	S014325-0								
1439	139.2	4.9	608	4	BG678047	BG678047	602625771								
1440	139.2	4.9	623	5	BQ197920	BQ197920	NKLV122.F								
1441	139.2	4.9	631	7	CF330508	CF330508	NACL--06								
1442	139.2	4.9	647	7	CV2222879	CV2222879	taj34a03								
1443	139.2	4.9	684	6	CD642149	CD642149	AGENCOURT								
1444	139.2	4.9	708	6	CD237931	CD237931	FNPARF04								
1445	139.2	4.9	709	7	CV480279	CV480279	AGENCOURT								
1446	139.2	4.9	712	4	BG739805	BG739805	602630530								
1447	139.2	4.9	717	6	CD5211752	CD5211752	AGENCOURT								
1448	139.2	4.9	762	6	CD638731	CD638731	AGENCOURT								
1449	139.2	4.9	769	6	CB320358	CB320358	AGENCOURT								
1450	139.2	4.9	777	7	CN322743	CN322743	AGENCOURT								
1451	139.2	4.9	778	5	BUS33506	BUS33506	AGENCOURT								
1452	139.2	4.9	790	5	BUS34395	BUS34395	AGENCOURT								
1453	139.2	4.9	794	8	AZ530415	AZ530415	ENTEX01TR								
1454	139.2	4.9	795	5	BUS79391	BUS79391	AGENCOURT								
1455	139.2	4.9	795	7	CF288665	CF288665	AGENCOURT								
1456	139.2	4.9	816	7	CV488826	CV488826	AGENCOURT								
1457	139.2	4.9	827	5	BUS93672	BUS93672	AGENCOURT								
1458	139.2	4.9	830	5	BUS65215	BUS65215	AGENCOURT								
1459	139.2	4.9	830	6	CA967674	CA967674	CCL03a10								
1460	139.2	4.9	834	7	CK788590	CK788590	AGENCOURT								
1461	139.2	4.9	852	6	CA971155	CA971155	AGENCOURT								
1462	139.2	4.9	858	7	CO810738	CO810738	AGENCOURT								
1463	139.2	4.9	863	5	BUS963584	BUS963584	AGENCOURT								
1464	139.2	4.9	865	5	BUS942519	BUS942519	AGENCOURT								
1465	139.2	4.9	866	7	CF289423	CF289423	AGENCOURT								
1466	139.2	4.9	873	5	BUS960662	BUS960662	AGENCOURT								
1467	139.2	4.9	889	5	BUS42522	BUS42522	AGENCOURT								
1468	139.2	4.9	899	7	CF579388	CF579388	AGENCOURT								
1469	139.2	4.9	942	9	CNS00601	AL065607	Drosophila								
1470	139.2	4.9	954	5	BQ433060	BQ433060	AGENCOURT								
1471	139.2	4.9	972	7	CF594816	CF594816	AGENCOURT								
1472	139.2	4.9	979	7	CF584689	CF584689	AGENCOURT								
1473	139.2	4.9	1017	4	BG108324	BG108324	602280329								
1474	139.2	4.9	1025	9	CNS01472	AL104216	Drosophila								
1475	139.2	4.9	1038	5	BUS36229	BUS36229	AGENCOURT								
1476	139.2	4.9	1061	4	BM803249	BM803249	AGENCOURT								
1477	139.2	4.9	1145	9	CL077970	CL077970	CH216-147								
1478	139.2	4.9	1150	5	BQ923903	BQ923903	AGENCOURT								
1479	139.2	4.9	1150	5	BUS902080	BUS902080	AGENCOURT								
1480	139.2	4.9	1168	4	BM464215	BM464215	AGENCOURT								
1481	139.2	4.9	1194	4	BM473912	BM473912	AGENCOURT								
1482	139.2	4.9	1270	4	BM456675	BM456675	AGENCOURT								
1483	139	4.9	183	5	BQ740714	BQ740714	saq51b07								
1484	139	4.9	195	4	BU251931	BU251931	BU251931								

FEATURES

source

1. 3165

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="RZPD:DKFZp686N24154Q"

/db_xref="taxon:9606"

/clone="DKFZp686N24154"

/tissue type="colon endothel, primary cell culture"

/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host DH10B; sites SfiI + SfiIb"

/dev stages="adult"

/note="hypothetical protein"

1. 3165

/gene="DKFZp686N24154"

447. .2609

/gene="DKFZp686N24154"

/codon_start=1

/product="hypothetical protein"

/protein_id="CAE45808.1"

/db_xref="GI:34364726"

/db_xref="UniProt/TREMBL:Q6N062"

/translation="MELGCVTQPLGLTFLQLLLISLPRYTVINACPGAENWIMCRE

CCRYDQIECVCPGRKREVVGYTIPCRNEENECDSCLIHFGCTIFENCCKSRGSGGT

ALIGNMENTS

3165 bp mRNA linear HTC 22-SEP-2004

HSM806734 Homo sapiens mRNA; cDNA DKFZp686N24154 (from clone DKFZp686N24154).

LOCUS HSM806734

DEFINITION Homo sapiens mRNA; cDNA DKFZp686N24154 (from clone DKFZp686N24154).

ACCESSION BX640676

VERSION BX640676.1

KEYWORDS HTc.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3165)

Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Oeinger, A., Pöbo, G., Han, M. and Wiemann, S.

The German cDNA Consortium

Direct Submission

Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY

Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686N24154) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.

Please contact RZPD for ordering:

http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686N24154

Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

LDDFYVGFYCAECRAGVYGGDMRCGQVLRAPKGOIILLESYPLNAHCWETIHAKPGF
VIQLRFVLSLEFDYMCQYDYVVDGDNRDGOIILKRVGNERPAPIOSIGSSLHVLF
HDSGKNFDGFHAIYEEITAGSSSPCFHDGTCVLDKAGSYKACLAGTGTQRCENLLE
ERNCSDPGPVNGYOKITGGPLINGRAKIGTVVFFCNNSYVLSNGEKRTQQNGE
WSGQPICTIKACREPKISDLVRRVRLPMQVOSRETPHLQLYSAAFSKQJLOSAPTKP
ALPFDGLPMGQHLHTQYECISPFYRLGSSRRCLRTGKWSGRAPSCPIOCKIE
NITAPKTOGLRWPQAAIYRRTSGVHDGSLHKWFLVCSGALVNERTVVVAACHVTD
LGKWTMIKTADLKVLKGFYRDDDEKTIQSLRISALILHPNDYDPIILLADIATLKL
LDKARISTRVQPICLAASRDLSISFQESHIIIVAGHNVLDVRSFGPKNDTLRSGVSV
VDSLCEQSHEDHGIPVSVDTNMFCASWEPTAPSDICTAEAGGIAAASFPGRASPEPR
WHLMLGVSWSYDKTCSHRLSTAFTKVLFPFKOWIERNMK"

ORIGIN

Query Match 96.1%; Score 2734.4; DB 3; Length 3165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2738; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	1	CGCTCGGGCACCAGCGCGGCAAGATGGAGCTGGGTGCTGCAGCGCAGTTGGGGCTCAC	60
Db	422	CGCTCGGGCACCAGCGCGGCAAGATGGAGCTGGGTGCTGCAGCGCAGTTGGGGCTCAC	481
Qy	61	TTTTCTTCAGCTCCTTCATCTCGTCTTGCCTGCAAGAGAGTACACAGTCATTAATGAAGC	120
Db	482	TTTTCTTCAGCTCCTTCATCTCGTCTTGCCTGCAAGAGAGTACACAGTCATTAATGAAGC	541
Qy	121	CTGCCCTGGAGCAGAGTGGAAATCATGTGTCGGGAGTGCTGTGAATATGATCAGATTGA	180
Db	542	CTGCCCTGGAGCAGAGTGGAAATCATGTGTCGGGAGTGCTGTGAATATGATCAGATTGA	601
Qy	181	GTGCGTCTGCCCGGAAAGAGGGAAGTCGTGGGTATACCATCCCTTGCTGCAGGAATGA	240
Db	602	GTGCGTCTGCCCGGAAAGAGGGAAGTCGTGGGTATACCATCCCTTGCTGCAGGAATGA	661
Qy	241	GGAGAAATGAGTGTGACTCTGCTGATCCACCCAGGTTGTACCATCTTTGAAAAATGCAA	300
Db	662	GGAGAAATGAGTGTGACTCTGCTGATCCACCCAGGTTGTACCATCTTTGAAAAATGCAA	721
Qy	301	GAGCTGCCGAATATGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCTA	360
Db	722	GAGCTGCCGAATATGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCTA	781
Qy	361	CTGTGCAGAGTCCGAGCAGGCTGTGTACGGAGGAGTGCATGCGATGTGGCCAGGTTCT	420
Db	782	CTGTGCAGAGTCCGAGCAGGCTGTGTACGGAGGAGTGCATGCGATGTGGCCAGGTTCT	841
Qy	421	CGAGCCCCAAAGGFTCAGATTTTGTGTGAAAGCTATCCCTTAATGTCTCATGTGAATG	480
Db	842	CGAGCCCCAAAGGFTCAGATTTTGTGTGAAAGCTATCCCTTAATGTCTCATGTGAATG	901
Qy	481	GACCATTCATGCTAAACCTGGGTGTGTCATCCAACTAAGATTTGTCAGTCTGGA	540
Db	902	GACCATTCATGCTAAACCTGGGTGTGTCATCCAACTAAGATTTGTCAGTCTGGA	961
Qy	541	GTTTGACTACATGTGCGAGTATGACTATGTGAGGTTCTGTGATGGAGACAAACCGGATGG	600
Db	962	GTTTGACTACATGTGCGAGTATGACTATGTGAGGTTCTGTGATGGAGACAAACCGGATGG	1021
Qy	601	CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCAGCTCTATCCAGAGCATAGGATC	660
Db	1022	CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCAGCTCTATCCAGAGCATAGGATC	1081
Qy	661	CTCAGTCCAGCTCTCTTCCACTCCGATGGCTCCAGAAATTTTGAGGTTTCATGCCAT	720
Db	1082	CTCAGTCCAGCTCTCTTCCACTCCGATGGCTCCAGAAATTTTGAGGTTTCATGCCAT	1141
Qy	721	TTATGAGGAGATCACAGCATGCTCTCATCCCTTGTTTTCCATGACGGCAGCTGGGTCT	780
Db	1142	TTATGAGGAGATCACAGCATGCTCTCATCCCTTGTTTTCCATGACGGCAGCTGGGTCT	1201
Qy	781	TGACAAGGCTGGATCTTACAAGTGTGCTGCTGTGGCAGGCTATATCTGGGCAGCGCTGTGA	840
Db	1202	TGACAAGGCTGGATCTTACAAGTGTGCTGCTGTGGCAGGCTATATCTGGGCAGCGCTGTGA	1261

Qy	841	AAATCTCTCTGAAGAAAGAAACTGCTCAGACCTGGGGCCCGAGTCAATGGGTACAGAA	900
Db	1262	AAATCTCTCTGAAGAAAGAAACTGCTCAGACCTGGGGCCCGAGTCAATGGGTACAGAA	1321
Qy	901	AATAACAGGGGGCCTTGGGCTTATCAACGGACGCCATGCTTAAATTTGGCACCGTGGTGC	960
Db	1322	AATAACAGGGGGCCTTGGGCTTATCAACGGACGCCATGCTTAAATTTGGCACCGTGGTGC	1381
Qy	961	TTTCTTTTGTAACTCCTATGTTCTTAGTGGCAATCAGAAAGAACTTGGCCACAGAA	1020
Db	1382	TTTCTTTTGTAACTCCTATGTTCTTAGTGGCAATCAGAAAGAACTTGGCCACAGAA	1441
Qy	1021	TGGAGATGGTTCAGGAAACAGCCCATCTGCATAAAAGCCTGCCAGAAACCAAAGATTTC	1080
Db	1442	TGGAGATGGTTCAGGAAACAGCCCATCTGCATAAAAGCCTGCCAGAAACCAAAGATTTC	1501
Qy	1081	AGACTGTGTGAGAGAGAGGATTTCTTCGATGCAAGTTCAGTCAAGGGAGACACCATTA	1140
Db	1502	AGACTGTGTGAGAGAGAGGATTTCTTCGATGCAAGTTCAGTCAAGGGAGACACCATTA	1561
Qy	1141	CCAGCTATCTCAGCGGCTTCAGCAACAGCAAACTGCAGAGTGCCCTTACCAAGAGCC	1200
Db	1562	CCAGCTATCTCAGCGGCTTCAGCAACAGCAAACTGCAGAGTGCCCTTACCAAGAGCC	1621
Qy	1201	AGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTA	1260
Db	1622	AGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTA	1681
Qy	1261	TTAGTGCATCTCACCCCTTCTACCGCGCTTGGGACAGCAGCAGGAGGACATGTCTGAGAC	1320
Db	1682	TTAGTGCATCTCACCCCTTCTACCGCGCTTGGGACAGCAGCAGGAGGACATGTCTGAGAC	1741
Qy	1321	TGGGAATGAGTGGGCGGACCATCTGCATCCCTATCTGCGGGAATTTGAGAACAT	1380
Db	1742	TGGGAATGAGTGGGCGGACCATCTGCATCCCTATCTGCGGGAATTTGAGAACAT	1801
Qy	1381	CACTCTCTCCAAAGACCCAAAGGTTGCGCTGGCGTGGCAGGAGGAGGACATCTACAGGAGAC	1440
Db	1802	CACTCTCTCCAAAGACCCAAAGGTTGCGCTGGCGTGGCAGGAGGAGGACATCTACAGGAGAC	1861
Qy	1441	CAGCGGGTGTGATGACGGCAGCCTACAAAGGAGCGTGGTTCCTAGTCTGAGCGGTGC	1500
Db	1862	CAGCGGGTGTGATGACGGCAGCCTACAAAGGAGCGTGGTTCCTAGTCTGAGCGGTGC	1921
Qy	1501	CCTGTGTAATGAGCCGACCTGTGTGGTGGCTGCCACCTGTGTACTGACCTGCGGAAGGT	1560
Db	1922	CCTGTGTAATGAGCCGACCTGTGTGGTGGCTGCCACCTGTGTACTGACCTGCGGAAGGT	1981
Qy	1561	CACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAATTTCTACCGGGATGATGA	1620
Db	1982	CACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAATTTCTACCGGGATGATGA	2041
Qy	1621	CCGGATGAGAAAGACCATCCAGAGCCTACGAGTTCTGCTATCATTTCTGATCCCACTA	1680
Db	2042	CCGGATGAGAAAGACCATCCAGAGCCTACGAGTTCTGCTATCATTTCTGATCCCACTA	2101
Qy	1681	TGACCCCATCTGCTGTGATGTCATCGCCATCTGAGCTCTAGAACGCGCGTAT	1740
Db	2102	TGACCCCATCTGCTGTGATGTCATCGCCATCTGAGCTCTAGAACGCGCGTAT	2161
Qy	1741	CAGCACCCGAGTCCAGCCCATCTGCTCGCTCGGATCGGGATCTCAGACCTTCTTCCA	1800
Db	2162	CAGCACCCGAGTCCAGCCCATCTGCTCGCTCGGATCGGGATCTCAGACCTTCTTCCA	2221
Qy	1801	GGAGTCCCAATCATCTGTGGTGGTGGAAATGCTCTGGCAGACGTTGAGAGGCTTGGCTT	1860
Db	2222	GGAGTCCCAATCATCTGTGGTGGTGGAAATGCTCTGGCAGACGTTGAGAGGCTTGGCTT	2281
Qy	1861	CAAGAACGACACACTGCGCTCTGGGGTGGTCAAGTGTGGTGGACTCGCTCTGTGTGAGGA	1920
Db	2282	CAAGAACGACACACTGCGCTCTGGGGTGGTCAAGTGTGGTGGACTCGCTCTGTGTGAGGA	2341
Qy	1921	GCAGCATGAGGACCATGGCATCCCGATGAGTGTCTACTGATAACATGTTTCTGTGCCAGCTG	1980

Db 602 CCAAGAAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCATGCTCCTCATCCC 661
Qy 753 CTTGTTTTCCATGACGGCAGTGGCTTCTTGACAAAGGCTGGATCTTTACAAAGTGTGGCTGCT 812
Db 662 CTTGTTTTCCATGACGGCAGTGGCTTCTTGACAAAGGCTGGATCTTTACAAAGTGTGGCTGCT 721
Qy 813 TGGCAGGCTTATCTGGGAGCGCTGTGAAATCTCTTTGAAGAAAGAACTGCTCAGACC 872
Db 722 TGGCAGGCTTATCTGGGAGCGCTGTGAAATCTCTTTGAAGAAAGAACTGCTCAGACC 781
Qy 873 CTGGGGGCCAGTCAATGGGTACCAAGAAATTAACAGGGGGCCCTGGGCTTATCAACGAGC 932
Db 782 CTGGGGGCCAGTCAATGGGTACCAAGAAATTAACAGGGGGCCCTGGGCTTATCAACGAGC 841
Qy 933 GCCATGCTAAATTTGGCAGCGGTGTCTTTCTTTTGTAACTCTTATGTTCTTAGTG 992
Db 842 GCCATGCTAAATTTGGCAGCGGTGTCTTTCTTTTGTAACTCTTATGTTCTTAGTG 901
Qy 993 GCAATGAGAAAGAACTTGCAGCAGATGGAGA-GTGGTCAAGGAAACAGGCCATCTGC 1051
Db 902 GCNATGAGAAAGAACTTGCAGCAGATGGAGAGTGGTCAAGGAAACAGGCCATCTGC 961
Qy 1052 ATAAAGGCTGCGGAGAACCAAGATTTCAACCTGGTGAAGAGAGTCTTCCGATG 1111
Db 962 ATAAAGGCTGCGGAGAACCAAGATTTCAACCTGGTGAAGAGAGTCTTCCGATG 1021
Qy 1112 CAGGTTCACTCAGGAGACCAATTAACCAAGCTTATCTCAGCGGCTTCAAGCAAGCAG 1171
Db 1022 CAGGTTCACTCAGGAGACCAATTAACCAAGCTTATCTCAGCGGCTTCAAGCAAGCAG 1081
Qy 1172 AAATGTCAGAGTGCCCTACCAAGAGCAGGCCCTTCCCTTTGGAGATCTGCCCATGGGA 1231
Db 1082 AAATGTCAGAGTGCCCTACCAAGAGCAGGCCCTTCCCTTTGGAGATCTGCCCATGGGA 1141
Qy 1232 TACCAACATCTGCATACCCAGCTCCAGTATGATGCATCTACCTTTTCAACGCGGCTG 1291
Db 1142 TACCAACATCTGCATACCCAGCTCCAGTATGATGCATCTACCTTTTCAACGCGGCTG 1201
Qy 1292 GGCAGCAGGAGACATGCTGAGGACTGGGAAGTGGAGTGGGGGGCACCATCTGTC 1351
Db 1202 GGCAGCAGGAGACATGCTGAGGACTGGGAAGTGGAGTGGGGGGCACCATCTGTC 1261
Qy 1352 ATCCCTATCTGGGGGAAATTCAGAAACATCACTGCTCCAAAGACCAGGGTGTGGCTGG 1411
Db 1262 ATCCCTATCTGGGGGAAATTCAGAAACATCACTGCTCCAAAGACCAGGGTGTGGCTGG 1321
Qy 1412 CCGTGGCAGGACCATCTACAGGAGGACAGCGGGGTGCATGACGGGAGCCTACACAG 1471
Db 1322 CCGTGGCAGGACCATCTACAGGAGGACAGCGGGGTGCATGACGGGAGCCTACACAG 1381
Qy 1472 GAGCGTGGTTCCTAGTCTGACGGGTGCCCTGGTGAATGAGCGCACTGTGGTGGCT 1531
Db 1382 GAGCGTGGTTCCTAGTCTGACGGGTGCCCTGGTGAATGAGCGCACTGTGGTGGCT 1441
Qy 1532 GCCCACTGTGTTACTGACCTGGGGAAGTCAACATGATCAAGACAGCAGACCTGAAAGTT 1591
Db 1442 GCCCACTGTGTTACTGACCTGGGGAAGTCAACATGATCAAGACAGCAGACCTGAAAGTT 1501
Qy 1592 GTTTTGGGAAATTCACCGGATGATGACCGGATGAGAGACCATCCAGAGCCTACAG 1651
Db 1502 GTTTTGGGAAATTCACCGGATGATGACCGGATGAGAGACCATCCAGAGCCTACAG 1561
Qy 1652 ATTTCTGCTATCTGATCCCACTATGACCCCATCTGTTGATGCTGACATGCC 1711
Db 1562 ATTTCTGCTATCTGATCCCACTATGACCCCATCTGTTGATGCTGACATGCC 1621
Qy 1712 ATCTGGAAGCTCTAGACAGGCCGTATACGACCCGAGTCCAGGCCCATCTGCTCGCT 1771
Db 1622 ATCTGGAAGCTCTAGACAGGCCGTATACGACCCGAGTCCAGGCCCATCTGCTCGCT 1681
Qy 1772 GCCAGTCGGATCTCAGCACTTCTTCCAGGAGTCCCAATCACTGTGGCTGGGAT 1831
Db 1682 GCCAGTCGGATCTCAGCACTTCTTCCAGGAGTCCCAATCACTGTGGCTGGGAT 1741

Qy 1832 GTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTC 1891
Db 1742 GTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTC 1801
Qy 1892 AGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGCGCATCCAGTGAGT 1951
Db 1802 AGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGCGCATCCAGTGAGT 1861
Qy 1952 GTCACTGATAACATGTTCTGTGCCAGCTGGGAAACCACTGCCCTTCTGATATCTGCAT 2011
Db 1862 GTCACTGATAACATGTTCTGTGCCAGCTGGGAAACCACTGCCCTTCTGATATCTGCAT 1921
Qy 2012 GCAGAGACAGGAGCATCGCGCTGTGTCTTCCGGGACGAGCATCTCTGAGCAAGC 2071
Db 1922 GCAGAGACAGGAGCATCGCGCTGTGTCTTCCGGGACGAGCATCTCTGAGCAAGC 1981
Qy 2072 TGGCATCTGATGGGACTGCTGCTGAGCTGAGCTATGATAAAACATGAGCCACAGGCTCTCC 2131
Db 1982 TGGCATCTGATGGGACTGCTGCTGAGCTGAGCTATGATAAAACATGAGCCACAGGCTCTCC 2041
Qy 2132 ACTGCTTCAACAGGCTGCTGCTTTAAAGACTGGATTGAAAGAAATATGAAATGAACC 2191
Db 2042 ACTGCTTCAACAGGCTGCTGCTTTAAAGACTGGATTGAAAGAAATATGAAATGAACC 2101
Qy 2192 ATGCTCATGCTCTCTGAGAAAGTGTCTGTATATCCGTCTGTACGTGTCTATGGGT 2251
Db 2102 ATGCTCATGCTCTCTGAGAAAGTGTCTGTATATCCGTCTGTACGTGTCTATGGGT 2161
Qy 2252 GAAGCAGTGTGGGCTGAAAGTGTGATTTGGGCTGTGAACTTGGCTGTGACAGGCTCTG 2311
Db 2162 GAAGCAGTGTGGGCTGAAAGTGTGATTTGGGCTGTGAACTTGGCTGTGACAGGCTCTG 2221
Qy 2312 ACTTCAGGACAAACACTCAGTGAAGGTGAGTAGACCTCCATTGCTGTGAGCTGATGCC 2371
Db 2222 ACTTCAGGACAAACACTCAGTGAAGGTGAGTAGACCTCCATTGCTGTGAGCTGATGCC 2281
Qy 2372 GCGTCCACTACTTAGGACAGCCAAATTTGGAAGATGCCAGGGCTTGCAAGAAATGAAATTTCT 2431
Db 2282 AGTCCACTACTTAGGACAGCCAAATTTGGAAGATGCCAGGGCTTGCAAGAAATGAAATTTCT 2341
Qy 2432 CAAAGAAGACCATATACAAAACCTCTCCACTCCACTGACCTGGTGGTCTTCCCAACTTT 2491
Db 2342 CAAAGAAGACCATATACAAAACCTCTCCACTCCACTGACCTGGTGGTCTTCCCAACTTT 2401
Qy 2492 CAGTTATACGATGSCCATCAGCTTGACAGGGAAGATCTGGGCTTCATGAGGCCCTTTT 2551
Db 2402 CAGTTATACGATGSCCATCAGCTTGACAGGGAAGATCTGGGCTTCATGAGGCCCTTTT 2461
Qy 2552 GAGGCTCTCAAGTTCTAGAGAGCTGCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATG 2611
Db 2462 GAGGCTCTCAAGTTCTAGAGAGCTGCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATG 2521
Qy 2612 TGGTGCATGCTTGTGTACATGGCCACAGTACAGTCTGGTCTTTTCTTCCCATCTC 2671
Db 2522 TGGTGCATGCTTGTGTACATGGCCACAGTACAGTCTGGTCTTTTCTTCCCATCTC 2581
Qy 2672 TTGTACATTTTAAATAAGGTTGGCTTCTGAACTACAAAATAAAAAA 2731
Db 2582 TTGTACATTTTAAATAAGGTTGGCTTCTGAACTACAAAATAAAAAA 2641
Qy 2732 AAAAAAAAA 2740
Db 2642 AAAAAAAAA 2650

RESULT 3
AY406074
LOCUS
DEFINITION
ACCESSION
VERSION

AY406074 2214 bp DNA linear GSS 12-DEC-2003
Homo sapiens HCM2436 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.

AY406074
AY406074.1 GI:39762048

```
KEYWORDS  GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
           1 (bases 1 to 2214)
           Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
           Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
           Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
           Adams, M.D. and Cargill, M.
TITLE      Inferring nonneutral evolution from human-chimp-mouse orthologous
           gene trios
JOURNAL    Science 302 (5652), 1960-1963 (2003)
PUBMED    14671302
REFERENCE  2 (bases 1 to 2214)
AUTHORS    Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
           Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
           Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
           Adams, M.D. and Cargill, M.
TITLE      Direct Submission
JOURNAL    Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
           Rockville, MD 20850, USA
COMMENT    This sequence was made by sequencing genomic exons and ordering
           them based on alignment.
FEATURES   Location/Qualifiers
           source
             1..2214
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
             <1..>2214
             /locus_tag="HCM2436"
gene
ORIGIN
Query Match      66.5%; Score 1893; DB 9; Length 2214;
Best Local Similarity 88.5%; Pred. No. 0;
Matches 1960; Conservative 0; Mismatches 203; Indels 51; Gaps 1;
Qy 26 ATGGAGCTGGGTTGTGGAACGAGTGGGGCTCACTTTTTCAGCTCCTTCTCATCTCG 85
Db 1 ATGGAGCTGGGTTGTGGAACGAGTGGGGCTCACTTTTTCAGCTCCTTCTCATCTCG 60
Qy 86 TCCTTGGCCAGAGAGTACACAGTCAATTAATGAGCTGCTGCCCGGAAAGAGGAA 145
Db 61 TCCTTGGCCAGAGAGTACACAGTCAATTAATGAGCTGCTGCCCGGAAAGAGGAA 120
Qy 146 ATGTCGCGGAGTGTGTAATATGATCAGATTGAGTGGTCTGCCCGGAAAGAGGAA 205
Db 121 ATGTCGCGGAGTGTGTAATATGATCAGATTGAGTGGTCTGCCCGGAAAGAGGAA 180
Qy 206 GTGCTGGGTTATACCATCCCTTGTGTCAGGAATGAGGAATGAGTGTGACTCTGCTG 265
Db 181 GTGCTGGGTTATACCATCCCTTGTGTCAGGAATGAGGAATGAGTGTGACTCTGCTG 240
Qy 266 ATCCACCCAGGTGTGATACATCTTTGAAACTGCAAGAGCTGCCGAATGGCTCATGGGG 325
Db 241 ATCCACCCAGGTGTGATACATCTTTGAAACTGCAAGAGCTGCCGAATGGCTCATGGGG 300
Qy 326 GTATCTTTGGATGACTTCTATGTGAAGGGTTCTACTGTGAGAGTGCAGAGCTGG 385
Db 301 GTATCTTTGGATGACTTCTATGTGAAGGGTTCTACTGTGAGAGTGCAGAGCTGG 360
Qy 386 TACGGAGGAGACTGTCATGCGATGTGGCCAGAGTTCTGCGAGGCCCAAGAGGTCAGATT 445
Db 361 TACGGAGGAGACTGTCATGCGATGTGGCCAGAGTTCTGCGAGGCCCAAGAGGTCAGATT 420
Qy 446 TTGGAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTCATGCTAAACCTGGGTT 505
Db 421 TTGGAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTCATGCTAAACCTGGGTT 480
Qy 506 GTCAATCCAACTAAGATTGTGATGTTGAGTGTGGAGTTGACTACATGTGCCAGTATGAC 565
Db 481 GTCAATCCAACTAAGATTGTGATGTTGAGTGTGGAGTTGACTACATGTGCCAGTATGAC 540
566 TATGTTGAGGTTGTTGATGGAGACAACCGCGATGGCCAGATCATCAAGCGTCTCTGTGCG 625
541 TATGTTGAGGTTGTTGATGGAGACAACCGCGATGGCCAGATCATCAAGCGTCTCTGTGCG 600
626 AACGAGCGCGCAGCTCCTATCCAGAGCATAGGATCCTCACTCCAGTCTCTCTTCCACTCC 685
601 AACGAGCGCGCAGCTCCTATCCAGAGCATAGGATCCTCACTCCAGTCTCTCTTCCACTCC 660
686 GATGCTCTCAAGAATTTTTCAGCGGTTTCCATGCGCATTTATGAGGAGATCACAGCATGCTCC 745
661 GATGCTCTCAAGAATTTTTCAGCGGTTTCCATGCGCATTTATGAGGAGATCACAGCATGCTCC 720
746 TCATCCCTCTGTTTCCATGAGCGGACGCGTGTCTTGAACAAGCTGGATCTTTACAAGTGT 805
721 TCATCCCTCTGTTTCCATGAGCGGACGCGTGTCTTGAACAAGCTGGATCTTTACAAGTGT 780
806 GCCTGCTGGCAGGCTATACCTGGGCGAGCGTGTGAAATCTCTTGAAGAAGAAGAACTGC 865
781 GCCTGCTGGCAGGCTATACCTGGGCGAGCGTGTGAAATCTCTTGAAGAAGTGGGAAGTCC 840
866 -----TCAGACCCCT 874
841 AAGATCAAGCGCTCAGAAGATTCTGTCCTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 900
875 GGGGGCCCGCATGATGGGTACAGAAAATAACAGGGGGCCCTGGGCTTATCAACGAGCGC 934
901 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 960
935 CATGCTAAATTTGGCACCGTGTCTTTCTTTTGTAACTCTCTATGTTCTTAGTGGC 994
961 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1020
995 AATGAGAAAAGAACTTTCAGCAGCAAAATGAGAGTGGTCAAGGAAACAGCCCATCTGCATA 1054
1021 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1080
1055 AAAGCTGCGCAGAAACAAAGATTTCAGACTGTTGAGAGAGAGTCTTCCGATGCGAG 1114
1081 NNNNNCTCCGCAAGAACAAAGATTTCAGACTGTTGAGAGAGAGTCTTCCGATGCGAG 1140
1115 GTTCAGTCAAGGGAGACACCATTAACAGCTATATCAGCGGCTTTCAGCAAGCAGAAA 1174
1141 GTTCAGTCAAGGGAGACACCATTAACAGCTATATCAGCGGCTTTCAGCAAGCAGAAA 1200
1175 CTGAGAGTGCCCTTACCAAGAACAGCCCTTCCCTTTGGAGATCTGCCCATGGGATAC 1234
1201 CTGAGAGTGCCCTTACCAAGAACAGCCCTTCCCTTTGGAGATCTGCCCATGGGATAC 1260
1235 CAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCCCTTCTACCGCGCTGGGC 1294
1261 CAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCCCTTCTACCGCGCTGGGC 1320
1295 AGCAGCAGGAGACATGCTGAGGACTGGGAAGTGGAGTGGGCGGCGGACCATCTCGCATC 1354
1321 AGCAGCAGGAGACATGCTGAGGACTGGGAAGTGGAGTGGGCGGCGGACCATCTCGCATC 1380
1355 CCTATCTGCGGGAATAATGAGAACATCACTGCTCCAAAGACCAGAGGTTGGCTGGGCG 1414
1381 CCTATCTGCGGGAATAATGAGAACATCACTGCTCCAAAGACCAGAGGTTGGCTGGGCG 1440
1415 TGGCAGGAGCCATCTTACAGGAGACCAAGCGGGTGCATGACGCGAGCTTACACAAGGA 1474
1441 TGGCAGGAGCCATCTTACAGGAGACCAAGCGGGTGCATGACGCGAGCTTACACAAGGA 1500
1475 GCGTGGTCTTCTAGTCTGCGAGCGGTCCTCTGTTGATGAGCGCATCTGTTGGTGGCTGCC 1534
1501 GCGTGGTCTTCTAGTCTGCGAGCGGTCCTCTGTTGATGAGCGCATCTGTTGGTGGCTGCC 1560
1535 CACTGTGTTACTGACCTGGGGAAGGTCAACATGATCAAGAGCAGCAGCTGAAAGTGT 1594
1561 CACTGTGTTACTGACCTGGGGAAGGTCAACATGATCAAGAGCAGCAGCTGAAAGTGT 1620
1595 TTGGGGAATAATCTTACCGGGATGATGACCCGGGATGAGAACCAATCCAGAGCCTACAGATT 1654
```



```
Db      |||||TTGGGGAATCTTACCGGATGATGACCGGATGAGAGACCATCCAGAGCTACAGATT 1680
Qy      TCTGCTATCATTTCTGCATCCCACTATGAGCCCATCTCTGCTGTGATGCTGACATGCCCATC 1714
Db      TCTGCTATCATTTCTGCATCCCACTATGAGCCCATCTCTGCTGTGATGCTGACATGCCCATC 1740
Qy      CTGAGCTCTCTAGACAAGCGCCGATATCAGCACCCGAGTCCAGCCCATCTGCTCTGCTGCC 1774
Db      CTGAGCTCTCTAGACAAGCGCCGATATCAGCACCCGAGTCCAGCCCATCTGCTCTGCTGCC 1800
Qy      AGTCGGGATCTCAGCACTTCTCTTCAGGAGTCCCACTCATCTGTGGCTGGCTGGGAATGTC 1834
Db      AGTCGGGATCTCAGCACTTCTCTTCAGGAGTCCCACTCATCTGTGGCTGGCTGGGAATGTC 1860
Qy      CTGGCAGAGCTGAGAGCGCTGCTTCAAGAACGACACACTGCGCTCTGGGGTGTGTCAGT 1894
Db      CTGGCAGAGCTGAGAGCGCTGCTTCAAGAACGACACACTGCGCTCTGGGGTGTGTCAGT 1920
Qy      GTGGTGGACTCGCTGCTGTGAGGAGCAGCATGAGGACCATGGCATCCCACTGAGTGTGC 1954
Db      GTGGTGGACTCGCTGCTGTGAGGAGCAGCATGAGGACCATGGCATCCCACTGAGTGTGC 1980
Qy      ACTGATAACATGTTCTGTGCCAGCTGGGAACCCACTGCGCCCTTCTGATATCTGCACCTGCA 2014
Db      ACTGATAACATGTTCTGTGCCAGCTGGGAACCCACTGCGCCCTTCTGATATCTGCACCTGCA 2040
Qy      GAGCAGAGGAGCATCGCGCTGTGCTTCCGGGACGAGCATCTCTGAGCAGCGTGG 2074
Db      GAGCAGAGGAGCATCGCGCTGTGCTTCCGGGACGAGCATCTCTGAGCAGCGTGG 2100
Qy      CATCTGATGGAGTGGTCACTGAGTGGATGATGATAAATGATGAGCATGAGCATCTCCACT 2134
Db      CATCTGATGGAGTGGTCACTGAGTGGATGATGATAAATGATGAGCATGAGCATCTCCACT 2160
Qy      GCCTTCAACAGGTGCTGCTTTAAAGATGATGATGAAAGAAATATGAATGA 2188
Db      GCCTTCAACAGGTGCTGCTTTAAAGATGATGATGAAAGAAATATGAATGA 2214

RESULT 4
LOCUS   AK088017
DEFINITION Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN
full-length enriched library, clone:E430002G05 product:hypothetical
EGF-like domain, CUB domain, Sushi domain / SCR repeat / CCP module
and Serine proteases, trypsin family domain containing protein,
full insert sequence.
ACCESSION AK088017
VERSION AK088017.1 GI:26352935
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
```

```
TITLE YAMAMOTO,R., MATSUMOTO,H., SAKAGUCHI,S., IKEGAMI,T., KASHIWAGI,K.,
FUJIWAKE,S., INOUE,K., TOGAWA,Y., IZAWA,M., OHARA,E., WATAHIKI,M.,
YONEDA,Y., ISHIKAWA,T., OZAWA,K., TANAKA,T., MATEMURA,S., KAWAI,J.,
OKAZAKI,Y., MURAMATSU,M., INOUE,Y., KIRA,A. and HAYASHIZAKI,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,N., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
1. 2746
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="FANTOM DB:E430002G05"
/db_xref="taxon:10090"
/clone="E430002G05"
/cell_type="thymic cells"
/tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="2 days neonate"
71. 2233
/note="unnamed protein product; hypothetical EGF-like
domain, CUB domain, Sushi domain / SCR repeat / CCP module
and Serine proteases, trypsin family domain containing
protein (InterPro|IPR000561, evidence: InterPro)
putative"
/codon_start=1
/protein_id="BAC40098.1"
FEATURES
source
```


/db_xref="GI:26352936"
/translation="MELDRWAQLGLVFLQLLLISLPREYTVINEACPGAENIMCRE
CCEYDIELCPGKEVVGYTPCCRNEDNECDCLIHPGCTTIFENCKSRGWSGGT
LDLDFPGFYCAEACRAGWYGDGMRGQVLRSKQILLESYPLNAHCWTHARPFG
IIQLRFGMLSLFDMCOYDYVEVRDGNDSPIIKRFGCNERPAPIRSTGSLHLVLF
HSDSKNFDGPHAFVEETACSSSPCFHDTCLLDITGSPKACLAGVTGORCENLLE
ERNSDLDGPNVYKKITEGGLLNEHVKIGTVVSPFCNGSYVLSGNEKRTCCQNGE
WSGQPVCMKACREPKISDLVRRRLVSMQVSRETPHLQLYSTAPSKOKLQDASTKRP
ALPFDGLTGPYQHLHTQVYECISPFYRLLGSSRRRTCLRTKWSRAPSCPIPGKIE
STPSFKTGTRWPMQAAIYRRTSGVHDGLHGKAWFLVCSGALVNRVTVVVAACHVTE
LGGKATIKTADVLKLVGFYRDDDRDEKSIQNLVSAIILHPNDPDIILDDTLVLLK
LDKATIRSVOPICLVTATRDLDLSTQESHITVAGWNILADVRSQPKNDTLHYGMVVR
VDPMLCEQHEHDHGLIPSVTDNMFCASKDPSTPSDICTAETGGIALLSPGRASPEPR
WHLVGLVSWSDKNSGLSTAFKTLVLPFKDWIERNMK"
2718..2723
/note="putative"
2746
/note="putative"

polyA_signal

polyA_site

ORIGIN

Query Match 62.8%; Score 1788.2; DB 3; Length 2746;
Best Local Similarity 80.5%; Pred. No. 0;
Matches 2174; Conservative 0; Mismatches 503; Indels 24; Gaps 6;

QY	19	GGCAAGGATGAGCTGGGTGCTGACCGAGTTGGGGCTCACTTTTCTCAGCTCCTTCT	78
DB	64	GGAAACGATGAGCTAGACAGATGGCGCGAGTTGGGGCTGGTGTCTTCGACGCTCTTCT	123
QY	79	CATCTCGTCTTGCCCAAGAGACTACACAGTCAATTAATGAAGCTCGCCCTGGAGCAGATG	138
DB	124	CATCTCATCTGTTGCCAAGAGACTACCGTCAATTAATGAAGCTCTCCGGAGCTGAGTG	183
QY	139	GAATATCATGTGTCGGGAGTGTGTAATATGATCAGATTGAGTGCCTGTGCCCGGAAA	198
DB	184	GAACATCATGTGAGAGAATGTTGTAATATGATCAGATTGAATGCTTGCCCAAGAAA	243
QY	199	GAGGAACTGCTGGGTATACATCCCTTGTCGAGGAATGAGGAGATGAGTGTGACTC	258
DB	244	GAAGGAAGTGGTGGGTACACATCCCATGCTGCAAGGAATGAGGATAATGATGTGACTC	303
QY	259	CTGCCGTGATCCACCAGGTGTGACCATCTTTGAAAACCTGCAAGAGCTGCCGAAATGGCTC	318
DB	304	CTGTCTAATTCACCAGGTGTGACCATCTTTGAAAACCTGCAAGAGCTGCCGCAATGGCTC	363
QY	319	ATGGGGGGTACTCTTGAGTACTTCTATGTGAAGGGGTTCTACTGTGAGAGTGCAGGC	378
DB	364	CTGGGGCGGAACCTCTGGATGACTTCTAGTGAAGGATTTACTTGGCAGAGTGCAGGC	423
QY	379	AGGCTGGTACGAGGAGACTGATCGGATGTGGCCAGGTTCGTGAGCCGCCAAAGGGTCA	438
DB	424	AGGCTGGTACGAGGAGACTGATCGGATGTGGCCAGGTTCGTGAGCCCTCAAAGGGTCA	483
QY	439	GATTTGTGGAAAGCTATCCCTAAATGCTCACTGTAAGGAGCAATTCATGCTAAACC	498
DB	484	GATCTGTGGAGAGCTATCCCTTAAACGCTCACTGTGAATGGACTATTATGCGCAGACC	543
QY	499	TGGGTTTGTATCCCAACTTAAGATTGTGATGTTGAGTCTGAGTGTGACTATCATGTGCCA	558
DB	544	TGGGTTTATCATCAGTGTGAGTTGTTGATGCTGAGCCTAGAGTTTGACTACATGTGCCA	603
QY	559	GTATGACTATGTTGAGTGTGAGTGGAGACAAACCGGATGCCAGATCATCAACGGTGT	618
DB	604	ATATGACTACGTGGAGGTCCGCGATGGGGATAATAGTGACAGCCCTATCATCAAGCGTTT	663
QY	619	CTGTGGCAACGAGCGGCGAGCTCCTATCCAGAGCATAGATCCTCACTCCAGCTCCTT	678
DB	664	CTGTGGCAACGAGCGGCGAGCTCCTATCCAGAGCACTGAGCTCTTCACTCCATGTCTTTT	723
QY	679	CCACTCCGATGCTCCAGAAATTTTGAACGGTTTCCATGCCATTTATGAGGAGATCACAGC	738
DB	724	CAATCTCATGAGCTCCAGAACTTCATGAGCTTCCACGCTGTCTTTTGGAGGATCACAGC	783
QY	739	ATGCTCCTCATCCCCCTGTTTCCATGACGGCACGTGCGCTCTTGAACAAGGCTGGATCTTA	798

DB	784	GTGCTCCTCATCCCCCTGTTTTCATGATGGCACATGCTCCTTTGACACCATCGGTCTTT	843
QY	799	CAAGTGTCCCTGCTTGGCAGGCTATACCTGGGGCAGCGCTGTGAAAAATCTCTTTGAAGAAAG	858
DB	844	CAAGTGTGCTGCTGCTGGCTGCTACACCTGGGCGAGCGCTGTGAAAAATCTACTTTGAAGAAAG	903
QY	859	AAATGCTCAGACCTTGGGGGCCCATGCAATGGGGTACAGAAAAATAACAGGGGGCCCTGG	918
DB	904	AAATGCTCAGACCTTGGGGGCCCATGCAATGGGGTACAGAAAAATAACAGAAAGTCTCTGG	963
QY	919	GCTTATCAACGAGCGCCATGCTAAAAATGGGCACCGTGTGTCTTTCTTTTGAACAATCTC	978
DB	964	ACTTCTCAATGAGCACCATGTAATAAATTTGGCACGGTGTGTCTTTCTTTTGAACGGCTC	1023
QY	979	CTATGTTCTTAGTGGCAATGAGAAAAAGAACTTTGCCAGCAGAAATGGAGAGTGGTCAAGGAA	1038
DB	1024	ATACGTTCTGAGTGGCAATGAGAAAAAGAACTTTGCCAGCAGAAATGGAGAGTGGTCAAGGAA	1083
QY	1039	ACAGCCCATCTGCATAAAAAGCTGCGGAGAACCAAGATTTTCAGACCTGGTGTGAGAAAGAG	1098
DB	1084	GCAACCTGCTGTCATGAAAGCTGCGGGAAACCGAAGATCTCAGACCTGGTGTGAGAAAGAG	1143
QY	1099	AGTTCTCCGATGAGGTTTCAGTCAAGGGAGACACCATTAACACAGCTATATCTACGCGGC	1158
DB	1144	AGTCTCTTCGATGAGGTTTCAGTCAAGGGAGACACCATTAACATCAGCTTTATTTCCACGGC	1203
QY	1159	CTTCAGCAAGCAGAAAACTGCAGAGTGGCCCTTACCAAGAAAGCAGCGCTTCCCTTTGGAGA	1218
DB	1204	TTTCAGCAAGCAGAAAAATTCAGAGATGCTCTTACCAAAAGCAGCGCTTCCATTTGGAGA	1263
QY	1219	TCGCGCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGATGATGATCTCACTTT	1278
DB	1264	CCTGCCCCCTGGATACCAACATCTGCATACCAAGTCCAGTATGATGATCTCCTCCCTT	1323
QY	1279	CTACCGCGCTGGGAGCAGCAGGAGCATGTCTGAGGAGTGGGAGTGGAGTGGGCG	1338
DB	1324	CTACCGCGCTGGGAGCAGCAGGAGCATGTCTGAGAACTGGGAAAGTGGAGTGGGCG	1383
QY	1339	GGCAACCTCTGCTATCCCTATCTGCGGAAAAATTGAGAAACATCACTGTCTCAAAGACCA	1398
DB	1384	GGCCCGCTCTGTATCCCAATCTGTGGAANAATCGAGAGCATCTCTTCTCAAAGACCA	1443
QY	1399	AGGTTGCGCTGGCGTGGCAGGAGCCATCTACAGGAGGACAGCGGGTGCATGACGG	1458
DB	1444	AGGCACCGCTGGCCATGCGCAGGAGCCATCTACCGAGGACCACTGTGTGTACAGATGG	1503
QY	1459	CAGCTACACAGGGAGCGTGTCTTAGTCTGACGCGTGGCTGTGTGTGTGTGTGTGTGTGT	1518
DB	1504	TGGTCTGCACAAAGGTGCATGGTCTTGGTCTGCAAGTGGTGTGTGTGTGTGTGTGTGTGT	1563
QY	1519	TGT	1578
DB	1564	TGT	1623
QY	1579	AGACTGAAAGT	1638
DB	1624	AGACTGAAAGT	1683
QY	1639	CCAGAGCCTACAGATTTTGT	1698
DB	1684	CCAGAAATTTACGGGTTTCTGT	1743
QY	1699	TGCTGACATCGCCATCTCTGAAAGCTCTTAGAAGGCGGTATTCAGACCCCGAGTCCAGCC	1758
DB	1744	CAGTACATCGCTGTCTGAAAGCTCTTAGAAGGCGGTATTCAGACCCCGAGTCCAGCC	1803
QY	1759	CATCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1818
DB	1804	CATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1863
QY	1819	GGTGGCTGGAATGTCTTGGCAGAGCGTGTGAGGAGCGCTTGTGTGTGTGTGTGTGTGTGTGT	1878

Db 1864 GCTGGCTGGAACATCCTCGCAGATGTGAGGAGCCCTGGCTTTAAGAATGATACCTTACA 1923
Qy 1879 CTCTGGGTGTGCTAGTGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGG 1938
Db 1924 TTATGGAATGGTTCAGAGTGGTAGACCAATGCTTTGTGAGGAACAGCATGAAGACCATGG 1983
Qy 1939 CATCCAGTGTGAGTGTCACTGATAACATGTTCTGTGCCAGCTGGGAACCACTGCCCTTC 1998
Db 1984 CATTCAGTGTGAGTGTCACTGACACATGTTCTGTGCCAGCAAGATCCAGTACCCCTTC 2043
Qy 1999 TGATATCTGCATCTGACAGACAGGAGGATCGCGCTGTGTCTTCCCGGAGCAGCATC 2058
Db 2044 TGACATCTGCATCTGACAGACAGGAGGATCGCTGCTTTGTCTTCCCGGAGCAGCATC 2103
Qy 2059 TCCTGAGCAGCTGGCATCTGATGGGACTGTGTGAGCTGGAGCTATGATAAACHATGAG 2118
Db 2104 CCCCAGGACGCTGGCATTTGTGGGGCTGTGACGTGGAGCTATGACAAGACATGTAG 2163
Qy 2119 CCACAGGCTCTCCAGTCTTCCACCAAGTGTGCTCTTTTAAAGACTGGATTGAAGAAA 2178
Db 2164 CAATGGCTATCCACAGCTTCCAAAGGTGTTCGCTTCAAGACTGGATTGAGAGAAA 2223
Qy 2179 TATGAATGAACCATGCTCATGCACTCTCTTGAGAGTGTCTGTATATCCGTCTGTACG 2238
Db 2224 CATGAATGAACCATGCAAGGCACTGAGA-AGCCTTTTCTAGCATCGTCTGTACA 2282
Qy 2239 TGTGTCACTGGTGAAGCAGTGTGGGCTGAAGTGTGATTGGCTGTGAACCTGGCTGT 2298
Db 2283 TATG---TTGTATAGAACAATCGGGGCTGAAGTGTAAATTTGGCCCACTCTTGGCTAC 2339
Qy 2299 GCCAGGCTTCTGACTTCAGGAGCAAAACTCAGTGAAGGGTGAAGTGAAGCTTCAATGTCTG 2358
Db 2340 TGAAAGGCTCTGGTTTCAGGAGCTTATCTCAATAGAGGGTGAACAGAGTTTACTTCAT- 2398
Qy 2359 GTAGGCTGATGCGCGTCCACTACTAGGACAGCCAAATTGGAAGATGCCAGGCTTGCAG 2418
Db 2399 -CAGGGAACCTGTCTCCCTGACTGCTTGG-GAATCATCTAAAAGATGCCAGGTCTTGAAC 2456
Qy 2419 AAGTAAGTTTCTTAAAGAGACCA-----TATACAAAACCTCTCCACTCCACTGACCT 2472
Db 2457 AACTGGATTTCTTCAAGAAGACCATGTGACTAGAGGAGAACCTCTTGTCTCTCTCCA 2516
Qy 2473 GGTGTCTTCCCAACTTTCAGTATATCAATATCGAATGCCATCAGCTTGACAGGGAAGATCTGG 2532
Db 2517 CTCAGAGTATGTGACTGTCAATCAGTTTGGGTTGAAAAGTTGATTGGGAGGCGCTGG 2576
Qy 2533 GCTTCATGAGGCCCCCTTTTGAGGCTCTCAAGTCTCTAGAGAGCTGCTGTGGGACAGCCCA 2592
Db 2577 GCTGCACCTGGCTTCTGTCAAAGTTCCAAAGAAACAAACAACCTT-----AGACTA 2625
Qy 2593 GGGCAGCAGAGCTGGGATGTGGTGCATGCGCTTTGTGTACATGGCCACACAGTACAGTCTGGT 2652
Db 2626 GCCCAGGGCAAGAGAGATTGGGTTGGCACCCTGTGTAAATTTGTCAACAGATTGTCTGAT 2685
Qy 2653 CTTTTTCTTCCCTCTCTCTGTACACATTTTATAAATAAGGTTGGCTTCTGAACTA 2712
Db 2686 CTTTCCCTTCCAAATCTCTGTACACATTTCAATTAACACAGGCTGTCTCTCCCTGACCTA 2745
Qy 2713 C 2713
Db 2746 C 2746

RESULT 5
LOCUS AY406076
DEFINITION Mus musculus HCM2436 gene, VIRTUAL TRANSCRIPT, partial sequence,
AY406076 genomic survey sequence.
ACCESSION AY406076
VERSION AY406076.1 GI:39762050
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2214)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 2214)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..2214
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>2214
/locus_tag="HCM2436"
gene
ORIGIN
Query Match 51.5%; Score 1466.6; DB 9; Length 2214;
Best Local Similarity 77.0%; Pred. No. 1.1e-278;
Matches 1704; Conservative 0; Mismatches 459; Indels 51; Gaps 1;
Qy 26 ATGAGCTGGGTGTGTGACGCGAGTTGGGGCTCACTTTTTCAGCTCCTCTCATCTCG 85
Db 1 ATGAGCTAGACAGATGGCGCAGTTGGGGCTGTGGTTCCTCGAGCTCCTCTCATCTCA 60
Qy 86 TCCTTGCCCAAGAGTACACAGTCATTAAATGAAGCTCGCTCGGAGCAGAGTGAATATC 145
Db 61 TCGTTGCCAAGAGAGTACACGGTCATTAAATGAAGCTCTGCCGGAGCTGAGTGAACATC 120
Qy 146 ATGTGTCGGGAGTGTGTGAATATGATCAGATTGAGTGCCTGTGCCCGGAAAGAGGAA 205
Db 121 ATGTGTAGAGATGTTGTGAATATGATCAGATTGAATGCTCTGCCAGGAAAGAGAA 180
Qy 206 GTGCTGGGTATATCATCCCTTGTGACAGGAATGAGGAGATGAGTGTGACTCTCGCTG 265
Db 181 GTGTGGGTTACACCATCCATGCTGCAGGAATGAGGATAATGAATGTGACTCTGTCTA 240
Qy 266 ATCCACCCAGGTTGPACCATCTTTGAAATCTGCAAGAGCTGCCGAAATGGCTCATGGGG 325
Db 241 ATTCACCCAGGTTGPACCATCTTTGAAATCTGCAAGAGCTGCCGCAATGGCTCTGGGG 300
Qy 326 GGTACTCTTGGATGACTTCTATGTGAAGGGTTCTACTGTGACAGTGTCCGAGCAGGCTGG 385
Db 301 GGAATCTCTGGATGACTTCTACGTGAAGGATTTCTACTGCGCAGAGTGCAGGCGAGCTG 360
Qy 386 TACGAGGAGACTGATCGGATGTGGCCAGAGTTCTGCCAGGCCCCAAAGGTCAGATTGTG 445
Db 361 TACGAGGAGACTGATCGGATGTGGCCAGGTTCTTCGAGGCTCAAGAGGTCAGATCTTTG 420
Qy 446 TTGGAAGCTATCCCTAAATGCTCAGCTGTGAATGGACCATTCATGCTAAACCTGGGTTT 505
Db 421 TTGGAGAGACTATCCCTTAAACGCTCCTGTGATGAGACTATTTTCATGCCAGACTGGGTTT 480
Qy 506 GTCTCCCACTAAGATTTTGTCAATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGAC 565
Db 481 ATCATCCAGTTGAGGTTTGGTATGCTGAGCTCTAGAGCTTAGAGTTTGACTACATGTGCCAATATGAC 540
Qy 566 TATGTTGAGGTTCTGATGAGGAGACAAACCGGATGGCCAGATCATCAAGGTCGTCTGTGGC 625
Db 541 TATGTGGAGGTCGCGATGGGATAATAGTGAACAGCCCTATCATCAAGGCTTCTGTGGC 600

```
QY 626 AAGAGGCGCCAGCTCTCTATCCAGAGCATAGGATCTCTCACTCAAGTCTCTTTCACCTCC 685
D 601 AACGAGAGCCAGCTCCCATCAGGAGCACTGGCTCTTCACTCATGTCTCTTTCATCTCT 660
QY 686 GATGCTCCAGAAATTTGACGGTTTCCATGCTCATTTATGAGGAGATCACAGCATGCTCC 745
D 661 GATGGTCCAGAACTTCGATGGCTTCCACGCTGTCTTTTGGAGGAGATCACAGCGTGCTCC 720
QY 746 TCATCCCTCTGTTTCCATGACGGCAGCTGCTGCTCTTGAACAAGCTGGATCTTACAAGTGT 805
D 721 TCATCCCTCTGTTTCCATGATGCGCATGCTCTTGAACAAGCTGGATCTTACAAGTGT 780
QY 806 GCTGCTGGCAGGCTATCTGGCAGCGCTGTGAAAATCTCTCTGAAGAAAGAACTGTC 865
D 781 GCTGCTGGCTGGCTTACATCTGGCAGCGCTGTGAAAATCTCTCTGGAGGCTGGGAAGTGC 840
QY 866 TCAGACCTCTGGGGGCCAGTCAATGGGT----- 893
D 841 AAGGTCAAGGTGGTGGCAGGTTAGGGTCTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 900
QY 894 -----ACCAGAAAATAACAGGGGGCCCTGGGCTTATCAACGACGC 934
D 901 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 960
QY 935 CATGCTAAATTTGGCACCGTGTGCTCTTCTTTTGTAACTCTCTATGTTCTTAAAGTGC 994
D 961 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1020
QY 995 AATGAGAAAAGAACTTGGCCAGCAGATGGAGAGTGGTCAAGGAAACAGCCCATCTGCATA 1054
D 1021 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1080
QY 1055 AAGGCTGCGGAGAACCAAGATTTTCAGACCTGGTGAGAGGAGAGTCTTCCGATGACG 1114
D 1081 NNNNNCTGCGGGAACCGAGATCTCAGACCTGGTGAGAGGAGAGTCTTTCGATGACG 1140
QY 1115 GTTCACTCAAGGAGACACCATTAACCAAGCTATATCAAGCGCTTCTCAGCAAGCAGAAA 1174
D 1141 GTTCACTCAAGGAGACACCATTAACATCAGCTTTTATTCACGCTTCTCAGCAAGCAGAAA 1200
QY 1175 CTGCAAGTGGCCCTACCAAGAGCAGCCCTTCCCTTTGGAGATCTGCCATGGGATAC 1234
D 1201 TTGCAAGTGGCTCTTACCAAAAGCAGCCCTTCCATTTGGAGATCTGCCCTGGATAC 1260
QY 1235 CAACATCTGCATACCCAGCTCCAGTATGATGATCTCAACCTTCTACCGCGCTGGGC 1294
D 1261 CAACATCTGCATACCCAGCTCCAGTATGATGATCTCGCCCTTCTACCGCGCTGGGA 1320
QY 1295 AGCAGCAGGAGCATGTCTGAGGACTGGGAAGTGGAGTGGCGGGCCACCATCTGCAATC 1354
D 1321 AGCAGCAGGAGCATGTCTGAGAACTGGGAAGTGGAGTGGCGGGCCCGCTCTGTATC 1380
QY 1355 CCTATCTGGGGAATTTGAGAAATCATCTGCTCCAAAGACCAAGGTTGGCTGGCGG 1414
D 1381 CCAATCTCTGGGAAAATCGAGAGCATCTCTTCCAAAAGACCAAGGCAACCGCTGGGCA 1440
QY 1415 TGGCAGGAGCCATCTACAGGAGGACCAAGCGGGTGCATGACGCGCATACACAAAGGA 1474
D 1441 TGGCAGGAGCCATCTACCGAGGACCAAGTGTGTACAGATGGTGTGTGCAAAAGT 1500
QY 1475 GCGTGGTCTTCTAGTCTGACGCGGTGCCCTGTGTAATGAGCGCATGTGTGTGGTGGCTGCC 1534
D 1501 GCATGGTCTTCTAGTCTGACGCGGTGCCCTGTGTAATGAGCGCATGTGTGTGGTGGCTGCC 1560
QY 1535 CACTGTGTATCTGACTGGGGAAGTCAACATGATCAAGACAGCAGATCTGAAAGTGTGT 1594
D 1561 CACTGTGTGACTGAGCTGGGGAAGCCACCATCATCAAGACAGCAGATCTCAAGTGTGT 1620
QY 1595 TTGGGGAATTTCTACCGGATCATGACCGGATGAGAGACCATCCAGAGCTTACAGATT 1654
D 1621 TTGGGGAATTTCTACAGGACCATGATCGGATGAGAGACCATCCAGATTTACGGGT 1680
```

```
QY 1655 TCTGTATCATTTCTGCATCCCAACTATGACCCCATCTGCTGTGATGCTGACATCGGCATC 1714
D 1681 TCTGTATCATTTCTGCACCCCAACTATGACCCCATCTGCTGTGATGCTGACATCGGTGT 1740
QY 1715 CTGAGCTCTTAGACAAGCCCGTATCAGCACCCAGTCCAGCCCATCTGCTCGCTGCC 1774
D 1741 CTGAAGCTCTTAGACAAGAGCTCGCATCAGTACCCGCTGTCACACCATCTGCTGGTACC 1800
QY 1775 AGTGGGATCTCAGCACTTCTTCCAGGAGTCCCACTCATCTGCTGGCTGGGATGTC 1834
D 1801 ACTGGGACCTCAGCACCTCTTTCAGGAAATCCCACTCATCTGCTGGCTGGGAAATC 1860
QY 1835 CTGGCAGAGTGAAGAGCCCTGGCTTCAAGAAAGACACTGCTGCTGGGCTGGTCACT 1894
D 1861 CTGGCAGATGAGAGGAGCCCTGGCTTAAAGATGATACCTTACATTAAGAAATGGTCA 1920
QY 1895 GTGGTGGACTCGCTGCTGTGAGGAGCAGATGAGGACCATGGCATCCCACTGATGTC 1954
D 1921 GTGGTAGACCCATGCTTGTGAGGAACAGCATGAAGACCATGGCATCTCAGTTAGTGT 1980
QY 1955 ACTGATAACATGTTCTGTGCCAGCTGGGAAACCACTGCCCCCTTCTGATATCTGCACTGCA 2014
D 1981 ACTGACAACATGTTCTGTGCCAGCAAGATCCCACTGACCTTCTGACATCTGCACTGCA 2040
QY 2015 GAGCAGAGGAGCATCGCGCTGTGCTTCCGCGGACGAGCATCTCTGAGCAGCGCTGG 2074
D 2041 GAGCAGGGGAGCATCGCTGCTTGTCTTCCAGCGGAGCATCCCGAGCAGCGCTGG 2100
QY 2075 CATCTGATGGGAGCTGCTGAGCTGAGCTATGATAAAGCATGAGCAGCAGCGCTCTCCACT 2134
D 2101 CATTTGGTGGGCTGGTCACTGAGCTGAGCTATGACAAGATGATGAGCAATGGCTATCCACA 2160
QY 2135 GCCTTCACAAAGTCTGCTCTTTTAAAGACTGGATTGAAAGAAATATGAAATGA 2188
D 2161 GCCTTCACAAAGTGTTCGCGTTCAAGACTGGATTGAGAGAAACATGAATGA 2214

RESULT 6
AY406075 2214 bp DNA linear GSS 12-DEC-2003
LOCUS Pan troglodytes HCM2436 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY406075
VERSION AY406075.1 GI:39762049
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 2214)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2214)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..2214
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
```

gene	<1..>2214			
ORIGIN	/locus_tag="HCM2436"			
Query Match	50.5%;	Score 1437.2;	DB 9;	Length 2214;
Best Local Similarity	68.2%;	Pred. No. 6.8e-273;	Mismatches 654;	Indels 51; Gaps 1;
Matches 1509;	Conservative	0;		
Qy	26	ATGGAGCTGGGTTGCTGGACGAGCTGGGGCTCACTTTTCTTCAGCTCCTTCTCATCTCG	85	
Db	1	ATGGAGCTGGGTTGCTGGACGAGCTGGGGCTCACTTTTCTTCAGCTCCTTCTCATCTCG	60	
Qy	86	TCCTTCCGAAGAGGTACACAGTCAATTAATGAAGCTGCCCTGGAGCAGAGTGAATATC	145	
Db	61	TCCTTCCGAAGAGGTACACAGTCAATTAATGAAGCTGCCCTGGAGCAGAGTGAATATC	120	
Qy	146	ATGTGTCGGAGTGCTGCAATATGATCAGATTGAGTGCCTGCCCGGAAAGAGGAA	205	
Db	121	ATGTGTCGGAGTGCTGCAATATGATCAGATTGAGTGCCTGCCCGGAAAGAGGAA	180	
Qy	206	GTCTGGGTTATACCATCCCTTGCCTGACGGAATGAGGAGATGAGTGTGACTCTCGCTG	265	
Db	181	GTCTGGGTTATACCATCCCTTGCCTGACGGAATGAGGAGATGAGTGTGACTCTCGCTG	240	
Qy	266	ATCCACCCAGGTTGACCATCTTTGAAACTGCAAGAGCTGCCGAAATGGCTCATGGGG	325	
Db	241	ATCCACCCAGGTTGACCATCTTTGAAACTGCAAGAGCTGCCGAAATGGCTCATGGGG	300	
Qy	326	GGTACTTTGGATGACTTCTATGTGAAGGGTTCTACTGTGCAGAGTGCCGACGAGCTGG	385	
Db	301	GGTACTTTGGATGACTTCTATGTGAAGGGTTCTACTGTGCAGAGTGCCGACGAGCTGG	360	
Qy	386	TACGAGAGACTGTCATCGATGTGGCCAGGTTCTGCGAGCCCCAAGGGTCAGATTTG	445	
Db	361	TACGAGAGACTGTCATCGNNGTGGCCAGGTTCTGCGAGCCCCAAGGGTCAGATTTG	420	
Qy	446	TTGGAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTCATGCTAAACCTGGGTTT	505	
Db	421	TTGGAAGCTATCCCTAAATGCTCACTGCGAATGGACCGTTTCATGCTAAACCTGGGTTT	480	
Qy	506	GTCAATCAACTAAGATTGTCTATGTGAGTCTGGAGTTTGACTACATGTGCCAGTATGAC	565	
Db	481	GTCAATCAACTAAGNNNTTCATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGAC	540	
Qy	566	TATGTTGAGTTCGTGATGGAGACAACCGCGATGGCCAGATCATCAAGCGTGTCTGTGGC	625	
Db	541	TATGTTGAGTTCGTGATGGAGACAACCGCGANNNNNNTTCATCAAGCGTGTCTGTGGC	600	
Qy	626	AACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCCAGTCTCTTCCACTCC	685	
Db	601	AACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCCAGTCTCTTCCACTCC	660	
Qy	686	GATGGCTCCAGAAATTTTGACCGGTTTCCATGCGCATTTATGAGGAGATCACAGCATGCTCC	745	
Db	661	GATGGCTCCAGAAATTTTGATGGTTTCCATGCGCATTTATGAGGAGATCACAGCATGCTCC	720	
Qy	746	TCATCCCTTGTTCATGACGGCAGCTGCGTCTTGTGACAGGCTGGATCTTACAAGTGT	805	
Db	721	TCATCCCTTGTTCATGACGGCAGCTGCGTCTTGTGACAGGCTGGATCTTACAAGTGT	780	
Qy	806	GCCTGCTTGGCAGGCTATACTGGGCGAGCGCTGTGAAAATCTCTTTGAAAGAAAGAACTGC	865	
Db	781	GCCTGCTTGGCAGGCTATACTGGGCGAGCGCTGTGAAAATCTTCTTGAGGCTGGGAAGTCC	840	
Qy	866	-----TCAGACCTT	874	
Db	841	AAAGTCAAGCGGCCAGAAAGATTCAATTGCTGNNNNNNNNNNNNNNNNNNNNNNNNNNNN	900	
Qy	875	GGGGGCCCAAGTCAATGGGTACAGAAAATAACAGGGGGCCCTGGGCTTATCAACGACGC	934	
Db	901	NN	960	
Qy	935	CATGCTAAAAATTGGCACCGTGTGTCTTTCTTTGTGAACTCCTCATGTTCTTAGTGGC	994	

Db	961	NN	1020
Qy	995	AATGAGAAAAGAACTTGCCAGCAGAAATGGAGAGTGGTCAGGGAACAGCCCATCTGCATA	1054
Db	1021	NN	1080
Qy	1055	AAAGCCTGCCGAGAACCAAGATTTCAGACCTGGTGAAGAGAGATTCTTCCGATGCAG	1114
Db	1081	NNNNCTGCCGAGAACCAAGATTTCAGACCTGGTGAAGAGAGATTCTTCCATGCAG	1140
Qy	1115	GTTCAGTCAAGGGAGACACCAATTACAACAGCTATCTCAGCGGCTTCAGCAAGCAGAAA	1174
Db	1141	GTTCAGTCAAGNN	1200
Qy	1175	CTGCAGAGTCCCTCAACAGAGCCAGCCCTTCCCTTGGAGATCTGCCCCATGGGATAC	1234
Db	1201	NN	1260
Qy	1235	CAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACTCTTCTACCGCGCTGGCC	1294
Db	1261	CAACATCTGCATACCCAGCTCCANNNTGAGTGCATCTCACTCTTCTACCGCGNTTGGC	1320
Qy	1295	AGCAGCAGGAGCATGTCTGAGGACTGGGAAGTGGAGTGGCGGCGCACCATCTCTGCATC	1354
Db	1321	NNAGCNNNNNNNNNGTCTGAGGACTGGGAAGTGGAGTGGCGGCGCACCATCTCTGCATC	1380
Qy	1355	CCTATCTCGGGGAAAAATTGAGAAATCACTCTCTCCAAAGACCAAGGGTTGGCTGGCGG	1414
Db	1381	CNN	1440
Qy	1415	TGGCAGGCAGCATCTACAGGAGGACACAGCGGGTGCATGACGGCAGCTTACACAAGGA	1474
Db	1441	NN	1500
Qy	1475	CGCTGGTTCCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCATGTGGTGGTGGCTGCC	1534
Db	1501	NN	1560
Qy	1535	CACGTGTTACTGACCTGGGGAAGGTACACATGATCAAGACAGCAGACCTGAAGTGTGT	1594
Db	1561	CACGTGTTACTGACCTGGGGAAGGTNNCATGATCAAAAACAGCANNCTTGAAGTGTGT	1620
Qy	1595	TTGGGAAATTTCTACCGGGATGATGACCGGATGAGAAAGACCATCCAGAGCCTACAGATT	1654
Db	1621	TTGGGAAATTTCTACCGGGAATGACCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNA	1680
Qy	1655	TCTGCTATCATTTCTGCATCCCAATATGACCCCATCTCTGCTTGTGATGCTGACATCGCCATC	1714
Db	1681	TCTGCTATCATTTCTGCATCCCAATATGACCCCATCTCTGCTTGTGATGCTGACATCGCCATC	1740
Qy	1715	CTGAAGCTCTTAGACAAGCGCGTATCAGACCCGAGTCCAGCCCATCTGCTCGCTGCC	1774
Db	1741	CTGAAGCTCTTAGACAAGCGCGTATCAGACCCGAGTCCAGCCCATCTGCTCGCTGCC	1800
Qy	1775	AGTGGGATCTCAGACATTTCTTCCAGAGTCCCAACATCACTGTGGCTGGCTGGAATGTC	1834
Db	1801	AGTGGGATCTCAGACATTTCTTCCAGAGTCCCAACATCACTGTGGCTGGCTGGAATGTC	1860
Qy	1835	CTGGCAGACGTGAGGAGCCTGGCTTCAAGAACGACACACTGCGCTCTGGGTGGTTCAGT	1894
Db	1861	CTGGCAGACGTGAGGAGCCTGGCTTCAAGAACGACACACTGCGCTCTGGGTGGTTCAGC	1920
Qy	1895	GTGTGGAGTCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGTGATGTC	1954
Db	1921	GTGTGNN	1980
Qy	1955	ACTGATAACATGTTCTGTGCCAGCTGGGAAACCACTGCCCTTCTGATATCTGCATGCA	2014
Db	1981	NN	2040
Qy	2015	GAGACAGGAGCATCGCGCTGTCTTCCGGGACGAGCATCTCTTGAGGACCACTGCTGG	2074

```

Db      2041 GAGACNNNGGATCGCGCTGTGTCTTCCGGGACNAGCATCTCCTGAGCCACNCTGG 2100
Qy      2075 CATCTGATGGGACTGGTCTGAGCTGATGATAAAACATGACAGCCAGCGCTCTCCACT 2134
Db      2101 CATCTGATGGGACTGGTCTGAGCTGATGATAAAACATGACAGCCAGCGCTCTCCACT 2160
Qy      2135 GCCTTACCAAGGCTGCTGCTTTTAAAGACTGGATGAAAGAAATATGAATGA 2188
Db      2161 GCCTTACCAAGGCTGCTGCTTTTAAAGACTGGATGAAAGAAATATGAATGA 2214

RESULT 7
BX337780/c
LOCUS      BX337780 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI051YA20 3-PRIME, mRNA sequence.
ACCESSION  BX337780
VERSION     BX337780
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1100)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 1, 2003 this sequence version replaced gi:30312629.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5757.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?a=CS0DI051BA1ONP1&c=5757.r.
FEATURES
source      1..1100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI051YA20"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match      33.9%; Score 965.8; DB 5; Length 1100;
Best Local Similarity 99.1%; Pred. No. 6.4e-180;
Matches 991; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

Qy      1685 CCCATCTGCTTGATGCTGATCGCATCGCATCTGAGCTCTTAGACAGCGCCGCTATCAGC 1744
Db      998  CCCATCTGCTTGATGCT-ACATCGCCATCTGAGCTTCTTAGACAGCGCCGCTATCAGC 940
Qy      1745 ACCGAGTCCAGCCCATCTGCTCGCTGCCAGTGGGATCTCAGCACTTCTCTCCAGGAG 1804
Db      939  ACCGAGTCCAGCCCATCTGCTCGCTGCCAGTGGGATCTCAGCACTTCTCTCCAGGAG 880
Qy      1805 TCCACATCACTGCTGGCTGGAAATGCTCTGGCAGACGTGAGAGCCCTGGCTTCAAG 1864
Db      879  TCCACATCACTGCTGGCTGGAAATGCTCTGGCAGACGTGAGAGCCCTGGCTTCAAG 820
Qy      1865 AACGACACACTGCGCTCTGGGGTGGTCTAGTGTGGTGGACTGCTGCTGTGTGAGAGCAG 1924
Db      819  AACGACACACTGCGCTCTGGGGTGGTCTAGTGTGGTGGACTGCTGCTGTGTGAGAGCAG 760

```

```

Qy      1925 CATGAGGACCATGGCATCCCGATGAGTGTCTACTGATAACATGTTCTGTGCCAGCTGGAA 1984
Db      759  CATGAGGACCATGGCATCCCGATGAGTGTCTACTGATAACATGTTCTGTGCCAGCTGGAA 700
Qy      1985 CCCACTGCCCCCTTCTGATATCTGCACTGCAGAGACAGGAGCATCGCGCTGTGTCTTC 2044
Db      699  CCCACTGCCCCCTTCTGATATCTGCACTGCAGAGACAGGAGCATCGCGCTGTGTCTTC 640
Qy      2045 CCGGACGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGCTCAGCTGGAGCTAT 2104
Db      639  CCGGACGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGCTCAGCTGGAGCTAT 580
Qy      2105 GATAAAACATGACGACACAGGCTCTCCACTGCTTCCAAAGGCTGCTGCTTTTAAAGAC 2164
Db      579  GATAAAACATGACGACACAGGCTCTCCACTGCTTCCAAAGGCTGCTGCTTTTAAAGAC 520
Qy      2165 TGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTTGAGAAGTGTCTGTA 2224
Db      519  TGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTTGAGAAGTGTCTGTA 460
Qy      2225 TATCGCTGTGACGTGTGTCATTGCGTGAACGAGTGTGGGCTGAAGTGTGATTTGGCT 2284
Db      459  TATCGCTGTGACGTGTGTCATTGCGTGAACGAGTGTGGGCTGAAGTGTGATTTGGCT 400
Qy      2285 GTGAACCTTGGCTGTGCCAGGCTTCTGACTTTCAGGGACAAAACCTCAGTGAAGGCTGAGTA 2344
Db      399  GTGAACCTTGGCTGTGCCAGGCTTCTGACTTTCAGGGACAAAACCTCAGTGAAGGCTGAGTA 340
Qy      2345 GACCTCCATTGCTGGTAGGCTGATGCGCGCTCCACTACTAGGACAGCAATTGGAAGATG 2404
Db      339  GACCTCCATTGCTGGTAGGCTGATGCGCGCTCCACTACTAGGACAGCAATTGGAAGATG 280
Qy      2405 CCAGGGCTTGAAGAAGTAAGTCTTCAAGAAGACCATATACAAAACCTCTCCACTCC 2464
Db      279  CCAGGGCTTGAAGAAGTAAGTCTTCAAGAAGACCATATACAAAACCTCTCCACTCC 220
Qy      2465 ACTGACCTGTGTGTCTTCCCAACCTTTCAGTATATACGAATGCCATCAGCTTGACAGGGA 2524
Db      219  ACTGACCTGTGTGTCTTCCCAACCTTTCAGTATATACGAATGCCATCAGCTTGACAGGGA 160
Qy      2525 AGATCTGGCTTCAATAGGCGCCCTTTTGGAGCTCTCAAGTCTTAGAGAGTGCCTGTGG 2584
Db      159  AGATCTGGCTTCAATAGGCGCCCTTTTGGAGCTCTCAAGTCTTAGAGAGTGCCTGTGG 100
Qy      2585 ACAGCCAGGCGACGACGAGCTGGGATGTTGGTGCATGCCCTTTGTGTACATGCCACAGTAC 2644
Db      99  ACAGCCAGGCGACGACGAGCTGGGATGTTGGTGCATGCCCTTTGTGTACATGCCACAGTAC 40
Qy      2645 AGTCTGTGCTCTTTTCCCTTCCCATCTCTTGTACACATTTT 2684
Db      39  AGTCTGTGCTCTTTTCC-TCCCATCTCTTGTACACATTTT 1

```

```

RESULT 8
BX399904/c
LOCUS      BX399904 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI086Y021 3-PRIME, mRNA sequence.
ACCESSION  BX399904
VERSION     BX399904
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1008)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30622027.
Contact: Genoscope
Genoscope - Centre National de Sequencage

```

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5757.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1086AH1NP1&c=5757.r.

FEATURES

Location/Qualifiers

source

1..1008
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1086Y021"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 33.1%; Score 942; DB 5; Length 1008;
Best Local Similarity 98.2%; Pred. No. 3.1e-175; Indels 1; Gaps 1;
Matches 950; Conservative 10; Mismatches 6;
QY 1718 AAGTCTCTAGACAGCCCGTATACAGCACCGAGTCCAGCCCATCTGCTCGTGCCAGT 1777
DB 966 RAGCTCTWGCACAGGCCCGTTTCAGCACCGAGTCCAGCCCTTCTGCTCGTGCCAGT 907
QY 1778 CGGGATCTCAGCATTCTTCAGAGATCCACATCATTGTGGCTGGTGGATGTCGTG 1837
DB 906 CGGGATYTCAGAACTTCTTCRAGATCCCAATCATTGTGGCTGGTGGATGTCCTK 847
QY 1838 GCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTCGCTCTGGGGTGGTCAAGTGTG 1897
DB 846 GCAGACGTGAGGAGCCCTGGCTTCAAGAACRACACACTCGCTCTGGGGTGGTCAAGTGTG 787
QY 1898 GTGGACTCGCTGCTGTGAGGAGCAGCATGAGGACCATGGCATCCCACTGAGTGTCACT 1957
DB 786 GTGGACTCGCTGCTGTGAGGAGCAGCATGAGGACCATGGCATCCCACTGAGTGTCACT 727
QY 1958 GATAACATGTTCTGTGCCAGCTGGGAGCCACTGCCCCCTTCTGATATCTGCATCTGCAG 2017
DB 726 GATAACATGTTCTGTGCCAGCTGGGAGCCACTGCCCCCTTCTGATATCTGCATCTGCAG 667
QY 2018 ACAGGAGCATCGCGCTGTGTCCTTCCGGGACGAGCATCTCCTGAGCCAGCTGGCAT 2077
DB 666 ACAGGAGCATCGCGCTGTGTCCTTCCGGGACGAGCATCTCCTGAGCCAGCTGGCAT 607
QY 2078 CTGATGGGACTGGTCACTGGAGCTATGATAAAACATGACGACAGGCTTCCACTGCC 2137
DB 606 CTGATGGGACTGGTCACTGGAGCTATGATAAAACATGACGACAGGCTTCCACTGCC 547
QY 2138 TTCACCAAGTCTGCTGCTTTAAAGACTGGATTGAAGAAATATGAATGAACCATGCTC 2197
DB 546 TTCACCAAGTCTGCTGCTTTAAAGACTGGATTGAAGAAATATGAATGAACCATGCTC 487
QY 2198 ATGCACTCTCTGAGAAGTGTGTTCTGTATATCGTCTGACGTGTGTCATTGGGTGAAGCA 2257
DB 486 ATGCACTCTCTGAGAAGTGTGTTCTGTATATCGTCTGACGTGTGTCATTGGGTGAAGCA 427
QY 2258 GTGTGGGCTGAAGTGTGATTGGCTGTGAATCTGGCTGTGCCAGGCTTCTGACTTCA 2317
DB 426 GTGTGGGCTGAAGTGTGATTGGCTGTGACTTGGCTGTGCCAGGCTTCTGACTTCA 367
QY 2318 GGGACAAAACCTCAGTGAAGGTGAGTAGACCTCCATTGCTAGGCTGATGCCGGTCC 2377
DB 366 GGGACAAAACCTCAGTGAAGGTGAGTAGACCTCCATTGCTAGGCTGATGCCAGTCC 307
QY 2378 ACTACTAGGACGCCAAATTGGAAGATGCCAGGCTTGCCAGAAAGTAAGTTTCTTCAAAGA 2437

Db 306 ACTACTAGGACGCCAAATTGGAAGATGCCAGGCTTGCAAGAAGTAAGTTTCTTCAAAGA 247
QY 2438 AGACATATACAAAACCTCTCCACTCCACTGACCTGGTGGTCTTCCCAACTTTCAGTTA 2497
Db 246 AGACATATACAAAACCTCTCCACTCCACTGACCTGGTGGTCTTCCCAACTTTCAGTTA 187
QY 2498 TACGAATGCCATCAGCTTTCAGCCAGGAGATCTGGGCTTTCATGAGGCCCTTTTGAGGCT 2557
Db 186 TACGAATGCCATCAGCTTTCAGCCAGGAGATCTGGGCTTTCATGAGGCCCTTTTGAGGCT 127
QY 2558 CTCAAGTTTCTAGAGAGCTGCTGTGGGACACGCCACCCAGGACAGCAGTGGATGTGTGC 2617
Db 126 CTCAAGTTTCTAGAGAGCTGCTGTGGGACACGCCACCCAGGACAGCAGTGGATGTGTGC 67
QY 2618 ATGCTTTGTGTATACATGAGGACAGTACAGTCTGGTCTTCTTCCCATCTCTGTGAC 2677
Db 66 ATGCTTTGTGTATACATGAGGACAGTACAGTCTGGTCTTCTTCCCATCTCTGTGAC 8
QY 2678 ACATTTT 2684
Db 7 ACATTTT 1

RESULT 9

BX434191/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On May 15, 2003 this sequence version replaced gi:30775248.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 5757.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0BAK025BH09NM1&c=5757.r.

Location/Qualifiers

1..897

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DE009YD01"

/tissue_type="PLACENTA"

/clone_lib="Homo sapiens PLACENTA"

/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed

with a NotI-oligo(dT) primer. Five prime end enriched,

double-strand cDNA was digested with Not I and cloned into

the Not I and EcoR V sites of the pCMVSPORT 6 vector.

Library was not normalized."

ORIGIN

Query Match 31.1%; Score 885.8; DB 5; Length 897;

Best Local Similarity 99.2%; Pred. No. 3.8e-164;

Matches 890; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1809 ACATCACTGTGGCTGGGAATGCTTGGCAGACGTGAGGAGCCCTTCAAGAACG 1868

```
Db      897 ACATCACTGGGCTGGCTGGAATGTTCTGCGCAACCTGAAGGAGCCCTGGCTCAAGAAACG 838
Qy      1869 ACACACTGGGCTCTGGGGTGGTCAAGTGTGGTGAATGCTGCTGTGTGTGAGGAGCAGCATG 1928
Db      837 ACACACTGGGCTCTGGGGTGGTCAAGTGTGGTGAATGCTGCTGTGTGTGAGGAGCAGCATG 778
Qy      1929 AGACCATGGCATCCCAAGTGAAGTGTCACTGATGAACATGTTCTGTGTCAGCTGGGAACCCA 1988
Db      777 AGACCATGGCATCCCAAGTGAAGTGTCACTGATGAACATGTTCTGTGTCAGCTGGGAACCCA 718
Qy      1989 CTGCCCCCTCTGATATCTGCACCTGACAGACAGGAGGCATCGCGGTGTGCTCTCCCGG 2048
Db      717 CTGCCCCCTCTGATATCTGCACCTGACAGACAGGAGGCATCGCGGTGTGCTCTCCCGG 658
Qy      2049 GACGAGCATCTCTGAGCCACGCTGCGCATCTGATGGGACTGTGTCAGCTGGAGCTATGATA 2108
Db      657 GACGAGCATCTCTGAGCCACGCTGCGCATCTGATGGGACTGTGTCAGCTGGAGCTATGATA 598
Qy      2109 AAACATGACGACACAGGCTCTCCACTGCTTCAACCAAGTGTGCTCTTTAAAGACTGA 2168
Db      597 AAACATGACGACACAGGCTCTCCACTGCTTCAACCAAGTGTGCTCTTTAAAGACTGA 538
Qy      2169 TTGAAGAAATATGAATGAACATGCTCATGCACTCTCTGAGAGTGTCTGTATATC 2228
Db      537 TTGAAGAAATATGAATGAACATGCTCATGCACTCTCTGAGAGTGTCTGTATATC 478
Qy      2229 CGTCTGACGTGTCTATGCGTGAAGCAGTGTGGGCTTGAAGTGTGATTTGGCCCTGTGA 2288
Db      477 CGTCTGACGTGTCTATGCGTGAAGCAGTGTGGGCTTGAAGTGTGATTTGGCCCTGTGA 418
Qy      2289 ACTTGCTGTGCGAGGCTTCTGACTTCAAGAGACCATATACAAACCTCTCCACTCCACTG 2468
Db      417 ACTTGCTGTGCGAGGCTTCTGACTTCAAGAGACCATATACAAACCTCTCCACTCCACTG 238
Qy      2469 ACCTGTGTGCTTCCCAACTTTCAGTTATAGCAATGCCATCAGCTTGACCGGGAAGAT 2528
Db      237 ACCTGTGTGCTTCCCAACTTTCAGTTATAGCAATGCCATCAGCTTGACCGGGAAGAT 178
Qy      2529 CTGGGCTTCAAGGCCCCCTTTGAGGCTCTCAAGTCTAGAGAGCTGCTGTGGACAG 2588
Db      177 CTGGGCTTCAAGGCCCCCTTTGAGGCTCTCAAGTCTAGAGAGCTGCTGTGGACAG 118
Qy      2589 CCAGGGCAGCAGAGCTGGGATGTGTGATGCTGCTTGTGATACATGCGCCACAGTACAGTC 2648
Db      117 CCAGGGCAGCAGAGCTGGGATGTGTGATGCTGCTTGTGATACATGCGCCACAGTACAGTC 58
Qy      2649 TGGTCTCTTCTCCCTCCCTCTCTCTGATACACATTTTAAATAAAGGGTGGCTTC 2705
Db      57 TGGTCTCTTCTCCCTCCCTCTCTCTGATACACATTTTAAATAAAGGGTGGCTTC 1
```

RESULT 10

BX399905

LOCUS

BX399905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

DEFINITION clone CS0D1086Y021 5-PRIME, mRNA sequence.

ACCESSION

BX399905

VERSION

BX399905.2

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1049)

AUTHORS

TITLE

JOURNAL

COMMENT

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30622029.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5757.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?sa=CS0D1086AH11QPl&c=5757.r.

FEATURES

Source

Location/Qualifiers

1..1049

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0D1086Y021"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

QY 614 CGTGTCTGTGGCAACGAGGGCCAGCTCTCTATCCAGAGCATAGGATCCTCACTCCACGTC 673
 Db 601 CGTGTCTGTGGCAACGAGGGCCAGCTCTCTATCCAGAGCATAGGATCCTCACTCCACGTC 660
 QY 674 CTCCTCCACTCCGATGGCTCCAAAGAAATTTGACGGTTTCCATGCCATTTATGAGGAGATC 733
 Db 661 CTCCTCCACTCCGATGGCTCCAAAGAAATTTGACGGTTTCCATGCCATTTATGAGGAGATC 720
 QY 734 ACAGCATGCTCTCATCCCTTTGTTCCATGACGGCAGCGCTGCTCTTGAACAAGCTGGA 793
 Db 721 ACAGCATGCTCTCATCCCTTTGTTCCATGACGGCA-STGGTCTTCTTGACAAGGCTGGA 779
 QY 794 TCTTACAGTGTGCTGCTTGGCAGGTATCTATGGCAGCGCTGTGAAAATCTCTTGA 853
 Db 780 TCTTACAGTGTGCTGCTTGGCAGGTATCTATGGCAGCGCTGTGAAAATCTCTTGGRG 839
 QY 854 GAAAGAACTGC 865
 Db 840 GCTGGGAAGTCC 851

RESULT 11
 BX439313
 LOCUS
 DEFINITION BX439313 Homo sapiens PLACENTA mRNA linear EST 04-MAY-2004
 5-PRIME, mRNA sequence.
 ACCESSION BX439313
 VERSION BX439313.2 GI:47007084
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 952)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 15, 2003 this sequence version replaced gi:30779754.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 5757.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?8=CSODE009CB01QP1&c=5757.r.
 Location/Qualifiers
 1..952
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODE009YD01"
 /tissue_type="PLACENTA"
 /clone_lib="Homo sapiens PLACENTA"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

FEATURES
 source

ORIGIN

Query Match 28.6%; Score 815.2; DB 5; Length 952;
 Best Local Similarity 98.3%; Pred. No. 3.2e-150;
 Matches 834; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
 QY 14 GCCGCGCAAGGATGAGCTGGGTGCTGGACGACGCTGGGGCTCACTTTCTTCAGCTC 73
 Db 1 GCCGCGCAAGGATGAGCTGGGTGCTGGACGCA-TTGGGGCTCACTTTCTTCAGCTC 59

QY 74 CTTCTCATCTCGTCTCTTGGCCAAAGAGATACACAGTCAATTAATGAAGCCTGCGCTCGAGCA 133
 Db 60 CTTCTCATCTCGTCTCTTGGCCAAAGAGATACACAGTCAATTAATGAAGCCTGCGCTCGAGCA 119
 QY 134 GAGTGGAAATATCATGTGTGCGGAGTGTGTGAATATGATCAGATTGAGTGGTCTGCCCC 193
 Db 120 GAGTGGAAATATCATGTGTGCGGAGTGTGTGAATATGATCAGATTGAGTGGTCTGCCCC 179
 QY 194 GGAAGAGGGAAGTGTGGGTATATACATCCCTTGTCTGACAGGAATGAGGAATCAGTGT 253
 Db 180 GGAAGAGGGAAGTGTGGGTATATACATCCCTTGTCTGACAGGAATGAGGAATCAGTGT 239
 QY 254 GACTCTCTCCCTGATCCACCCAGAGTGTGTACCATCTTTTGAATACTGCAAGAGCTGCCAAAT 313
 Db 240 GACTCTCTCCCTGATCCACCCAGAGTGTGTACCATCTTTTGAATACTGCAAGAGCTGCCAAAT 299
 QY 314 GGTCTATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTCTTACTGTGACAGTGC 373
 Db 300 GGTCTATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTCTTACTGTGACAGTGC 359
 QY 374 CGAGCAGGCTGGTACCGAGGAGACTGCGATGCGATGTGGCCAGGTTCTGGAGCCCCAAG 433
 Db 360 CGAGCAGGCTGGTACCGAGGAGACTGCGATGCGATGTGGCCAGGTTCTGGAGCCCCAAG 419
 QY 434 GGTCTAGATTTTGTGGAAAGCTATCCCTTAAATGCTCACTGTGAATGGACCATTCATGCT 493
 Db 420 GGTCTAGATTTTGTGGAAAGCTATCCCTTAAATGCTCACTGTGAATGGACCATTCATGCT 479
 QY 494 AAACCTGGGTTTGTTCATCCAACTAAGATTTGTCTATGTTGAGTCTGGAGTTTGACTACATG 553
 Db 480 AAACCTGGGTTTGTTCATCCAACTAAGATTTGTCTATGTTGAGTCTGGAGTTTGACTACATG 539
 QY 554 TCCAGTATGACTATGTTGAGTTCGTATGAGAGCAACCGCATGGCCAGATCATCAAG 613
 Db 540 TCCAGTATGACTATGTTGAGTTCGTATGAGAGCAACCGCATGGCCAGATCATCAAG 599
 QY 614 CGTGTCTGTGGCAACGAGCGGCCAGCTCTCTATCCAGAGCATAGGATCCTCACTCCACGTC 673
 Db 600 CGTGTCTGTGGCAACGAGCGGCCAGCTCTCTATCCAGAGCATAGGATCCTCACTCCACGTC 659
 QY 674 CTCCTCCACTCCGATGGCTCCAAAGAAATTTTGAACGTTTCCATGCGCATTTATGAGAGATC 733
 Db 660 CTCCTCCACTCCGATGGCTCCAAAGAAATTTTGAACGTTTCCATGCGCATTTATGAGAGATC 719
 QY 734 ACAGCATGCTCTCATCCCTTTGTTCCATGACGCGACGTCGCTCTTGACAGGCTGGA 793
 Db 720 ACAGCATGCTCTCATCCCTTTGTTCCATGACGCGACGTCGCTCTTGACAGGCTGGA 779
 QY 794 TCTTACAAAGTGTGCTGCTTGGCAGGCTATCTATGGCAGCGCTGTGAAAATCTCTCTTGA 853
 Db 780 TCTTACAAAGTGTGCTGCTTGGCAGGCTATCTATGGCAGCGCTGTGAAAATCTGATTA 839
 QY 854 GAAAGAA 861
 Db 840 GATACGAA 847

RESULT 12
 CD514783

LOCUS
 DEFINITION AGENCOURT 14376424 NIH.MGC 181 Homo sapiens cDNA clone
 IMAGE:30396311 5', mRNA sequence.

ACCESSION CD514783

VERSION CD514783.1 GI:31446501

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM477 row: m column: 24
High quality sequence stop: 613.

FEATURES
source

Location/Qualifiers
1. 879
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30396311"
/tissue_type="White Matter"
/dev_stage="Unknown"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_181"
/note="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV
(destroyed); Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.42 kb. Library was constructed by
(Invitrogen). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 28.5%; Score 809.8; DB 6; Length 879;
Best Local Similarity 99.2%; Pred. No. 3.7e-149;
Matches 844; Conservative 0; Mismatches 4; Indels 3; Gaps 3;
Qy 952 CGTGTGTCCTTTCTTTGTAACAATCTCTATGTTCTTAGTGCAATGAGAAAGAACTTG 1011
Db 1 CGTGTGTCCTTTCTTTGTAACAATCTCTATGTTCTTAGTGCAATGAGAAAGAACTTG 60
Qy 1012 CCAGCAGATGGAGTGTGTCAGGAGAACGCCATCTGCATTAAGCTCGCGAGACC 1071
Db 61 CCAGCAGATGGAGTGTGTCAGGAGAACGCCATCTGCATTAAGCTCGCGAGACC 120
Qy 1072 AAAGATTTTCCAGCTGTGTCAGAGGAGAGTCTTCCCGATGTCAGTTCAGTCAAGGGAGAC 1131
Db 121 AAAGATTTTCCAGCTGTGTCAGAGGAGAGTCTTCCCGATGTCAGTTCAGTCAAGGGAGAC 180
Qy 1132 ACCATTACACAGCTATATCTAGCGGCTTCAGCAAGCAGAAACTGCAAGAGTGCCTTAC 1191
Db 181 ACCATTACACAGCTATATCTAGCGGCTTCAGCAAGCAGAAACTGCAAGAGTGCCTTAC 240
Qy 1192 CAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGGATACCAATCTTCGCATACCCA 1251
Db 241 CAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGGATACCAATCTTCGCATACCCA 300
Qy 1252 GCTCCAGTATGATGTCATCTCACCCTTCTACCGCGCTGCGGACAGCAGGAGGACATG 1311
Db 301 GCTCCAGTATGATGTCATCTCACCCTTCTACCGCGCTGCGGACAGCAGGAGGACATG 360
Qy 1312 TCTGAGGACTGGGAAGTGGAGTGGCGGGACCATCTTCGATCTCCATCTATCTGCGGAAAT 1371
Db 361 TCTGAGGACTGGGAAGTGGAGTGGCGGGACCATCTTCGATCTCCATCTATCTGCGGAAAT 420
Qy 1372 TGAGAACATCTGCTCCAAAGACCAAGGCTTGGCTGGCGCTGGCAGGAGGACCATCTA 1431
Db 421 TGAGAACATCTGCTCCAAAGACCAAGGCTTGGCTGGCGCTGGCAGGAGGACCATCTA 480
Qy 1432 CAGGAGGACCAAGCGGGTGCATGACGCGAGCTTACCAAGGAGGCTGTTCTCTAGTCTG 1491
Db 481 CAGGAGGACCAAGCGGGTGCATGACGCGAGCTTACCAAGGAGGCTGTTCTCTAGTCTG 540
Qy 1492 CAGCGGTGCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTACTGACCT 1551

Db 541 CAGCGGTGCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTACTGACCT 600
Qy 1552 GGGGAAGGTCAACATGATCAAGACAGCAGACTGAAAGTGTGTTGGGGAATTTCTACCG 1611
Db 601 GNGGAGGTCAACATGATCAAGACAGCAGACTGAAAGTGTGTTGGGGAATTTCTACCG 660
Qy 1612 GGATGATCAACCGGATGAGAGACATCCAGAGCCTACAGATTTCTGTATCATTTCTGCA 1671
Db 661 GGATGATCAACCGGATGAGAGACATCCAGAGCCTACAGATTTCTGTATCATTTCTGCA 720
Qy 1672 TCCCAACTATGACCCCATCTGCTGTGATGCTGACATCGCCATCTCTGAAGCTCTAGACAA 1731
Db 721 TCCCAACTATGACCCCATCTGCTGTGATGCTGACATCGCCATCTCTGAAGCTCTAGACAA 780
Qy 1732 GGCCCG-TATCAGCACCCGAGTCCAGGCCATC-TGCCTCGCTG-CCAGTCGGGATCTCAG 1788
Db 781 GGCCCGTATCAGCACCCGAGTCCAGGCCATCTTGCCTCGCTGCGCCAGTCGGGATCTCAG 840
Qy 1789 CACTTCCTTCC 1799
Db 841 CACTTCCTTCC 851
RESULT 13
BX337781
LOCUS
DEFINITION
BX337781 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1051YA20 5-PRIME, mRNA sequence.
ACCESSION
BX337781
VERSION
BX337781.2 GI:46268407
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (Bases 1 to 886)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30333640.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5757.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CS0D1051BA10QPl&c=5757.r.
Location/Qualifiers
1. 886
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1051YA20"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was
normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5757.r
Query Match 28.4%; Score 809.4; DB 5; Length 886;
Best Local Similarity 98.6%; Pred. No. 4.5e-149;
Matches 835; Conservative 2; Mismatches 8; Indels 2; Gaps 2;
Qy 1 CGCTCGGCAACAGCCGCGGCAAGATGGAGCTGGTGTGTCGACGCGAGTTGGGGCTCAC 60

Db 38 CGCTGGGACACAGCCGGCAAGGATGGAGCTGGGTTGCTGGACGCGAGTTGGGGCTCAC 97

Qy 61 TTTTCTTCAGCTCTTCTCATCTCGTCTTGGCAAGAGAGTACAGTCATTAATGAAGC 120

Db 98 TTTTCTTCAGCTCTTCTCATCTCGTCTTGGCAAGAGAGTACAGTCATTAATGAAGC 157

Qy 121 CTGCGCTGGAGCAGAGTGGAAATATCATCTGTGCGGAGTGCTGTGAATATCATCATGATGA 180

Db 158 CTGCGCTGGAGCAGAGTGGAAATATCATCTGTGCGGAGTGCTGTGAATATCATCATGATGA 217

Qy 181 GTGCGTCTGCCCCGAAAGAGGAAGTCTGTGGGTTATACCATCCCTTCTGCTGACGAATGA 240

Db 218 GTGCGTCTGCCCCGAAAGAGGAAGTCTGTGGGTTATACCATCCCTTCTGCTGACGAATGA 277

Qy 241 GGAGATGAGTGTGATCTCTGCTGATCCACCCAGGTTGTACCATCTTTGAAACTGCAA 300

Db 278 GGAGATGAGTGTGATCTCTGCTGATCCACCCAGGTTGTACCATCTTTGAAACTGCAA 337

Qy 301 GAGCTGCCGAATGGCTCATGCGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCCTA 360

Db 338 GAGCTGCCGAATGGCTCATGCGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCCTA 397

Qy 361 CTGTGCAGAGTCCGAGCAGGCTGTGTACGAGGAGACTGCATGCGATGTGCCAGGTTCT 420

Db 398 CTGTGCAGAGTCCGAGCAGGCTGTGTACGAGGAGACTGCATGCGATGTGCCAGGTTCT 457

Qy 421 GCGAGCCCCAAGGTCAGATTTTGTGGAAGCTATCCCTAAATGCTCATCTGTGAATG 480

Db 458 GCGAGCCCCAAGGTCAGATTTTGTGGAAGCTATCCCTAAATGCTCATCTGTGAATG 517

Qy 481 GACCATTCATGCTAAACCT-GGGTTTGTTCATCCAACTAAGATTTGTCTATGTGAGTCTGG 539

Db 518 GACCATTCATGCTAAACCTGGGGTTGTCTCACTAAGATTTGTCTATGTGAGCTTGG 577

Qy 540 AGTTTGACTACATGTSCCAGTATGACTATGTGAGGTTCTGATGGAGACAAACCGCATG 599

Db 578 AGTTTGACTACATGTSCCAGTATGACTATGTGAGGTTCTGATGGAGACAAACCGCATG 637

Qy 600 GCCAGATCATCAGGCTGTGTGCAAGAGGCGGAGCTCTCTATCCAGAGCATAGAT 659

Db 638 GCCAGATCATCAGGCTGTGTGCAAGAGGCGGAGCTCTCTATCCAGAGCATAGAT 697

Qy 660 CTTCACTCCAGCTCTCTTCCACTCCGATGGCTCCAAAGATTTTTCACGGTTTCCATGCCA 719

Db 698 CTTCACTCCAGCTCTCTTCCACTCCGATGGCTCCAAAGATTTTTCACGGTTTCCATGCCA 757

Qy 720 TTTATGAGGAGATCAGCATGCTCTCTCATCCCTTGTTCATGACGCGACGTCGCTCC 779

Db 758 TTTATGAGGAGATCAGCATGCTCTCTCATCCCTTGTTCATGACGCGACGTCGCTCC 817

Qy 780 TTGACAAGGCTGGATCTTACAAGTGTGCTGTGGCAGGCTATCTACTGGGAGCGCTGTG 839

Db 818 TTGACAAGGCTGGATCTTACAAGTGTGCTGTGGCAGGCTATCTACTGGGAGCGCTGTG 876

Qy 840 AAAATCT 846

Db 877 AATCTCY 883

RESULT 14

AK031254
LOCUS AK031254 2184 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930437L24 product:hypothetical BGF-like domain, CUB domain, Sushi domain / SCR repeat / CCP module and Serine proteases, trypsin family domain containing protein, full insert sequence.
ACCESSION AK031254
VERSION AK031254.1 GI:26082224
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

11076861

5 The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2184)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hirakawa, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,

Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,

Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,

URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,

Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://phantom.gsc.riken.jp/

Location/Qualifiers

1. 2184

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CS7BL/6J"

from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558 (2001). [PMID:11544199]) Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACGATCTAGATCGGAGCGGCCCTTTTCTTTT-3'] from 3.4g of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LI-Sal4, purified by phenol/chloroform extraction, and separated from free linkers by Centricon-100 column. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The average insert size is about 3.6kb."

Search completed: May 6, 2005, 15:01:47
Job time : 6113 secs

ORIGIN

Query Match		26.1%;	Score 742.2;	DB 6;	Length 795;
Best Local Similarity		98.8%;	Pred. No. 8e-136;		
Matches 758;		Conservative 0;	Mismatches 8;	Indels 1;	Gaps 1;
QY	637	AGCTCCTATCCAGAGCATAGGATCCTCACTCACTCTCTTCCACTCCGATGGCTCCAA	696		
Db	3	AGGTAATCCCGAGAGCATAGGATCCTCACTCCAGCTCCTTCCACTCCGATGGCTCCAA	62		
QY	697	GAAATTTTACCGTTTCCATGCCATTTATGAGGAGATCACAGCATGCTCCTCATCCCTTG	756		
Db	63	GAAATTTTACCGTTTCCATGCCATTTATGAGGAGATCACAGCATGCTCCTCATCCCTTG	122		
QY	757	TTTCCATGACGGCAGCTGGTCTTTGACAGAGCTGGATCTTACAACTGCTGCTTGGC	816		
Db	123	TTTCCATGACGGCAGCTGGTCTTTGACAGAGCTGGATCTTACAACTGCTGCTTGGC	182		
QY	817	AGGCTATATCGGCGACGCTGTGAAAATCTCTTGAAGAAAAGAACTGCTCAGACCTGG	876		
Db	183	AGGCTATATCGGCGACGCTGTGAAAATCTCTTGAAGAAAAGAACTGCTCAGACCTGG	242		
QY	877	GGGCCCCAGTCAATGGGTACCAGAAAATAACAGGGGGCCCTGGGCTTATCAAGGACGCA	936		
Db	243	GGGCCCCAGTCAATGGGTACCAGAAAATAACAGGGGGCCCTGGGCTTATCAAGGACGCA	302		
QY	937	TGCTAAAATTTGGCACCGTGGTCTTTCTTTTGTAACTCTATGTTCTTAGTGCAA	996		
Db	303	TGCTAAAATTTGGCACCGTGGTCTTTCTTTTGTAACTCTATGTTCTTAGTGCAA	362		
QY	997	TGAGAAAAGAACTTCCAGAGAGAAATGGAGAGTGGTCAGGGAAAAGCCCATCTGCATAAA	1056		
Db	363	TGAGAAAAGAACTTCCAGAGAGAAATGGAGAGTGGTCAGGGAAAAGCCCATCTGCATAAA	422		
QY	1057	AGCCTGCCGAGAACCAAGATTTACAGCTGGTGAGAGGAGAGTTCTTCGATGCAGGT	1116		
Db	423	AGCCTGCCGAGAACCAAGATTTACAGCTGGTGAGAGGAGAGTTCTTCGATGCAGGT	482		
QY	1117	TCAGTCAAGGGAGACACCATACACAGCTATCTCAGCGGCTTTCAGCAAGCAGAACT	1176		
Db	483	TCAGTCAAGGGAGACACCATACACAGCTATCTCAGCGGCTTTCAGCAAGCAGAACT	542		
QY	1177	GCAGAGTCCCTTACCAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCA	1236		
Db	543	GCAGAGTCCCTTACCAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCA	602		
QY	1237	ACATCTGCATACCCAGCTCCAGTATGATGATCTCACCTTCTACCGCGCTGGGCAG	1296		
Db	603	ACATCTGCATACCCAGCTCCAGTATGATGATCTCACCTTCTACCGCGCTGGGCAG	662		
QY	1297	CAGCAGGAGGACATGCTGAGGACTTGGGAAAGTGGAGTGGCGGGCACCATCTCGATCCC	1356		
Db	663	CAGCAGGAGGACATGCTGAGGACTTGGGAAAGTGGAGTGGCGGGCACCATCTCGATCCC	722		
QY	1357	TATCTGGGGAAAATTGAGAAATCATCTGCTCCAAAGCCCAAGGGT	1403		
Db	723	TATCTGGGGAAAATTGAG-ACATCACTGCTCCAAAGACCAAGGTT	768		

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2005, 12:57:47 ; Search time 332 Seconds
(without alignments)
14026.637 Million cell updates/sec

Title: US-10-063-692-37

Perfect score: 2846

Sequence: 1 cgcctgggaccagccggc.....aaaaaaaaaaaaaaaaaa 2846

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2259.4	79.4	2886	3	US-09-280-116-104
2	2142.2	75.3	2259	4	US-10-067-422-2
3	1988.4	69.9	2144	4	US-09-620-312D-969
4	1984.8	69.7	2142	4	US-09-620-312D-1006
5	479.4	16.8	505	3	US-09-280-116-179
6	140.8	4.9	1696	4	US-09-835-811-1
7	140.8	4.9	240	1	US-08-628-417-6
8	138.4	4.9	396	4	US-09-640-173-53
9	138.4	4.9	396	4	US-09-713-550-53
10	138.4	4.9	396	4	US-09-825-294-53
11	138.4	4.9	396	4	US-09-970-966-53
12	138.2	4.9	3275	3	US-09-370-838-151
13	138.2	4.9	3275	4	US-09-854-133-151
14	137.8	4.8	1798	3	US-09-797-906-1
15	137	4.8	2447	2	US-09-014-969-14
16	136.6	4.8	2262	4	US-09-311-021-171
17	135.6	4.8	1459	4	US-09-537-654-3
18	135.4	4.8	2146	4	US-10-003-392-3
19	135.2	4.8	2394	4	US-09-800-729-33
20	134.4	4.7	6409	4	US-09-967-908A-1
21	134.4	4.7	6409	4	US-10-159-151-1
22	132.8	4.7	1985	4	US-09-707-794A-212
23	132.8	4.7	1985	4	US-09-905-125A-212
24	132.8	4.7	1985	4	US-09-902-775A-212
25	132.8	4.7	1985	4	US-09-906-700-212
26	132.8	4.7	1985	4	US-09-903-603A-212
27	132.8	4.7	1985	4	US-09-904-920A-212
28	132.8	4.7	1985	4	US-09-909-064-212
29	132.8	4.7	1985	4	US-09-905-381A-212
30	132.8	4.7	1985	4	US-09-906-618-212
31	132.6	4.7	612	4	US-09-902-540-1357
32	131.8	4.6	2674	3	US-09-817-180-1
33	131.8	4.6	2674	4	US-10-003-295-1
34	131.6	4.6	1051	3	US-09-245-041-10
35	131.6	4.6	1051	4	US-09-358-055B-10
36	131.6	4.6	1051	4	US-09-893-238-10
37	130.8	4.6	1447	3	US-09-443-041A-27
38	130.4	4.6	1738	4	US-09-918-909A-27
39	128.4	4.5	569	4	US-09-461-325-44
40	128.4	4.5	569	4	US-10-012-542-44
41	128.4	4.5	569	4	US-10-115-123-44
42	127.6	4.5	674	4	US-09-620-405B-465
43	127.6	4.5	674	4	US-09-433-826B-465
44	127.6	4.5	674	4	US-09-604-287A-465
45	127.6	4.5	674	4	US-09-834-759-465
46	127.6	4.5	674	4	US-09-590-751A-465
47	127.6	4.5	674	4	US-09-551-621-465
48	125.8	4.4	2082	2	US-08-785-310A-2
49	125.6	4.4	614	4	US-09-902-540-1318
50	124	4.4	144	1	US-08-702-344-26
51	123.4	4.3	396	4	US-09-640-173-33
52	123.4	4.3	396	4	US-09-713-550-33
53	123.4	4.3	396	4	US-09-825-294-33
54	123.4	4.3	396	4	US-09-970-966-33
55	121.8	4.3	441	4	US-09-601-537-10
56	121.8	4.3	1117	3	US-09-247-373B-33
57	121.8	4.3	4121	4	US-09-601-537-9
58	119.4	4.2	2634	3	US-09-463-238-3
59	119.2	4.2	1813	3	US-09-071-224-3
60	119	4.2	1020	4	US-09-328-475C-43
61	118.8	4.2	1733	3	US-09-073-569-1
62	118.4	4.2	249	4	US-09-621-976-1322
63	117.2	4.1	4064	4	US-09-873-717A-3
64	117	4.1	117	1	US-08-702-344-3
65	116.8	4.1	1024	4	US-09-328-475C-50
66	116.8	4.1	1034	4	US-09-311-021-105
67	116.4	4.1	396	4	US-09-640-173-16
68	116.4	4.1	396	4	US-09-713-550-16
69	116.4	4.1	396	4	US-09-825-294-16
70	116.4	4.1	396	4	US-09-970-966-16
71	116.2	4.1	2269	3	US-09-394-645-1
72	116.2	4.1	2269	3	US-09-243-560B-1
73	116.2	4.1	6671	1	US-08-280-443-1
74	116.2	4.1	6671	1	US-08-457-459-1
75	116.2	4.1	6671	1	US-08-555-678-1
76	116.2	4.1	6671	5	PCT-US95-02275-1
77	115.2	4.0	1048	4	US-09-489-847-38
78	115.2	4.0	2246	3	US-09-363-708-3
79	115.2	4.0	2246	4	US-09-083-587-3
80	115	4.0	1039	4	US-09-902-540-1280
81	113.8	4.0	882	4	US-09-311-021-107
82	113.4	4.0	2186	3	US-09-360-545-66
83	113	4.0	130	4	US-09-621-976-12892
84	111.4	3.9	194	4	US-09-621-976-9596
85	111.4	3.9	2608	4	US-09-904-615-16
86	111	3.9	111	4	US-09-621-976-14677
87	111	3.9	282	4	US-09-621-976-18648
88	110.8	3.9	2038	4	US-09-885-723-6
89	110.6	3.9	708	4	US-09-270-767-13081
90	110.4	3.9	1066	1	US-08-157-101A-4
91	110.4	3.9	1474	3	US-08-821-994-64
92	110.2	3.9	6243	2	US-09-056-075-1
93	110	3.9	578	3	US-09-602-877A-95
94	109.6	3.9	396	4	US-09-640-173-10
95	109.6	3.9	396	4	US-09-713-550-10
96	109.6	3.9	396	4	US-09-825-294-10
97	109.6	3.9	396	4	US-09-970-966-10
98	109.4	3.8	140	1	US-08-628-417-5
99	109.4	3.8	1771	4	US-09-907-794A-158
100	109.4	3.8	1771	4	US-09-866-028-36

Sequence 212, App
Sequence 212, App
Sequence 212, App
Sequence 1357, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 465, App
Sequence 465, App
Sequence 465, App
Sequence 465, App
Sequence 2, Appli
Sequence 1318, Ap
Sequence 26, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 10, Appl
Sequence 33, Appl
Sequence 9, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 43, Appl
Sequence 1, Appli
Sequence 1322, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 50, Appl
Sequence 105, App
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 107, App
Sequence 66, Appl
Sequence 12892, A
Sequence 9596, Ap
Sequence 16, Appl
Sequence 14677, A
Sequence 18648, A
Sequence 6, Appli
Sequence 13081, A
Sequence 4, Appli
Sequence 64, Appl
Sequence 1, Appli
Sequence 95, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 5, Appli
Sequence 158, App
Sequence 36, Appli

101	109.4	3.8	1771	4	US-09-905-125A-158	Sequence 158, App	174	98.4	3.5	19557	5	PCT-US92-06300-1	Sequence 1, Appli
102	109.4	3.8	1771	4	US-09-902-775A-158	Sequence 158, App	175	98	3.4	98	1	US-08-088-658-42	Sequence 42, Appl
103	109.4	3.8	1771	4	US-09-906-700-158	Sequence 158, App	176	98	3.4	98	2	US-08-471-907A-42	Sequence 42, Appl
104	109.4	3.8	1771	4	US-09-944-457-36	Sequence 36, Appl	177	98	3.4	98	4	US-09-621-976-12160	Sequence 12160, A
105	109.4	3.8	1771	4	US-09-903-603A-158	Sequence 158, App	178	98	3.4	98	4	US-09-621-976-15091	Sequence 15091, A
106	109.4	3.8	1771	4	US-09-904-920A-158	Sequence 158, App	179	98	3.4	196	4	US-09-442-054A-42	Sequence 42, Appl
107	109.4	3.8	1771	4	US-09-905-064-158	Sequence 158, App	c 180	98	3.4	196	4	US-09-442-054A-42	Sequence 42, Appl
108	109.4	3.8	1771	4	US-09-905-381A-158	Sequence 158, App	181	97.8	3.4	3438	4	US-10-164-595-29	Sequence 29, Appl
109	109.4	3.8	1771	4	US-09-906-618-158	Sequence 158, App	182	97.2	3.4	3438	4	US-09-270-767-11902	Sequence 11902, A
110	109.4	3.8	1771	4	US-09-906-618-158	Sequence 158, App	183	97.2	3.4	272	4	US-09-621-976-16026	Sequence 16026, A
111	109.2	3.8	359	4	US-09-621-976-16008	Sequence 16008, A	184	97	3.4	347	4	US-09-621-976-12430	Sequence 12430, A
112	109.2	3.8	359	4	US-09-621-976-16019	Sequence 16019, A	185	97	3.4	97	4	US-09-621-976-12430	Sequence 12430, A
113	109.2	3.8	362	4	US-09-621-976-16010	Sequence 16010, A	186	96.8	3.4	1098	3	US-09-248-335-35	Sequence 35, Appl
114	109	3.8	365	4	US-09-621-976-16042	Sequence 16042, A	187	96.8	3.4	1342	4	US-09-489-847-89	Sequence 89, Appl
115	109	3.8	111	3	US-09-297-535-23	Sequence 23, Appl	188	96.6	3.4	2665	3	US-08-971-089-5	Sequence 5, Appli
116	109	3.8	121	3	US-09-297-535-20	Sequence 20, Appl	c 189	96.4	3.4	1445	2	US-08-814-951A-1	Sequence 1, Appli
117	108.6	3.8	371	4	US-09-621-976-16048	Sequence 16048, A	c 189	96.4	3.4	260	2	US-08-520-678A-29	Sequence 29, Appl
118	108.6	3.8	949	4	US-09-489-847-35	Sequence 35, Appl	c 190	96.4	3.4	260	3	US-08-897-126-29	Sequence 29, Appl
119	108.6	3.8	1493	1	US-08-340-820-24	Sequence 24, Appl	c 191	96.4	3.4	268	4	US-09-621-976-73	Sequence 73, Appl
120	108	3.8	2327	1	US-08-593-535-24	Sequence 24, Appl	c 192	96.4	3.4	582	4	US-09-787-292-3	Sequence 3, Appli
121	108	3.8	2434	4	US-10-066-130-20	Sequence 20, Appl	193	96.4	3.4	2852	3	US-09-027-137-2	Sequence 2, Appli
122	108	3.8	2674	4	US-10-066-130-19	Sequence 19, Appl	194	96.4	3.4	2852	3	US-09-344-441-2	Sequence 2, Appli
123	108	3.8	2771	4	US-10-066-130-18	Sequence 18, Appl	195	96.2	3.4	194	4	US-09-621-976-801	Sequence 801, App
124	108	3.8	5860	4	US-10-066-130-17	Sequence 17, Appl	196	96.2	3.4	3116	4	US-09-311-021-187	Sequence 187, App
c 125	108	3.8	9589	1	US-07-925-695-1	Sequence 1, Appli	197	96.2	3.4	4086	4	US-09-702-705-1801	Sequence 1801, Ap
c 126	108	3.8	9589	1	US-07-925-695-2	Sequence 2, Appli	198	96.2	3.4	4086	4	US-09-736-457-1801	Sequence 1801, Ap
c 127	108	3.8	12980	3	US-08-811-566-5	Sequence 5, Appli	199	96.2	3.4	4086	4	US-09-671-325-1801	Sequence 1801, Ap
c 128	108	3.8	12980	3	US-09-034-756-5	Sequence 5, Appli	c 200	96	3.4	537	4	US-09-720-201A-4	Sequence 4, Appli
129	107.8	3.8	357	4	US-09-621-976-16058	Sequence 16058, A	c 201	96	3.4	644	4	US-09-720-201A-6	Sequence 6, Appli
130	107.8	3.8	1872	3	US-09-801-052-1	Sequence 1, Appli	202	96	3.4	2323	3	US-09-149-476-24	Sequence 24, Appl
131	107.6	3.8	1141	4	US-09-800-729-78	Sequence 78, Appl	203	95.4	3.4	1406	4	US-10-000-489-81	Sequence 81, Appl
132	107.6	3.8	2184	3	US-08-955-918C-1	Sequence 1, Appli	204	95.4	3.4	3334	4	US-09-668-119-2	Sequence 2, Appli
133	107.6	3.8	2184	3	US-08-697-766A-1	Sequence 1, Appli	205	95.2	3.3	105	4	US-09-621-976-13820	Sequence 13820, A
134	107.6	3.8	356	2	US-08-520-678A-22	Sequence 22, Appl	206	95.2	3.3	351	4	US-09-559-023-1	Sequence 1, Appli
c 135	107	3.8	356	3	US-08-897-126-22	Sequence 22, Appl	207	95	3.3	331	4	US-09-621-976-15134	Sequence 15134, A
c 136	107	3.8	9646	3	US-08-811-566-1	Sequence 1, Appli	208	95	3.3	1277	4	US-09-720-317A-19	Sequence 19, Appl
c 137	107	3.8	9646	3	US-09-034-756-1	Sequence 1, Appli	209	94.8	3.3	3556	4	US-09-270-767-25838	Sequence 25838, A
c 138	107	3.8	1641	1	US-08-300-903A-8	Sequence 8, Appli	210	94.6	3.3	2216	2	US-09-426-783-5	Sequence 5, Appli
139	106.6	3.7	1641	4	US-08-988-197A-8	Sequence 8, Appli	211	94.6	3.3	2621	2	US-08-553-619B-8	Sequence 8, Appli
140	106.6	3.7	1641	4	US-08-385-072-8	Sequence 8, Appli	212	94.6	3.3	3715	4	US-09-234-245-1	Sequence 1, Appli
141	106.6	3.7	1641	4	US-09-372-432A-19	Sequence 19, Appl	213	94.4	3.3	333	3	US-09-018-584A-27	Sequence 27, Appl
142	106	3.7	1454	3	US-09-370-253-1	Sequence 1, Appli	214	94.4	3.3	1091	4	US-09-328-965-1	Sequence 1, Appli
143	105.6	3.7	1882	3	US-09-621-976-1324	Sequence 1324, Ap	215	94.4	3.3	333	3	US-09-784-423-27	Sequence 27, Appl
144	105.4	3.7	1273	4	US-09-621-976-14731	Sequence 14731, A	216	94.4	3.3	2625	4	US-09-270-767-10080	Sequence 10080, A
145	104	3.7	177	4	US-09-621-976-1047	Sequence 1047, Ap	217	94.4	3.3	2239	3	US-09-196-390-1	Sequence 1, Appli
146	104	3.7	177	4	US-09-653-839-9	Sequence 9, Appli	218	94.2	3.3	2239	3	US-09-952-677-1	Sequence 1, Appli
147	103.6	3.6	2806	4	US-10-202-619-9	Sequence 9, Appli	219	94.2	3.3	601	4	US-09-949-016-195763	Sequence 195763, A
148	103.6	3.6	41736	4	US-09-949-016-17091	Sequence 17091, A	220	93.8	3.3	997	4	US-09-907-794A-376	Sequence 376, App
149	103.6	3.6	147	4	US-09-621-976-10254	Sequence 10254, A	221	93.8	3.3	997	4	US-09-905-125A-376	Sequence 376, App
150	103.4	3.6	147	4	US-09-621-976-10254	Sequence 10254, A	222	93.8	3.3	997	4	US-09-905-125A-376	Sequence 376, App
151	102.6	3.6	147	4	US-09-621-976-10254	Sequence 10254, A	223	93.8	3.3	997	4	US-09-906-700-376	Sequence 376, App
152	102.2	3.6	1052	4	US-09-489-847-23	Sequence 23, Appl	224	93.8	3.3	997	4	US-09-906-700-376	Sequence 376, App
153	102.2	3.6	2527	4	US-09-244-805-29	Sequence 29, Appl	225	93.8	3.3	997	4	US-09-904-920A-376	Sequence 376, App
154	102	3.6	102	4	US-09-621-976-14804	Sequence 14804, A	226	93.8	3.3	997	4	US-09-909-064-376	Sequence 376, App
155	101.8	3.6	558	4	US-09-043-861-3	Sequence 3, Appli	227	93.8	3.3	997	4	US-09-905-381A-376	Sequence 376, App
156	100.4	3.5	123	4	US-09-621-976-12330	Sequence 12330, A	228	93.8	3.3	997	4	US-09-906-618-376	Sequence 376, App
c 157	100.4	3.5	251672	4	US-09-949-016-17296	Sequence 17296, A	229	93.8	3.3	1895	3	US-09-444-336-7	Sequence 7, Appli
c 158	100.4	3.5	251682	4	US-10-151-832-1	Sequence 11973, A	230	93.6	3.3	903	5	PCT-US95-06406A-21	Sequence 21, Appl
159	100.2	3.5	1308	4	US-08-545-196B-10	Sequence 10, Appl	231	93.6	3.3	1248	4	US-09-489-847-101	Sequence 101, App
160	100.2	3.5	1582	3	US-08-545-196B-12	Sequence 12, Appl	232	93.4	3.3	2223	1	US-08-257-073-4	Sequence 4, Appli
161	100.2	3.5	1582	3	US-08-545-196B-12	Sequence 12, Appl	233	93.2	3.3	1069	3	US-09-372-422A-7	Sequence 7, Appli
c 162	100.2	3.5	4419	4	US-09-620-312D-187	Sequence 187, App	234	93	3.3	1172	1	US-07-945-288-9	Sequence 9, Appli
163	100	3.5	2671	6	5168051-9	Patent No. 5168051	235	93	3.3	1172	1	US-08-462-831-9	Sequence 9, Appli
164	100	3.5	2671	6	5168051-9	Patent No. 5168051	236	93	3.3	1172	1	US-08-461-809-9	Sequence 9, Appli
165	99.4	3.5	550	4	US-09-010-147B-5	Sequence 5, Appli	237	93	3.3	1172	1	US-08-461-809-9	Sequence 9, Appli
166	99	3.5	1411	3	US-08-964-127-5	Sequence 5, Appli	238	93	3.3	1172	5	PCT-US93-08518-9	Sequence 9, Appli
167	99	3.5	1411	3	US-09-496-692-5	Sequence 5, Appli	239	92.8	3.3	179	4	US-09-621-976-9575	Sequence 9575, Ap
168	99	3.5	1411	4	US-10-000-273-5	Sequence 5, Appli	240	92.4	3.2	1114	3	US-09-152-060-41	Sequence 41, Appl
169	99	3.5	1414	4	US-09-501-115-5	Sequence 5, Appli	241	92.4	3.2	1249	4	US-09-461-325-128	Sequence 128, App
170	98.8	3.5	193	4	US-09-621-976-10543	Sequence 10543, A	242	92.4	3.2	1249	4	US-10-012-542-128	Sequence 128, App
171	98.8	3.5	790	3	US-09-363-970-4	Sequence 4, Appli	243	92.4	3.2	1249	4	US-10-115-123-128	Sequence 128, App
c 172	98.4	3.5	270	2	US-08-520-678A-30	Sequence 30, Appl	c 244	92.4	3.2	1260	4	US-09-461-325-93	Sequence 93, Appl
c 173	98.4	3.5	270	3	US-08-897-126-30	Sequence 30, Appl	c 245	92.4	3.2	1260	4	US-10-012-542-93	Sequence 93, Appl

C 247	92.4	3.2	1260	4	US-10-115-123-93	Sequence 93, Appl	320	89	3.1	3410	4	US-09-651-236-110	Sequence 110, App
248	92.2	3.2	244	4	US-09-621-976-484	Sequence 484, App	321	88.8	3.1	1190	4	US-09-390-207-1	Sequence 1, Appl
249	92.2	3.2	271	4	US-09-621-976-10380	Sequence 10380, A	322	88.8	3.1	1508	3	US-09-039-046-1	Sequence 1, Appl
250	92.2	3.2	1193	3	US-09-372-422A-23	Sequence 23, Appl	323	88.6	3.1	1636	4	US-09-578-194-6	Sequence 6, Appl
251	92.2	3.2	1662	4	US-09-668-097A-13	Sequence 13, Appl	324	88.6	3.1	331	4	US-09-621-976-16100	Sequence 16100, A
252	92.2	3.2	2406	4	US-09-594-506-37	Sequence 37, Appl	325	88.6	3.1	339	4	US-09-621-976-16015	Sequence 16015, A
253	92	3.2	92	4	US-09-621-976-14689	Sequence 14689, A	326	88.6	3.1	601	4	US-09-949-016-40844	Sequence 40844, A
254	92	3.2	242	4	US-09-621-976-16324	Sequence 16324, A	327	88.6	3.1	601	4	US-09-949-016-40845	Sequence 40845, A
255	92	3.2	19124	2	US-08-487-826B-13	Sequence 13, Appl	328	88.6	3.1	601	4	US-09-949-016-40846	Sequence 40846, A
C 256	91.8	3.2	367	4	US-09-270-767-14713	Sequence 14713, A	C 329	88.6	3.1	462589	4	US-09-949-016-12900	Sequence 12900, A
257	91.8	3.2	601	4	US-09-949-016-160412	Sequence 160412, A	C 330	88.6	3.1	476044	4	US-09-949-016-12412	Sequence 12412, A
258	91.8	3.2	601	4	US-09-949-016-160413	Sequence 160413, A	C 331	88.4	3.1	146	4	US-09-621-976-8550	Sequence 8550, Ap
259	91.6	3.2	195	4	US-09-621-976-18062	Sequence 18062, A	C 332	88.4	3.1	160	4	US-09-621-976-10335	Sequence 10335, A
260	91.6	3.2	1878	3	US-09-465-558-39	Sequence 39, Appl	C 333	88.4	3.1	334	4	US-09-621-976-150044	Sequence 16004, A
261	91.6	3.2	2311	4	US-09-800-729-66	Sequence 66, Appl	C 334	88.4	3.1	601	4	US-09-949-016-150083	Sequence 150083, A
262	91.4	3.2	176	4	US-09-621-976-13903	Sequence 13903, A	C 335	88.4	3.1	2445	4	US-09-949-016-781	Sequence 781, App
263	91	3.2	92	4	US-09-621-976-13903	Sequence 13903, A	C 336	88.4	3.1	2539	4	US-10-144-198-21	Sequence 21, Appl
264	91	3.2	242	4	US-09-621-976-13920	Sequence 13920, A	C 337	88.4	3.1	26115	4	US-09-949-016-15959	Sequence 15959, A
265	91	3.2	246	4	US-09-621-976-13617	Sequence 13617, A	C 338	88	3.1	184	4	US-09-270-767-30942	Sequence 30942, A
266	90.8	3.2	601	4	US-09-949-016-182221	Sequence 182221, A	C 339	88	3.1	196	4	US-09-644-460-40	Sequence 40, Appl
C 267	90.8	3.2	133358	4	US-09-949-016-16964	Sequence 16964, A	C 340	88	3.1	332	4	US-09-621-976-16050	Sequence 16050, A
C 268	90.8	3.2	133360	4	US-09-949-016-12651	Sequence 12651, A	C 341	88	3.1	332	4	US-09-621-976-16032	Sequence 16032, A
269	90.6	3.2	163	4	US-09-621-976-9608	Sequence 9608, Ap	C 342	88	3.1	333	4	US-09-621-976-16045	Sequence 16045, A
270	90.6	3.2	454	2	US-08-623-908A-6	Sequence 6, Appl	C 343	88	3.1	2149	4	US-09-949-016-456	Sequence 456, App
271	90.6	3.2	1198	3	US-09-248-335-27	Sequence 27, Appl	C 344	88	3.1	3124	3	US-09-734-030-1	Sequence 1, Appl
C 272	90.6	3.2	7218	1	US-08-232-463-14	Sequence 14, Appl	C 345	88	3.1	3124	4	US-10-153-921-1	Sequence 1, Appl
C 273	90.6	3.2	57139	4	US-09-949-016-11771	Sequence 11771, A	C 346	88	3.1	3124	4	US-10-669-689-1	Sequence 1, Appl
C 274	90.6	3.2	57150	4	US-09-949-016-16233	Sequence 16233, A	C 347	87.8	3.1	336	4	US-09-621-976-16051	Sequence 16051, A
275	90.4	3.2	990	4	US-09-800-723-79	Sequence 79, Appl	C 348	87.8	3.1	376	2	US-08-623-906A-18	Sequence 18, Appl
276	90.4	3.2	1297	4	US-09-800-723-80	Sequence 80, Appl	C 349	87.8	3.1	1008	4	US-09-780-641-1	Sequence 1, Appl
277	90.4	3.2	1361	4	US-09-489-847-64	Sequence 64, Appl	C 350	87.8	3.1	1736	3	US-09-182-816-22	Sequence 22, Appl
278	90.4	3.2	1683	3	US-09-347-803-11	Sequence 11, Appl	C 351	87.8	3.1	1736	3	US-09-182-816-24	Sequence 24, Appl
279	90.4	3.2	2280	3	US-08-813-150-1	Sequence 1, Appl	C 352	87.8	3.1	1736	3	US-09-471-528-22	Sequence 22, Appl
280	90.4	3.2	2280	3	US-09-546-553-1	Sequence 1, Appl	C 353	87.8	3.1	1736	3	US-09-471-528-24	Sequence 24, Appl
281	90.2	3.2	1746	4	US-09-485-523-57	Sequence 57, Appl	C 354	87.8	3.1	1736	3	US-09-634-530-22	Sequence 22, Appl
282	90.2	3.2	1768	4	US-09-485-523-13	Sequence 13, Appl	C 355	87.8	3.1	1736	3	US-09-634-530-24	Sequence 24, Appl
C 283	90	3.2	601	4	US-09-949-016-150084	Sequence 150084, A	C 356	87.4	3.1	332	4	US-09-621-976-16053	Sequence 16053, A
284	89.8	3.2	1492	3	US-09-369-247-23	Sequence 23, Appl	C 357	87.4	3.1	639	4	US-09-482-273-49	Sequence 49, Appl
285	89.8	3.2	1817	1	US-08-473-981A-5	Sequence 5, Appl	C 358	87.4	3.1	1602	1	US-08-530-950-3	Sequence 3, Appl
286	89.8	3.2	1817	2	US-08-474-087-5	Sequence 5, Appl	C 359	87.4	3.1	1602	3	US-08-888-429A-3	Sequence 3, Appl
C 287	89.6	3.1	601	4	US-09-949-016-150085	Sequence 150085, A	C 360	87.4	3.1	1602	3	US-09-149-879-3	Sequence 3, Appl
288	89.6	3.1	711	4	US-09-621-976-17854	Sequence 17854, A	C 361	87.4	3.1	1602	4	US-09-057-009-3	Sequence 3, Appl
289	89.6	3.1	795	4	US-09-270-767-14068	Sequence 14068, A	C 362	87.4	3.1	1602	4	US-09-593-653-3	Sequence 3, Appl
290	89.6	3.1	1134	3	US-09-248-335-29	Sequence 29, Appl	C 363	87.4	3.1	131332	4	US-09-949-016-15535	Sequence 15535, A
291	89.6	3.1	1700	2	US-08-897-340-4	Sequence 4, Appl	C 364	87.4	3.1	360470	4	US-09-949-016-13173	Sequence 13173, A
292	89.6	3.1	1700	3	US-09-252-329-4	Sequence 4, Appl	C 365	87.2	3.1	812	3	US-09-091-097-7	Sequence 7, Appl
293	89.4	3.1	335	4	US-09-621-976-16061	Sequence 16061, A	C 366	87.2	3.1	1512	2	US-08-909-965C-8	Sequence 8, Appl
294	89.4	3.1	336	4	US-09-621-976-16013	Sequence 16013, A	C 367	86.8	3.0	593	3	US-09-385-982-282	Sequence 282, App
295	89.4	3.1	338	4	US-09-621-976-16041	Sequence 16041, A	C 368	86.8	3.0	601	4	US-09-949-016-29142	Sequence 29142, A
296	89.4	3.1	2628	1	US-08-143-219-1	Sequence 1, Appl	C 369	86.8	3.0	601	4	US-09-949-016-29143	Sequence 29143, A
297	89.2	3.1	1037	4	US-09-489-847-112	Sequence 112, App	C 370	86.8	3.0	601	4	US-09-949-016-29144	Sequence 29144, A
298	89.2	3.1	2010	1	US-07-864-475A-4	Sequence 4, Appl	C 371	86.8	3.0	601	4	US-09-949-016-41097	Sequence 41097, A
299	89.2	3.1	2010	2	US-08-468-249A-4	Sequence 4, Appl	C 372	86.8	3.0	601	4	US-09-949-016-41098	Sequence 41098, A
300	89	3.1	89	4	US-09-621-976-14749	Sequence 14749, A	C 373	86.8	3.0	601	4	US-09-949-016-41099	Sequence 41099, A
301	89	3.1	89	4	US-09-621-976-14974	Sequence 14974, A	C 374	86.8	3.0	1921	2	US-08-557-128-11	Sequence 11, Appl
302	89	3.1	147	4	US-09-621-976-8551	Sequence 8551, Ap	C 375	86.8	3.0	2202	3	US-09-465-558-59	Sequence 59, Appl
303	89	3.1	318	4	US-09-621-976-10247	Sequence 10247, A	C 376	86.8	3.0	16073	4	US-09-949-016-12312	Sequence 12312, A
304	89	3.1	554	4	US-09-696-169A-14	Sequence 14, Appl	C 377	86.8	3.0	16073	4	US-09-949-016-12905	Sequence 12905, A
305	89	3.1	688	6	5498694-3	Patent No. 5498694	C 378	86.6	3.0	1781	4	US-09-818-512-1	Sequence 1, Appl
306	89	3.1	688	6	5498694-3	Patent No. 5498694	C 379	86.4	3.0	332	4	US-09-621-976-16031	Sequence 16031, A
307	89	3.1	3410	3	US-09-020-956-110	Sequence 110, App	C 380	86.4	3.0	658	3	US-08-998-416-595	Sequence 595, App
308	89	3.1	3410	3	US-09-030-607-110	Sequence 110, App	C 381	86.4	3.0	2218	4	US-09-016-434-1157	Sequence 1157, Ap
309	89	3.1	3410	3	US-09-439-313-110	Sequence 110, App	C 382	86.4	3.0	2218	4	US-10-329-668-7	Sequence 7, Appl
310	89	3.1	3410	3	US-09-352-616A-110	Sequence 110, App	C 383	86.4	3.0	2233	1	US-08-496-631-1	Sequence 1, Appl
311	89	3.1	3410	3	US-09-602-877A-100	Sequence 100, App	C 384	86.2	3.0	329	4	US-09-621-976-16012	Sequence 16012, A
312	89	3.1	3410	3	US-09-232-149A-110	Sequence 110, App	C 385	86.2	3.0	443	4	US-09-621-976-17631	Sequence 17631, A
313	89	3.1	3410	4	US-09-159-812-110	Sequence 110, App	C 386	86.2	3.0	602	1	US-08-764-100-8	Sequence 8, Appl
314	89	3.1	3410	4	US-09-636-215-110	Sequence 110, App	C 387	86.2	3.0	642	1	US-08-764-100-13	Sequence 13, Appl
315	89	3.1	3410	4	US-09-685-166A-110	Sequence 110, App	C 388	86.2	3.0	643	1	US-08-764-100-7	Sequence 7, Appl
316	89	3.1	3410	4	US-09-115-453-110	Sequence 110, App	C 389	86.2	3.0	2993	1	US-08-764-100-2	Sequence 2, Appl
317	89	3.1	3410	4	US-09-688-489-110	Sequence 110, App	C 390	86.2	3.0	2993	1	US-08-764-100-10	Sequence 10, Appl
318	89	3.1	3410	4	US-09-679-426-110	Sequence 110, App	C 391	86.2	3.0	3000	1	US-08-764-100-9	Sequence 9, Appl
319	89	3.1	3410	4	US-09-759-143-110	Sequence 110, App	C 392	86.2	3.0	3001	1	US-08-764-100-1	Sequence 1, Appl

393	86.2	3.0	161124	4	US-09-949-016-11760	Sequence 11760, A	466	83.4	2.9	2230	3	US-08-378-313-24	Sequence 24, Appl
394	86	3.0	630	1	US-08-185-414E-1	Sequence 1, Appl	467	83.4	2.9	2550	6	5258287-23	Patent No. 5258287
C 395	86	3.0	27687	4	US-09-949-016-13840	Sequence 13840, A	468	83.4	2.9	2550	6	5258287-23	Patent No. 5258287
396	85.8	3.0	326	4	US-09-621-976-16024	Sequence 16024, A	469	83.4	2.9	2989	6	5378464-1	Patent No. 5378464
397	85.8	3.0	601	4	US-09-949-016-175160	Sequence 175160, A	470	83.4	2.9	2989	6	5378464-1	Patent No. 5378464
398	85.8	3.0	1835	3	US-09-485-549-1	Sequence 1, Appl	471	83.4	2.9	168174	4	US-10-071-411A-63	Sequence 63, Appl
399	85.8	3.0	2320	3	US-09-203-904A-13	Sequence 13, Appl	472	83.4	2.9	168273	4	US-10-071-411A-2	Sequence 2, Appl
C 400	85.8	3.0	2638	4	US-10-029-907-6	Sequence 6, Appl	C 473	83.4	2.9	250958	4	US-09-949-016-16061	Sequence 16061, A
C 401	85.8	3.0	19601	4	US-09-949-016-15629	Sequence 15629, A	C 474	83.2	2.9	300	4	US-09-621-976-16227	Sequence 16227, A
402	85.8	3.0	31111	4	US-09-949-016-15628	Sequence 15628, A	C 475	83.2	2.9	844	4	US-09-690-942-3	Sequence 3, Appl
403	85.6	3.0	273	4	US-09-809-545A-31	Sequence 31, Appl	476	83	2.9	83	4	US-08-621-976-14751	Sequence 14751, A
404	85.6	3.0	73519	4	US-09-949-016-16344	Sequence 16344, A	477	83	2.9	83	4	US-09-621-976-14959	Sequence 14959, A
405	85.6	3.0	105919	4	US-09-949-016-11769	Sequence 11769, A	478	83	2.9	188	4	US-09-621-976-10364	Sequence 10364, A
406	85.4	3.0	1325	1	US-08-306-691B-51	Sequence 51, Appl	C 479	83	2.9	253	2	US-08-520-678A-25	Sequence 25, Appl
407	85.4	3.0	1378	3	US-09-149-476-208	Sequence 208, App	C 480	83	2.9	253	2	US-08-897-126-25	Sequence 25, Appl
408	85.4	3.0	2276	4	US-09-203-258-183	Sequence 183, App	C 481	83	2.9	601	4	US-09-949-016-193621	Sequence 193621, A
409	85.2	3.0	323	4	US-09-621-976-10374	Sequence 10374, A	482	83	2.9	1192	4	US-09-439-554-23	Sequence 23, Appl
C 410	85.2	3.0	349	4	US-09-270-767-6612	Sequence 6612, Ap	C 483	83	2.9	54033	4	US-09-949-016-12091	Sequence 12091, A
C 411	85.2	3.0	309	4	US-09-270-767-21894	Sequence 21894, A	C 484	83	2.9	54033	4	US-09-949-016-14325	Sequence 14325, A
412	85.2	3.0	601	4	US-09-949-016-29145	Sequence 29145, A	485	82.8	2.9	190	4	US-09-621-976-16784	Sequence 16784, A
413	85.2	3.0	601	4	US-09-949-016-41100	Sequence 41100, A	486	82.8	2.9	293	4	US-09-621-976-16965	Sequence 16965, A
C 414	85.2	3.0	175265	4	US-09-949-016-16089	Sequence 16089, A	487	82.8	2.9	1212	3	US-09-182-145-34	Sequence 34, Appl
C 415	85.2	3.0	312470	4	US-09-949-016-14043	Sequence 14043, A	C 488	82.8	2.9	1212	3	US-09-182-145-35	Sequence 35, Appl
C 416	85.2	3.0	336024	4	US-09-949-016-12373	Sequence 12373, A	489	82.8	2.9	1307	2	US-08-960-022-17	Sequence 17, Appl
C 417	85.2	3.0	85	4	US-09-621-976-13395	Sequence 13395, A	490	82.8	2.9	5021	4	US-09-949-016-786	Sequence 786, App
418	85	3.0	85	4	US-09-621-976-14949	Sequence 14949, A	491	82.8	2.9	152070	4	US-09-949-016-15402	Sequence 15402, A
419	85	3.0	299	4	US-09-621-976-16226	Sequence 16226, A	C 492	82.6	2.9	124	6	5185243-1	Patent No. 5185243
420	85	3.0	635	1	US-08-455-633A-35	Sequence 35, Appl	C 493	82.6	2.9	124	6	5185243-1	Patent No. 5185243
421	85	3.0	635	1	US-08-416-336-5	Sequence 5, Appl	494	82.6	2.9	291	1	US-07-922-723A-7	Sequence 7, Appl
422	85	3.0	635	1	US-08-416-336-5	Sequence 5, Appl	495	82.6	2.9	291	1	US-07-799-828C-7	Sequence 7, Appl
423	85	3.0	635	2	US-08-456-460C-35	Sequence 35, Appl	496	82.6	2.9	291	1	US-08-074-275-7	Sequence 7, Appl
424	85	3.0	635	5	PCT-US94-05354-35	Sequence 35, Appl	497	82.6	2.9	291	1	US-08-480-366-7	Sequence 7, Appl
C 425	85	3.0	9636	1	US-08-323-170B-1	Sequence 1, Appl	498	82.6	2.9	291	2	US-07-952-277A-7	Sequence 7, Appl
C 426	85	3.0	9636	1	US-08-323-170B-1	Sequence 1, Appl	499	82.6	2.9	3448	1	US-08-296-014A-3	Sequence 3, Appl
C 427	85	3.0	59841	4	US-09-949-016-16602	Sequence 16602, A	500	82.6	2.9	3448	2	US-08-596-405-3	Sequence 3, Appl
428	84.8	3.0	601	4	US-09-621-976-16038	Sequence 16038, A	501	82.6	2.9	3448	2	US-08-877-620-3	Sequence 3, Appl
429	84.8	3.0	1074	3	US-09-248-335-67	Sequence 67, Appl	502	82.6	2.9	3448	4	US-09-287-368-3	Sequence 3, Appl
430	84.8	3.0	1210	3	US-09-443-041A-29	Sequence 29, Appl	503	82.6	2.9	3448	4	US-09-626-795-3	Sequence 3, Appl
C 431	84.8	3.0	1709	3	US-09-426-783-6	Sequence 6, Appl	504	82.6	2.9	4182	1	US-08-296-014A-1	Sequence 1, Appl
C 432	84.8	3.0	1925	4	US-09-148-545-128	Sequence 128, App	505	82.6	2.9	4182	2	US-08-596-405-1	Sequence 1, Appl
C 433	84.8	3.0	2028	4	US-09-426-783-9	Sequence 9, Appl	506	82.6	2.9	4182	2	US-08-877-620-1	Sequence 1, Appl
C 434	84.8	3.0	2028	4	US-09-426-783-9	Sequence 9, Appl	507	82.6	2.9	4182	2	US-08-287-368-1	Sequence 1, Appl
C 435	84.6	3.0	2797	4	US-09-949-016-376	Sequence 376, App	508	82.6	2.9	4182	4	US-09-626-795-1	Sequence 1, Appl
436	84.6	3.0	145928	4	US-09-949-016-15444	Sequence 15444, A	509	82.6	2.9	786431	4	US-09-751-389-3	Sequence 3, Appl
437	84.4	3.0	1725	4	US-09-668-097A-21	Sequence 21, Appl	510	82.4	2.9	84	4	US-09-621-976-14571	Sequence 14571, A
438	84.4	3.0	2271	4	US-09-205-258-243	Sequence 243, App	511	82.2	2.9	169	4	US-09-621-976-11249	Sequence 11249, A
C 439	84.4	3.0	3079	4	US-09-426-783-14	Sequence 14, Appl	512	82.2	2.9	1133	4	US-09-916-204-1	Sequence 1, Appl
440	84.4	3.0	3080	3	US-09-099-041A-25	Sequence 25, Appl	513	82.2	2.9	1133	4	US-10-282-048-1	Sequence 1, Appl
441	84.4	3.0	3080	3	US-09-245-281-25	Sequence 25, Appl	514	82.2	2.9	1441	3	US-08-821-994-63	Sequence 63, Appl
442	84.4	3.0	3080	3	US-09-207-359B-25	Sequence 25, Appl	515	82	2.9	179	4	US-09-621-976-18054	Sequence 18054, A
443	84.4	3.0	3080	4	US-09-340-620A-25	Sequence 25, Appl	516	82	2.9	329	4	US-09-621-976-16052	Sequence 16052, A
444	84.4	3.0	3080	4	US-09-865-364-25	Sequence 25, Appl	C 517	82	2.9	601	4	US-09-949-016-80450	Sequence 80450, A
C 445	84.4	3.0	250352	4	US-09-949-016-14724	Sequence 14724, A	C 518	82	2.9	1013	4	US-09-322-409-6	Sequence 6, Appl
446	84.2	3.0	324	4	US-09-621-976-16027	Sequence 16027, A	C 519	82	2.9	1013	4	US-09-322-409-8	Sequence 8, Appl
447	84.2	3.0	19727	3	US-09-336-536-66	Sequence 66, Appl	520	82	2.9	1013	4	US-09-451-527-6	Sequence 6, Appl
C 448	84.2	3.0	15722	4	US-09-949-016-16709	Sequence 16709, A	C 521	82	2.9	1013	4	US-09-451-527-8	Sequence 8, Appl
C 449	84.2	3.0	237510	4	US-09-949-016-14273	Sequence 14273, A	522	82	2.9	1461	3	PCT-US95-04258-4	Sequence 4, Appl
450	84	3.0	127	4	US-09-621-976-13933	Sequence 13933, A	523	82	2.9	1461	5	PCT-US95-04258-4	Sequence 4, Appl
451	84	3.0	215	4	US-09-621-976-15321	Sequence 15321, A	C 524	82	2.9	90541	4	US-09-759-359A-3	Sequence 3, Appl
C 452	84	3.0	601	4	US-09-949-016-175321	Sequence 175321, A	C 525	82	2.9	90541	4	US-10-207-973-3	Sequence 3, Appl
453	84	3.0	1507	3	US-09-453-323-1	Sequence 1, Appl	C 526	82	2.9	90541	4	US-10-207-973-3	Sequence 3, Appl
454	84	3.0	7724	4	US-08-486-049-1	Sequence 17096, A	C 527	82	2.9	113701	4	US-09-949-016-13214	Sequence 13214, A
C 455	84	3.0	12603	4	US-09-949-016-17096	Sequence 17096, A	C 528	82	2.9	670689	4	US-09-949-016-11894	Sequence 11894, A
456	83.8	2.9	1325	2	US-08-464-517-1	Sequence 1, Appl	C 529	82	2.9	670690	4	US-09-949-016-14207	Sequence 14207, A
457	83.8	2.9	1325	2	US-08-246-361A-1	Sequence 1, Appl	C 530	81.8	2.9	316	4	US-09-513-999C-838	Sequence 838, App
458	83.8	2.9	1325	2	US-08-463-772-1	Sequence 1, Appl	C 531	81.8	2.9	2147	4	US-09-949-016-5245	Sequence 5245, App
459	83.8	2.9	1325	5	PCT-US93-05000-1	Sequence 1, Appl	C 532	81.8	2.9	13818	4	US-09-949-016-12198	Sequence 12198, A
460	83.8	2.9	94877	4	US-09-949-016-16114	Sequence 16114, A	C 533	81.8	2.9	19819	4	US-09-949-016-16987	Sequence 16987, A
461	83.8	2.9	118143	4	US-09-949-016-17196	Sequence 17196, A	534	81.6	2.9	189	4	US-09-621-976-14761	Sequence 14761, A
462	83.6	2.9	84	4	US-09-949-016-17196	Sequence 17196, A	535	81.6	2.9	89689	4	US-09-949-016-13089	Sequence 13089, A
463	83.6	2.9	84	4	US-09-621-976-14577	Sequence 14577, A	C 536	81.4	2.9	601	4	US-09-949-016-193622	Sequence 193622, A
C 464	83.6	2.9	5852	1	US-07-867-106-2	Sequence 2, Appl	C 537	81.4	2.9	601	4	US-09-949-016-193623	Sequence 193623, A
C 465	83.6	2.9	12703	4	US-09-949-016-16685	Sequence 16685, A	C 538	81.4	2.9	601	4	US-09-949-016-193624	Sequence 193624, A

539	81.4	2.9	730	4	US-09-270-767-14600	Sequence 14600, A	612	80.4	2.8	10442	4	US-09-595-526C-1	Sequence 1, Appli
540	81.4	2.9	3527	2	US-08-909-965C-7	Sequence 7, Appli	613	80.4	2.8	10474	4	US-09-596-141C-7	Sequence 7, Appli
541	81.4	2.9	268494	4	US-09-949-016-17244	Sequence 17244, A	614	80.4	2.8	10474	4	US-09-596-141C-9	Sequence 9, Appli
C 542	81.2	2.9	604	4	US-09-334-819A-8	Sequence 8, Appli	615	80.4	2.8	10474	4	US-09-595-526C-7	Sequence 7, Appli
C 543	81.2	2.9	8643	4	US-10-029-907-4	Sequence 4, Appli	616	80.4	2.8	10474	4	US-09-595-526C-9	Sequence 9, Appli
544	81.2	2.9	39433	4	US-09-949-016-12014	Sequence 12014, A	C 617	80.4	2.8	42348	4	US-09-949-016-17157	Sequence 17157, A
C 545	81.2	2.9	68283	4	US-09-949-016-12261	Sequence 12261, A	618	80.4	2.8	49401	4	US-09-949-016-17080	Sequence 17080, A
C 546	81.2	2.9	156851	4	US-09-949-016-17349	Sequence 17349, A	619	80.4	2.8	113701	4	US-09-949-016-13214	Sequence 13214, A
C 547	81.2	2.9	254366	4	US-09-822-871-3	Sequence 3, Appli	C 620	80.4	2.8	275110	4	US-09-949-016-12706	Sequence 12706, A
548	81	2.8	81	4	US-09-621-976-13152	Sequence 13152, A	C 621	80.4	2.8	275110	4	US-09-949-016-16070	Sequence 16070, A
C 549	81	2.8	224	2	US-08-731-272A-26	Sequence 26, Appli	C 622	80.4	2.8	421491	4	US-09-949-016-12805	Sequence 12805, A
550	81	2.8	336	4	US-09-248-796A-13866	Sequence 13866, A	C 623	80.4	2.8	421494	4	US-09-949-016-14060	Sequence 14060, A
C 551	81	2.8	389	4	US-09-513-999C-420	Sequence 420, App	624	80.2	2.8	601	4	US-09-949-016-186943	Sequence 186943, A
552	81	2.8	601	4	US-09-949-016-155436	Sequence 155436, A	625	80.2	2.8	2407	3	US-09-370-807-7	Sequence 7, Appli
553	81	2.8	601	4	US-09-949-016-204599	Sequence 204599, A	626	80.2	2.8	2407	3	US-09-921-259-7	Sequence 7, Appli
554	81	2.8	601	4	US-09-949-016-204600	Sequence 204600, A	C 627	80.2	2.8	9558	4	US-09-949-016-13026	Sequence 13026, A
555	81	2.8	601	4	US-09-949-016-204601	Sequence 204601, A	C 628	80.2	2.8	10451	4	US-09-949-016-12192	Sequence 12192, A
556	81	2.8	601	4	US-09-949-016-204602	Sequence 204602, A	C 629	80	2.8	601	4	US-09-949-016-80449	Sequence 80449, A
557	81	2.8	601	4	US-09-949-016-204603	Sequence 204603, A	630	80	2.8	1332	2	US-09-057-762-1	Sequence 1, Appli
558	81	2.8	601	4	US-09-949-016-204604	Sequence 204604, A	631	80	2.8	1332	3	US-08-326-119A-1	Sequence 1, Appli
559	81	2.8	601	4	US-09-949-016-204605	Sequence 204605, A	632	80	2.8	258775	4	US-09-949-016-16435	Sequence 16435, A
560	81	2.8	601	4	US-09-949-016-204606	Sequence 204606, A	633	79.8	2.8	164	4	US-09-621-976-16692	Sequence 16692, A
561	81	2.8	601	4	US-09-949-016-204607	Sequence 204607, A	634	79.8	2.8	601	4	US-09-949-016-19137	Sequence 19137, A
562	81	2.8	700	3	US-09-152-060-26	Sequence 26, Appli	635	79.8	2.8	601	4	US-09-949-016-19138	Sequence 19138, A
563	81	2.8	29221	4	US-09-949-016-14257	Sequence 14257, A	636	79.8	2.8	601	4	US-09-949-016-19139	Sequence 19139, A
564	81	2.8	29221	4	US-09-949-016-14258	Sequence 14258, A	637	79.8	2.8	601	4	US-09-949-016-122876	Sequence 122876, A
565	81	2.8	55298	4	US-09-491-356C-1	Sequence 1, Appli	638	79.8	2.8	601	4	US-09-949-016-122877	Sequence 122877, A
566	81	2.8	87734	4	US-09-949-016-17521	Sequence 17521, A	639	79.8	2.8	601	4	US-09-949-016-122878	Sequence 122878, A
567	81	2.8	100877	4	US-09-949-016-13276	Sequence 13276, A	640	79.8	2.8	601	4	US-09-949-016-203158	Sequence 203158, A
568	81	2.8	132438	4	US-09-949-016-14349	Sequence 14349, A	641	79.8	2.8	601	4	US-09-949-016-203159	Sequence 203159, A
569	81	2.8	132438	4	US-09-949-016-14350	Sequence 14350, A	642	79.8	2.8	601	4	US-09-949-016-203160	Sequence 203160, A
570	81	2.8	151089	4	US-09-949-016-14348	Sequence 14348, A	643	79.8	2.8	601	4	US-09-949-016-203200	Sequence 203200, A
571	81	2.8	524032	4	US-09-949-016-15928	Sequence 15928, A	644	79.8	2.8	601	4	US-09-949-016-203201	Sequence 203201, A
572	81	2.8	524032	4	US-09-949-016-15929	Sequence 15929, A	645	79.8	2.8	601	4	US-09-949-016-203202	Sequence 203202, A
573	81	2.8	524032	4	US-09-949-016-15930	Sequence 15930, A	646	79.8	2.8	6920	4	US-09-949-016-15211	Sequence 15211, A
574	81	2.8	524032	4	US-09-949-016-15931	Sequence 15931, A	647	79.8	2.8	29927	4	US-09-949-016-11814	Sequence 11814, A
575	81	2.8	529885	4	US-09-949-016-14340	Sequence 14340, A	C 648	79.8	2.8	29927	4	US-09-949-016-17474	Sequence 17474, A
576	81	2.8	529885	4	US-09-949-016-14341	Sequence 14341, A	649	79.8	2.8	29927	4	US-09-949-016-17475	Sequence 17475, A
577	81	2.8	529885	4	US-09-949-016-14342	Sequence 14342, A	C 650	79.8	2.8	37802	4	US-09-949-016-13639	Sequence 12639, A
578	81	2.8	529885	4	US-09-949-016-14343	Sequence 14343, A	651	79.8	2.8	38566	4	US-09-949-016-15271	Sequence 15271, A
579	81	2.8	529885	4	US-09-949-016-14344	Sequence 14344, A	652	79.8	2.8	38566	4	US-09-949-016-15272	Sequence 15272, A
580	81	2.8	529885	4	US-09-949-016-14345	Sequence 14345, A	C 653	79.8	2.8	118067	4	US-09-497-855A-32	Sequence 32, Appli
581	81	2.8	529885	4	US-09-949-016-14346	Sequence 14346, A	654	79.6	2.8	173	4	US-09-621-976-9851	Sequence 9851, Ap
582	81	2.8	529885	4	US-09-949-016-14347	Sequence 14347, A	655	79.6	2.8	473	1	US-08-764-100-16	Sequence 16, Appli
583	80.8	2.8	333	4	US-09-248-796A-11241	Sequence 11241, A	656	79.6	2.8	601	4	US-09-949-016-45911	Sequence 45911, A
584	80.8	2.8	2744	3	US-09-071-101-1	Sequence 1, Appli	657	79.6	2.8	601	4	US-09-949-016-69770	Sequence 69770, A
585	80.8	2.8	2744	3	US-09-369-618-1	Sequence 1, Appli	658	79.6	2.8	601	4	US-09-949-016-69771	Sequence 69771, A
586	80.8	2.8	2744	3	US-09-369-617-1	Sequence 1, Appli	659	79.6	2.8	601	4	US-09-949-016-69771	Sequence 69771, A
587	80.8	2.8	5096	4	US-09-949-016-15105	Sequence 15105, A	660	79.6	2.8	601	4	US-09-949-016-162332	Sequence 162332, A
588	80.8	2.8	5173	1	US-08-242-677-1	Sequence 1, Appli	661	79.6	2.8	601	4	US-09-949-016-162333	Sequence 162333, A
C 589	80.8	2.8	23193	4	US-09-949-016-17215	Sequence 17215, A	662	79.6	2.8	601	4	US-09-949-016-162335	Sequence 162335, A
590	80.6	2.8	318	4	US-09-621-976-16040	Sequence 16040, A	663	79.6	2.8	601	4	US-09-949-016-162335	Sequence 162335, A
C 591	80.6	2.8	601	4	US-09-949-016-88560	Sequence 88560, A	664	79.6	2.8	601	4	US-09-949-016-204598	Sequence 204598, A
C 592	80.6	2.8	601	4	US-09-949-016-88565	Sequence 88565, A	665	79.6	2.8	601	4	US-08-252-966B-16	Sequence 16, Appli
593	80.6	2.8	601	4	US-09-949-016-89215	Sequence 89215, A	666	79.6	2.8	1606	4	US-09-820-004-1	Sequence 1, Appli
594	80.6	2.8	741	4	US-09-621-976-1894	Sequence 1894, Ap	C 667	79.6	2.8	4970	1	US-08-764-100-20	Sequence 20, Appli
595	80.6	2.8	763	4	US-09-743-207-3	Sequence 3, Appli	C 668	79.6	2.8	11890	4	US-09-949-016-13794	Sequence 13794, A
596	80.6	2.8	887	4	US-09-270-767-9818	Sequence 9818, Ap	669	79.6	2.8	30000	4	US-10-007-010-10	Sequence 10, Appli
597	80.6	2.8	1129	3	US-09-227-357-40	Sequence 40, Appli	C 670	79.6	2.8	39433	4	US-09-949-016-12014	Sequence 12014, A
598	80.6	2.8	1558	1	US-08-455-550-7	Sequence 7, Appli	671	79.6	2.8	35362	4	US-09-949-016-16286	Sequence 16286, A
599	80.6	2.8	1663	4	US-09-489-847-42	Sequence 42, Appli	672	79.6	2.8	113876	4	US-09-949-016-14828	Sequence 14828, A
600	80.6	2.8	3243	4	US-09-464-535-43	Sequence 43, Appli	673	79.6	2.8	113876	4	US-09-949-016-14829	Sequence 14829, A
601	80.6	2.8	72604	3	US-09-949-016-12186	Sequence 12186, A	674	79.6	2.8	115508	4	US-09-949-016-11800	Sequence 11800, A
602	80.6	2.8	72604	3	US-09-268-992-7	Sequence 7, Appli	675	79.6	2.8	115508	4	US-09-949-016-14826	Sequence 14826, A
603	80.6	2.8	72604	3	US-09-657-474-7	Sequence 7, Appli	C 676	79.6	2.8	115508	4	US-09-949-016-14827	Sequence 14827, A
C 604	80.6	2.8	26247	4	US-09-949-016-13358	Sequence 13358, A	C 677	79.4	2.8	601	4	US-09-949-016-84943	Sequence 84943, A
605	80.4	2.8	231	4	US-09-621-976-16317	Sequence 16317, A	678	79.4	2.8	601	4	US-09-949-016-155437	Sequence 155437, A
C 606	80.4	2.8	601	4	US-09-949-016-80451	Sequence 80451, A	679	79.4	2.8	601	4	US-09-949-016-155438	Sequence 155438, A
607	80.4	2.8	1692	4	US-09-821-803A-5	Sequence 5, Appli	680	79.4	2.8	601	4	US-09-949-016-155439	Sequence 155439, A
608	80.4	2.8	2045	3	US-09-153-060-22	Sequence 22, Appli	681	79.4	2.8	601	4	US-09-949-016-155441	Sequence 155441, A
609	80.4	2.8	3366	4	US-09-596-141C-6	Sequence 6, Appli	682	79.4	2.8	601	4	US-09-949-016-155442	Sequence 155442, A
610	80.4	2.8	3366	4	US-09-595-526C-6	Sequence 6, Appli	683	79.4	2.8	601	4	US-09-949-016-155445	Sequence 155445, A
611	80.4	2.8	10442	4	US-09-596-141C-1	Sequence 1, Appli	C 684	79.4	2.8	601	4	US-09-949-016-204750	Sequence 204750, A

c 685	79.4	2.8	13047	2	US-09-022-461-1	Sequence 1, Appli	c 758	78	2.7	65744	4	US-09-949-016-12591	Sequence 12591, A
c 686	79.4	2.8	12047	3	US-09-033-556-3	Sequence 3, Appli	c 759	78	2.7	65745	4	US-09-949-016-15871	Sequence 15871, A
c 687	79.4	2.8	12047	4	US-09-474-699-11	Sequence 11, Appl	c 760	78	2.7	106746	4	US-09-326-402C-1	Sequence 1, Appli
c 688	79.4	2.8	12047	4	US-09-151-376-3	Sequence 3, Appli	c 761	78	2.7	106746	4	US-09-326-402C-12	Sequence 12, Appl
c 689	79.4	2.8	12047	4	US-09-814-351-11	Sequence 11, Appl	c 762	78	2.7	118868	4	US-09-949-016-15746	Sequence 15746, A
c 690	79.4	2.8	53769	4	US-09-949-016-17527	Sequence 17, Appl	c 763	78	2.7	128175	4	US-09-949-016-16268	Sequence 16268, A
c 691	79.4	2.8	58407	4	US-08-916-421B-2	Sequence 2, Appli	c 764	77.8	2.7	212	4	US-09-621-976-1325	Sequence 1325, Ap
c 692	79.4	2.8	58407	4	US-09-692-570-2	Sequence 2, Appli	c 765	77.8	2.7	601	4	US-09-949-016-155440	Sequence 155440, A
c 693	79.4	2.8	93398	4	US-09-943-016-14167	Sequence 14167, A	c 766	77.8	2.7	601	4	US-09-949-016-155443	Sequence 155443, A
c 694	79.4	2.8	97376	4	US-09-949-016-16093	Sequence 16093, A	c 767	77.8	2.7	601	4	US-09-949-016-182153	Sequence 182153, A
c 695	79.4	2.8	254405	4	US-09-949-016-14381	Sequence 14381, A	c 768	77.8	2.7	601	4	US-09-949-016-182154	Sequence 182154, A
c 696	79.4	2.8	389504	4	US-09-949-016-11774	Sequence 11774, A	c 769	77.8	2.7	1509	3	US-09-149-476-179	Sequence 179, App
c 697	79.2	2.8	196	4	US-09-270-767-29394	Sequence 29394, A	c 770	77.6	2.7	166	4	US-09-621-976-18390	Sequence 18390, A
c 698	79.2	2.8	601	4	US-09-949-016-179690	Sequence 179690, A	c 771	77.6	2.7	185	4	US-09-621-976-16779	Sequence 16779, A
c 699	79.2	2.8	624	3	US-09-270-767-13424	Sequence 13424, A	c 772	77.6	2.7	394	2	US-08-623-906A-7	Sequence 7, Appli
c 700	79.2	2.8	1027	3	US-09-465-558-57	Sequence 57, Appl	c 773	77.6	2.7	601	4	US-09-949-016-76961	Sequence 76961, A
c 701	79.2	2.8	1738	2	US-08-379-482A-2	Sequence 2, Appli	c 774	77.6	2.7	601	4	US-09-949-016-76962	Sequence 76962, A
c 702	79.2	2.8	3975	4	US-09-270-767-3	Sequence 3, Appli	c 775	77.6	2.7	601	4	US-09-949-016-76963	Sequence 76963, A
c 703	79.2	2.8	142783	4	US-09-949-016-15127	Sequence 15127, A	c 776	77.6	2.7	601	4	US-09-949-016-76964	Sequence 76964, A
c 704	79.2	2.8	202001	4	US-09-734-674-3	Sequence 3, Appli	c 777	77.6	2.7	601	4	US-09-949-016-179688	Sequence 179688, A
c 705	79	2.8	361	3	US-09-018-584A-9	Sequence 9, Appli	c 778	77.6	2.7	601	4	Sequence 179692,	Sequence 179692, A
c 706	79	2.8	601	4	US-09-784-423-9	Sequence 9, Appli	c 779	77.6	2.7	1798	2	US-08-557-128-12	Sequence 12, Appl
c 707	79	2.8	361	4	US-09-949-016-155444	Sequence 155444, A	c 780	77.6	2.7	25175	4	US-09-949-016-16247	Sequence 16247, A
c 708	79	2.8	958	2	US-08-757-046A-5	Sequence 5, Appli	c 781	77.6	2.7	25175	4	US-09-949-016-16248	Sequence 16248, A
c 709	79	2.8	958	3	US-09-447-208-5	Sequence 5, Appli	c 782	77.6	2.7	25175	4	US-09-949-016-16273	Sequence 16273, A
c 710	79	2.8	958	3	US-09-135-988-5	Sequence 5, Appli	c 783	77.6	2.7	38772	4	US-09-949-016-12382	Sequence 12382, A
c 711	79	2.8	958	3	US-09-277-716-5	Sequence 5, Appli	c 784	77.6	2.7	38772	4	US-09-949-016-12729	Sequence 12729, A
c 712	79	2.8	958	3	US-08-597-274A-5	Sequence 5, Appli	c 785	77.6	2.7	44453	3	US-09-146-053-5	Sequence 5, Appli
c 713	79	2.8	958	3	US-08-908-909-5	Sequence 5, Appli	c 786	77.6	2.7	236341	4	US-09-949-016-13978	Sequence 13978, A
c 714	79	2.8	958	3	US-09-609-161B-5	Sequence 5, Appli	c 787	77.6	2.7	390416	4	US-09-949-016-16923	Sequence 16923, A
c 715	79	2.8	958	3	US-08-990-103-5	Sequence 5, Appli	c 788	77.4	2.7	593	4	US-09-904-615-59	Sequence 59, Appl
c 716	79	2.8	958	3	US-09-746-485A-5	Sequence 5, Appli	c 789	77.4	2.7	601	4	US-09-949-016-161983	Sequence 161983, A
c 717	79	2.8	958	4	US-10-126-139-5	Sequence 5, Appli	c 790	77.4	2.7	25431	4	US-09-949-016-13234	Sequence 13234, A
c 718	79	2.8	958	4	US-10-126-798-5	Sequence 5, Appli	c 791	77.4	2.7	144158	4	US-09-949-016-11755	Sequence 11755, A
c 719	79	2.8	958	4	US-10-126-777-5	Sequence 5, Appli	c 792	77.4	2.7	144158	4	US-09-949-016-12936	Sequence 12936, A
c 720	79	2.8	32721	4	US-09-949-016-14100	Sequence 14100, A	c 793	77.4	2.7	211049	4	US-09-949-016-15770	Sequence 15770, A
c 721	79	2.8	45469	4	US-09-949-016-14100	Sequence 14100, A	c 794	77.4	2.7	238815	4	US-09-949-016-16274	Sequence 16274, A
c 722	78.8	2.8	319	4	US-09-621-976-18055	Sequence 16055, A	c 795	77.2	2.7	443	4	US-09-936-885A-1	Sequence 1, Appli
c 723	78.8	2.8	601	4	US-09-949-016-179687	Sequence 179687, A	c 796	77.2	2.7	601	4	US-09-949-016-19140	Sequence 19140, A
c 724	78.8	2.8	664	4	US-09-949-016-66	Sequence 66, Appl	c 797	77.2	2.7	601	4	US-09-949-016-31458	Sequence 31458, A
c 725	78.8	2.8	2500	4	US-09-579-383-5	Sequence 5, Appli	c 798	77.2	2.7	601	4	US-09-949-016-31459	Sequence 31459, A
c 726	78.8	2.8	25659	4	US-09-949-016-15052	Sequence 15052, A	c 799	77.2	2.7	601	4	US-09-949-016-122875	Sequence 122875, A
c 727	78.8	2.8	36731	4	US-09-949-016-13770	Sequence 13770, A	c 800	77.2	2.7	601	4	US-09-949-016-127124	Sequence 127124, A
c 728	78.6	2.8	79	4	US-09-621-976-15090	Sequence 15090, A	c 801	77.2	2.7	601	4	US-09-949-016-127125	Sequence 127125, A
c 729	78.6	2.8	601	4	US-09-949-016-17919	Sequence 17919, A	c 802	77.2	2.7	601	4	US-09-949-016-127891	Sequence 127891, A
c 730	78.6	2.8	601	4	US-09-949-016-17920	Sequence 17920, A	c 803	77.2	2.7	601	4	US-09-949-016-128228	Sequence 128228, A
c 731	78.6	2.8	601	4	US-09-949-016-41809	Sequence 41809, A	c 804	77.2	2.7	601	4	US-09-949-016-203161	Sequence 203161, A
c 732	78.6	2.8	601	4	US-09-949-016-41810	Sequence 41810, A	c 805	77.2	2.7	601	4	US-09-949-016-203203	Sequence 203203, A
c 733	78.6	2.8	62908	4	US-09-949-016-17554	Sequence 17554, A	c 806	77.2	2.7	1100	3	US-07-861-458C-4	Sequence 4, Appli
c 734	78.6	2.8	93894	4	US-09-949-016-13629	Sequence 13629, A	c 807	77.2	2.7	17132	4	US-09-949-016-15361	Sequence 15361, A
c 735	78.6	2.8	137394	4	US-09-949-016-13872	Sequence 13872, A	c 808	77.2	2.7	24150	4	US-09-949-016-12438	Sequence 12438, A
c 736	78.6	2.8	137743	4	US-09-949-016-12178	Sequence 12178, A	c 809	77.2	2.7	300598	4	US-09-949-016-11868	Sequence 11868, A
c 737	78.4	2.8	601	4	US-09-949-016-127893	Sequence 127893, A	c 810	77.2	2.7	302604	4	US-09-949-016-14589	Sequence 14589, A
c 738	78.4	2.8	601	4	US-09-949-016-127894	Sequence 127894, A	c 811	77.2	2.7	302604	4	US-09-949-016-14589	Sequence 14589, A
c 739	78.4	2.8	601	4	US-09-949-016-128230	Sequence 128230, A	c 812	77.2	2.7	304533	4	US-09-949-016-15371	Sequence 15371, A
c 740	78.4	2.8	601	4	US-09-949-016-128231	Sequence 128231, A	c 813	77.2	2.7	304533	4	US-09-949-016-15372	Sequence 15372, A
c 741	78.4	2.8	731	1	US-08-451-405A-2	Sequence 2, Appli	c 814	77.2	2.7	308362	4	US-09-949-016-17119	Sequence 17119, A
c 742	78.4	2.8	960	3	US-09-248-335-57	Sequence 57, Appl	c 815	77	2.7	77	4	US-08-956-171E-2883	Sequence 2883, Ap
c 743	78.4	2.8	1147	1	US-08-665-716-1	Sequence 1, Appli	c 816	77	2.7	77	4	US-08-781-966A-2883	Sequence 2883, Ap
c 744	78.4	2.8	24634	4	US-09-270-767-12063	Sequence 12063, A	c 817	77	2.7	552	4	US-09-461-325-111	Sequence 111, App
c 745	78.4	2.8	3450	4	US-09-949-016-15141	Sequence 15141, A	c 818	77	2.7	552	4	US-10-012-542-111	Sequence 111, App
c 746	78.2	2.7	1292	4	US-09-270-767-12238	Sequence 12238, A	c 819	77	2.7	552	4	US-10-115-123-111	Sequence 111, App
c 747	78.2	2.7	1740	4	US-09-709-103-45	Sequence 45, Appl	c 820	77	2.7	572	3	US-09-342-653-5	Sequence 5, Appli
c 748	78.2	2.7	1740	4	US-09-439-410A-45	Sequence 45, Appl	c 821	77	2.7	601	4	US-09-949-016-17921	Sequence 17921, A
c 749	78.2	2.7	1801	4	US-09-709-103-3	Sequence 3, Appli	c 822	77	2.7	601	4	US-09-949-016-41811	Sequence 41811, A
c 750	78.2	2.7	1801	4	US-09-439-410A-3	Sequence 3, Appli	c 823	77	2.7	1296	4	US-09-461-325-29	Sequence 29, Appl
c 751	78.2	2.7	2445	6	5215909-9	Patent No. 5215909	c 824	77	2.7	1296	4	US-10-012-542-29	Sequence 29, Appl
c 752	78.2	2.7	2445	6	5215909-9	Patent No. 5215909	c 825	77	2.7	1296	4	US-10-115-123-29	Sequence 29, Appl
c 753	78	2.7	78	4	US-09-621-976-14824	Sequence 14824, A	c 826	77	2.7	1872	3	US-09-291-923-27	Sequence 27, Appl
c 754	78	2.7	78	4	US-09-621-976-15092	Sequence 15092, A	c 827	77	2.7	3581	2	US-09-291-923-27	Sequence 27, Appl
c 755	78	2.7	601	4	US-09-949-016-45912	Sequence 45912, A	c 828	77	2.7	8642	4	US-08-738-349-1	Sequence 1, Appli
c 756	78	2.7	601	4	US-09-949-016-45913	Sequence 45913, A	c 829	77	2.7	74177	4	US-10-023-907-2	Sequence 2, Appli
c 757	78	2.7	30337	4	US-09-949-016-13053	Sequence 13053, A	c 830	77	2.7	74177	4	US-09-949-016-17388	Sequence 17388, A

831	76.8	2.7	259	4	US-09-621-976-16294	Sequence 16294, A	904	75.8	2.7	250	4	US-09-621-976-18893	Sequence 18893, A
c 832	76.8	2.7	601	4	US-09-949-016-127892	Sequence 127892, A	905	75.8	2.7	320	4	US-09-621-976-16056	Sequence 16056, A
c 833	76.8	2.7	601	4	US-09-949-016-128229	Sequence 128229, A	c 906	75.8	2.7	601	4	US-09-949-016-132559	Sequence 132559, A
834	76.8	2.7	1518	4	US-09-614-912-1191	Sequence 191, App	c 907	75.8	2.7	601	4	US-09-949-016-132561	Sequence 132561, A
835	76.8	2.7	4949	3	US-09-138-024-22	Sequence 22, Appl	c 908	75.8	2.7	601	4	US-09-949-016-155362	Sequence 155362, A
836	76.8	2.7	4949	3	US-09-404-066-22	Sequence 22, Appl	c 909	75.8	2.7	601	4	US-09-949-016-155364	Sequence 155364, A
837	76.8	2.7	4949	3	US-09-573-322-22	Sequence 22, Appl	910	75.8	2.7	931	4	US-09-482-273-31	Sequence 31, Appl
c 838	76.8	2.7	1664976	4	US-08-916-421B-1	Sequence 1, Appl	911	75.8	2.7	7286	3	US-09-331-581-3	Sequence 14, Appl
c 839	76.8	2.7	1664976	4	US-09-692-570-1	Sequence 1, Appl	912	75.8	2.7	7938	3	US-09-331-581-14	Sequence 14, Appl
840	76.6	2.7	232	4	US-09-621-976-17701	Sequence 17701, A	913	75.8	2.7	53337	4	US-09-949-016-12500	Sequence 12500, A
841	76.6	2.7	451	4	US-09-270-767-2429	Sequence 2429, Ap	914	75.8	2.7	53337	4	US-09-949-016-16092	Sequence 16092, A
842	76.6	2.7	451	4	US-09-270-767-17711	Sequence 17711, A	915	75.8	2.7	113100	4	US-09-949-016-12245	Sequence 12245, A
843	76.6	2.7	588	4	US-09-205-258-64	Sequence 64, Appl	916	75.8	2.7	462589	4	US-09-949-016-12900	Sequence 12900, A
844	76.6	2.7	601	4	US-09-949-016-20852	Sequence 20852, A	917	75.8	2.7	476044	4	US-09-949-016-12412	Sequence 12412, A
845	76.6	2.7	601	4	US-09-949-016-110199	Sequence 110199, A	918	75.6	2.7	100	4	US-09-621-976-13412	Sequence 12774, A
846	76.6	2.7	675	4	US-09-621-976-2461	Sequence 2461, Ap	c 919	75.6	2.7	601	4	US-09-949-016-21578	Sequence 21578, A
847	76.6	2.7	1279	3	US-09-248-335-25	Sequence 25, Appl	c 920	75.6	2.7	601	4	US-09-949-016-21579	Sequence 21579, A
c 848	76.6	2.7	1467	4	US-09-949-016-2761	Sequence 2761, Ap	c 921	75.6	2.7	601	4	US-09-949-016-130330	Sequence 130330, A
849	76.6	2.7	1558	1	US-08-467-607-2	Sequence 2, Appl	c 922	75.6	2.7	601	4	US-09-949-016-130331	Sequence 130331, A
850	76.6	2.7	1558	2	US-08-469-362-2	Sequence 2, Appl	c 923	75.6	2.7	601	4	US-09-949-016-155055	Sequence 155055, A
851	76.6	2.7	1558	2	US-08-850-392-2	Sequence 2, Appl	924	75.6	2.7	601	4	US-09-949-016-161729	Sequence 161729, A
c 852	76.6	2.7	17331	4	US-09-949-016-14503	Sequence 14503, A	925	75.6	2.7	2908	4	US-09-904-615-35	Sequence 35, Appl
c 853	76.6	2.7	24040	4	US-09-949-016-12118	Sequence 12118, A	926	75.6	2.7	3848	3	US-09-112-096-28	Sequence 28, Appl
c 854	76.6	2.7	253345	4	US-09-949-016-13656	Sequence 12556, A	927	75.6	2.7	4285	3	US-09-410-464-1	Sequence 1, Appl
c 855	76.6	2.7	253364	4	US-09-949-016-13639	Sequence 13639, A	c 928	75.6	2.7	4600	4	US-09-702-705-1797	Sequence 1797, Ap
856	76.4	2.7	84	1	US-08-664-596B-3	Sequence 3, Appl	c 929	75.6	2.7	4600	4	US-09-736-457-1797	Sequence 1797, Ap
857	76.4	2.7	84	1	US-08-738-367-3	Sequence 3, Appl	c 930	75.6	2.7	4600	4	US-09-671-325-1797	Sequence 1797, Ap
858	76.4	2.7	159	4	US-09-621-976-17448	Sequence 17448, A	931	75.6	2.7	5668	3	US-09-112-096-14	Sequence 14, Appl
859	76.4	2.7	1046	1	US-08-361-467B-4	Sequence 4, Appl	932	75.6	2.7	5668	4	US-09-636-215-777	Sequence 777, App
860	76.4	2.7	1046	1	US-08-484-332C-4	Sequence 4, Appl	933	75.6	2.7	5668	4	US-09-685-166A-777	Sequence 777, App
861	76.4	2.7	1544	4	US-09-187-999-14	Sequence 14, Appl	934	75.6	2.7	5668	4	US-09-679-426-777	Sequence 777, App
862	76.4	2.7	1546	4	US-09-901-151-1	Sequence 1, Appl	935	75.6	2.7	5668	4	US-09-759-143-777	Sequence 777, App
863	76.2	2.7	348	4	US-09-621-976-16137	Sequence 16137, A	936	75.6	2.7	87617	4	US-09-651-236-777	Sequence 777, App
864	76.2	2.7	601	4	US-09-949-016-102626	Sequence 102626, A	937	75.6	2.7	87617	4	US-09-949-016-16551	Sequence 16551, A
865	76.2	2.7	601	4	US-09-949-016-102738	Sequence 102738, A	c 938	75.6	2.7	92227	4	US-09-949-016-11929	Sequence 11929, A
866	76.2	2.7	601	4	US-09-949-016-193087	Sequence 193087, A	c 939	75.6	2.7	92227	4	US-09-949-016-15421	Sequence 15421, A
867	76.2	2.7	601	4	US-09-949-016-193088	Sequence 193088, A	c 940	75.6	2.7	124110	4	US-09-949-016-13353	Sequence 13353, A
868	76.2	2.7	601	4	US-09-949-016-193180	Sequence 193180, A	c 941	75.6	2.7	130724	4	US-09-949-016-13753	Sequence 13753, A
869	76.2	2.7	601	4	US-09-949-016-193181	Sequence 193181, A	c 942	75.6	2.7	144922	4	US-09-949-016-15890	Sequence 15890, A
870	76.2	2.7	601	4	US-09-949-016-193273	Sequence 193273, A	c 943	75.6	2.7	152331	3	US-09-128-155-16	Sequence 16, Appl
871	76.2	2.7	601	4	US-09-949-016-193274	Sequence 193274, A	c 944	75.6	2.7	176373	3	US-09-128-155-17	Sequence 17, Appl
872	76.2	2.7	601	4	US-09-949-016-193366	Sequence 193366, A	945	75.4	2.6	98	4	US-09-621-976-11744	Sequence 11744, A
873	76.2	2.7	601	4	US-09-949-016-193367	Sequence 193367, A	c 946	75.4	2.6	257	2	US-08-520-676A-24	Sequence 24, Appl
874	76.2	2.7	1476	4	US-09-248-796A-5437	Sequence 5437, Ap	c 947	75.4	2.6	257	3	US-08-897-126-24	Sequence 24, Appl
875	76.2	2.7	86213	4	US-09-949-016-17240	Sequence 17240, A	c 948	75.4	2.6	25458	4	US-09-949-016-13986	Sequence 13986, A
876	76.2	2.7	86213	4	US-09-949-016-17241	Sequence 17241, A	c 949	75.4	2.6	41863	4	US-09-949-016-14948	Sequence 14948, A
877	76.2	2.7	86213	4	US-09-949-016-17242	Sequence 17242, A	c 950	75.4	2.6	129415	4	US-09-949-016-16997	Sequence 16997, A
878	76.2	2.7	86213	4	US-09-949-016-17243	Sequence 17243, A	c 951	75.4	2.6	312474	4	US-09-949-016-17434	Sequence 17434, A
c 879	76.2	2.7	133559	4	US-09-949-016-15845	Sequence 15845, A	952	75.2	2.6	8220	2	US-08-568-459A-11	Sequence 11, Appl
880	76.2	2.7	174020	4	US-09-949-016-12610	Sequence 12610, A	953	75.2	2.6	8220	3	US-09-210-288-11	Sequence 11, Appl
881	76.2	2.7	174030	4	US-09-949-016-13880	Sequence 13880, A	954	75.2	2.6	8220	3	US-09-210-288-11	Sequence 11, Appl
c 882	76.2	2.7	191433	4	US-09-949-016-16144	Sequence 16144, A	955	75	2.6	75	4	US-09-621-976-14892	Sequence 14892, A
c 883	76.2	2.7	678533	4	US-09-949-016-1577	Sequence 1577, A	956	75	2.6	77	4	US-09-621-976-14176	Sequence 14176, A
c 884	76.2	2.7	678533	4	US-09-949-016-14578	Sequence 14578, A	957	75	2.6	601	4	US-09-949-016-20851	Sequence 20851, A
885	76	2.7	76	4	US-09-621-976-14831	Sequence 14831, A	958	75	2.6	601	4	US-09-949-016-20853	Sequence 20853, A
886	76	2.7	76	4	US-09-621-976-14915	Sequence 14915, A	959	75	2.6	601	4	US-09-949-016-20854	Sequence 20854, A
887	76	2.7	109	4	US-09-621-976-14592	Sequence 14592, A	960	75	2.6	601	4	US-09-949-016-20855	Sequence 20855, A
888	76	2.7	415	3	US-09-018-584A-18	Sequence 18, Appl	961	75	2.6	601	4	US-09-949-016-20856	Sequence 20856, A
889	76	2.7	415	4	US-09-784-421-18	Sequence 18, Appl	962	75	2.6	601	4	US-09-949-016-65454	Sequence 65454, A
c 890	76	2.7	601	4	US-09-949-016-179689	Sequence 179689, A	963	75	2.6	601	4	US-09-949-016-110198	Sequence 110198, A
c 891	76	2.7	601	4	US-09-949-016-179691	Sequence 179691, A	964	75	2.6	601	4	US-09-949-016-110200	Sequence 110200, A
892	76	2.7	1298	3	US-08-971-089-1	Sequence 1, Appl	965	75	2.6	601	4	US-09-949-016-110201	Sequence 110201, A
c 893	76	2.7	2239	4	US-10-380-105-7	Sequence 7, Appl	966	75	2.6	601	4	US-09-949-016-110202	Sequence 110202, A
894	76	2.7	13184	4	US-09-949-016-16573	Sequence 16573, A	967	75	2.6	601	4	US-09-949-016-110203	Sequence 110203, A
c 895	76	2.7	23222	4	US-09-949-016-15949	Sequence 15949, A	c 968	75	2.6	601	4	US-09-949-016-149960	Sequence 149960, A
c 896	76	2.7	25922	4	US-09-949-016-11874	Sequence 11874, A	969	75	2.6	746	3	US-09-013-810-1	Sequence 1, Appl
c 897	76	2.7	35064	4	US-09-949-016-12778	Sequence 12778, A	970	75	2.6	3200	1	US-08-444-405-1	Sequence 1, Appl
c 898	76	2.7	35065	4	US-09-949-016-13196	Sequence 13196, A	971	75	2.6	3200	1	US-08-384-850-1	Sequence 1, Appl
c 899	76	2.7	40408	4	US-09-949-016-16331	Sequence 16331, A	972	75	2.6	14082	4	US-09-949-016-11898	Sequence 11898, A
900	75.8	2.7	62072	4	US-09-949-016-16331	Sequence 16331, A	973	75	2.6	14082	4	US-09-949-016-14783	Sequence 14783, A
901	75.8	2.7	165	4	US-09-621-976-8127	Sequence 8127, Ap	c 974	75	2.6	85675	4	US-09-949-016-12333	Sequence 12333, A
902	75.8	2.7	208	1	US-08-686-878A-37	Sequence 37, Appl	c 975	75	2.6	85675	4	US-09-949-016-15956	Sequence 15956, A
903	75.8	2.7	208	3	US-09-175-928-37	Sequence 37, Appl	c 976	75	2.6	87648	4	US-09-949-016-13655	Sequence 13655, A

977	74.8	2.6	351	4	US-09-621-976-16140	Sequence 16140, A	1050	73.8	2.6	1419	4	US-09-270-767-13127	Sequence 13127, A
c 978	74.8	2.6	80411	4	US-09-949-016-15777	Sequence 15777, A	1051	73.8	2.6	28438	4	US-09-820-790B-3	Sequence 3, Appli
c 979	74.8	2.6	100836	4	US-09-949-016-12871	Sequence 12871, A	1052	73.8	2.6	96327	4	US-09-949-016-16541	Sequence 16541, A
c 980	74.8	2.6	100837	4	US-09-949-016-17063	Sequence 17063, A	1053	73.8	2.6	194937	4	US-09-949-016-17032	Sequence 17032, A
981	74.8	2.6	225127	4	US-09-949-016-16480	Sequence 16480, A	1054	73.6	2.6	194937	4	US-09-949-016-17033	Sequence 17033, A
982	74.6	2.6	258	4	US-09-621-976-15353	Sequence 15353, A	1055	73.6	2.6	132	4	US-09-621-976-13468	Sequence 13468, A
c 983	74.6	2.6	318	3	US-09-134-001C-2112	Sequence 2112, Ap	1056	73.6	2.6	299	4	US-09-621-976-10211	Sequence 10211, A
c 984	74.6	2.6	601	4	US-09-949-016-47327	Sequence 47327, A	1057	73.6	2.6	334	2	US-08-623-906A-9	Sequence 9, Appli
985	74.6	2.6	760	4	US-09-205-258-232	Sequence 232, App	1058	73.6	2.6	601	4	US-09-949-016-79787	Sequence 79787, A
c 986	74.6	2.6	986	4	US-09-328-475C-141	Sequence 141, App	1059	73.6	2.6	601	4	US-09-949-016-126414	Sequence 126414, A
987	74.6	2.6	2163	4	US-09-710-279-2057	Sequence 2057, Ap	1060	73.6	2.6	1486	4	US-09-461-325-73	Sequence 73, Appl
c 988	74.6	2.6	2218	4	US-09-134-001C-2131	Sequence 2131, Ap	1061	73.6	2.6	1486	4	US-10-012-542-73	Sequence 73, Appl
989	74.6	2.6	3792	4	US-09-205-258-103	Sequence 103, App	1062	73.6	2.6	1486	4	US-10-115-123-73	Sequence 73, Appl
c 990	74.6	2.6	7992	4	US-09-710-279-3396	Sequence 3396, Ap	1063	73.6	2.6	96202	4	US-09-949-016-16433	Sequence 16433, A
c 991	74.6	2.6	7998	4	US-09-710-279-3962	Sequence 3962, Ap	1064	73.4	2.6	204	4	US-08-621-976-1323	Sequence 1323, Ap
c 992	74.6	2.6	8888	4	US-09-539-601-10	Sequence 10, Appl	1065	73.4	2.6	227	2	US-08-520-678A-28	Sequence 28, Appl
c 993	74.6	2.6	8001	4	US-09-539-601-7	Sequence 7, Appli	1066	73.4	2.6	227	3	US-08-897-126-28	Sequence 28, Appl
c 994	74.6	2.6	8001	4	US-09-539-601-16	Sequence 16, Appl	1067	73.4	2.6	601	4	US-09-949-016-25850	Sequence 25850, A
c 995	74.6	2.6	8001	4	US-09-539-601-22	Sequence 22, Appl	1068	73.4	2.6	601	4	US-09-949-016-55172	Sequence 55172, A
c 996	74.6	2.6	8001	4	US-09-539-601-28	Sequence 28, Appl	1069	73.4	2.6	4456	3	US-09-095-443-1	Sequence 1, Appli
c 997	74.6	2.6	8637	4	US-09-539-601-4	Sequence 4, Appli	1070	73.4	2.6	6755	3	US-08-931-939-4	Sequence 4, Appli
c 998	74.6	2.6	8638	4	US-10-029-907-7	Sequence 7, Appli	1071	73.4	2.6	8648	4	US-10-029-907-5	Sequence 5, Appli
c 999	74.6	2.6	8638	4	US-10-029-907-24	Sequence 24, Appl	1072	73.4	2.6	22301	4	US-09-949-016-12924	Sequence 12924, A
c1000	74.6	2.6	8638	4	US-10-029-907-25	Sequence 25, Appl	1073	73.4	2.6	23465	4	US-09-949-016-12487	Sequence 12487, A
c1001	74.6	2.6	8639	4	US-10-029-907-1	Sequence 1, Appli	1074	73.4	2.6	118868	4	US-09-949-016-15746	Sequence 15746, A
c1002	74.6	2.6	8649	4	US-09-539-601-13	Sequence 13, Appl	1075	73.4	2.6	152331	3	US-09-128-155-16	Sequence 16, Appl
c1003	74.6	2.6	11076	4	US-09-539-601-1	Sequence 1, Appli	1076	73.2	2.6	250	4	US-09-621-976-18363	Sequence 18363, A
c1004	74.6	2.6	11076	4	US-09-539-601-19	Sequence 19, Appl	1077	73.2	2.6	1702	4	US-09-799-451-574	Sequence 574, App
c1005	74.6	2.6	11076	4	US-09-539-601-25	Sequence 25, Appl	1078	73.2	2.6	2329	4	US-09-800-729-11	Sequence 11, Appl
c1006	74.6	2.6	11076	4	US-09-539-601-31	Sequence 31, Appl	1079	73.2	2.6	6065	4	US-09-800-729-35	Sequence 35, Appl
c1007	74.6	2.6	11338	4	US-09-949-016-1583	Sequence 1583, A	1080	73.2	2.6	13146	2	US-08-724-354D-3	Sequence 3, Appli
c1008	74.6	2.6	21593	4	US-09-949-016-15979	Sequence 15979, A	1081	73.2	2.6	8850	4	US-09-270-984A-3	Sequence 3, Appli
c1009	74.6	2.6	41743	4	US-09-949-016-13796	Sequence 13796, A	1082	73.2	2.6	8850	4	US-09-949-016-13424	Sequence 13424, A
c1010	74.6	2.6	57267	4	US-09-949-016-11899	Sequence 11899, A	1083	73.2	2.6	92155	4	US-09-949-016-17484	Sequence 17484, A
c1011	74.6	2.6	96878	4	US-09-949-016-12551	Sequence 12551, A	1084	73.2	2.6	143550	4	US-09-949-016-14143	Sequence 14143, A
c1012	74.6	2.6	101015	4	US-09-949-016-16981	Sequence 16981, A	1085	73.2	2.6	143550	4	US-09-949-016-15947	Sequence 15947, A
c1013	74.6	2.6	422592	4	US-09-949-016-14182	Sequence 14182, A	1086	73.2	2.6	149543	4	US-09-949-016-14083	Sequence 14083, A
c1014	74.4	2.6	378	4	US-09-248-796A-11672	Sequence 11672, A	1087	73.2	2.6	199471	4	US-09-949-016-14083	Sequence 14083, A
c1015	74.4	2.6	1123	3	US-09-152-060-15	Sequence 15, Appl	1088	73	2.6	73	4	US-09-621-976-14963	Sequence 29, Appl
c1016	74.4	2.6	1949	4	US-09-270-767-30986	Sequence 30986, A	1089	73	2.6	271	2	US-08-731-272A-29	Sequence 29, Appl
c1017	74.4	2.6	3290	4	US-09-270-767-14750	Sequence 14750, A	1090	73	2.6	601	4	US-09-949-016-201490	Sequence 201490, A
c1018	74.4	2.6	21862	4	US-09-949-016-17319	Sequence 17319, A	1091	73	2.6	1069	4	US-09-949-016-201491	Sequence 201491, A
c1019	74.4	2.6	49440	4	US-09-949-016-14150	Sequence 14150, A	1092	73	2.6	1709	4	US-09-205-258-74	Sequence 74, Appl
c1020	74.2	2.6	321	2	US-08-520-678A-23	Sequence 23, Appl	1093	73	2.6	2028	4	US-09-426-783-9	Sequence 9, Appli
c1021	74.2	2.6	321	3	US-08-897-126-23	Sequence 23, Appl	1094	73	2.6	2065	3	US-09-370-473-5	Sequence 5, Appli
c1022	74.2	2.6	472	4	US-09-270-767-12212	Sequence 12212, A	1095	73	2.6	2837	2	US-08-993-228-11	Sequence 11, Appl
c1023	74.2	2.6	601	4	US-09-949-016-32560	Sequence 32560, A	1096	73	2.6	4880	3	US-09-392-277-1	Sequence 1, Appli
c1024	74.2	2.6	601	4	US-09-949-016-60625	Sequence 60625, A	1097	73	2.6	4880	3	US-09-392-277-1	Sequence 1, Appli
c1025	74.2	2.6	601	4	US-09-949-016-155363	Sequence 155363, A	1098	73	2.6	4880	3	US-09-258-000-1	Sequence 1, Appli
c1026	74.2	2.6	1214	4	US-09-780-717-28	Sequence 28, Appl	1099	73	2.6	5125	3	US-09-031-563-4	Sequence 4, Appli
c1027	74.2	2.6	2083	4	US-09-716-129-41	Sequence 41, Appl	1100	73	2.6	5125	3	US-09-392-277-4	Sequence 4, Appli
c1028	74.2	2.6	102409	4	US-09-949-016-15148	Sequence 15148, A	1101	73	2.6	5125	3	US-09-258-000-4	Sequence 4, Appli
c1029	74.2	2.6	360470	4	US-09-949-016-13173	Sequence 13173, A	1102	73	2.6	16664	4	US-09-949-016-13308	Sequence 13308, A
c1030	74	2.6	347	4	US-09-621-976-16136	Sequence 16136, A	1103	73	2.6	86639	4	US-09-949-016-17397	Sequence 17397, A
c1031	74	2.6	601	4	US-09-949-016-21580	Sequence 21580, A	1104	73	2.6	117838	4	US-09-949-016-17595	Sequence 17595, A
c1032	74	2.6	601	4	US-09-949-016-126416	Sequence 126416, A	1105	73	2.6	138049	4	US-09-949-016-17030	Sequence 17030, A
c1033	74	2.6	601	4	US-09-949-016-127057	Sequence 127057, A	1106	73	2.6	146095	4	US-09-949-016-12872	Sequence 12872, A
c1034	74	2.6	601	4	US-09-949-016-130332	Sequence 130332, A	1107	73	2.6	146095	4	US-09-949-016-13239	Sequence 13239, A
c1035	74	2.6	601	4	US-09-949-016-173109	Sequence 173109, A	1108	73	2.6	186959	4	US-09-949-016-13125	Sequence 13125, A
c1036	74	2.6	1206	3	US-09-465-558-53	Sequence 53, Appl	1109	73	2.6	190078	4	US-09-949-016-12707	Sequence 12707, A
c1037	74	2.6	1637	4	US-09-205-258-178	Sequence 178, App	1110	73	2.6	202007	4	US-09-949-016-17026	Sequence 17026, A
c1038	74	2.6	4055	4	US-09-620-312D-706	Sequence 706, App	1111	73	2.6	190078	4	US-09-734-674-3	Sequence 3, Appli
c1039	74	2.6	8100	4	US-09-554-337-4	Sequence 4, Appli	1112	73	2.6	245286	4	US-09-949-016-15497	Sequence 15497, A
c1040	74	2.6	11517	1	US-07-920-281C-1	Sequence 1, Appli	1113	73	2.6	283538	4	US-09-949-016-13506	Sequence 13506, A
c1041	74	2.6	11517	3	US-08-466-277-1	Sequence 1, Appli	1114	73	2.6	413	3	US-09-227-357-71	Sequence 71, Appl
c1042	74	2.6	11517	3	US-09-688-842-1	Sequence 1, Appli	1115	72.8	2.6	510	4	US-09-248-796A-13735	Sequence 13735, A
c1043	74	2.6	15538	4	US-09-554-337-1	Sequence 1, Appli	1116	72.8	2.6	601	4	US-09-949-016-127054	Sequence 127054, A
c1044	74	2.6	20229	4	US-09-949-016-16549	Sequence 16549, A	1117	72.8	2.6	601	4	US-09-949-016-127056	Sequence 127056, A
c1045	74	2.6	41062	4	US-09-949-016-12761	Sequence 12761, A	1118	72.8	2.6	601	4	US-09-949-016-127058	Sequence 127058, A
c1046	74	2.6	41062	4	US-09-949-016-16796	Sequence 16796, A	1119	72.8	2.6	601	4	US-09-949-016-127059	Sequence 127059, A
c1047	73.8	2.6	601	4	US-09-949-016-48520	Sequence 48520, A	1120	72.8	2.6	601	4	US-09-949-016-127060	Sequence 127060, A
c1048	73.8	2.6	601	4	US-09-949-016-184917	Sequence 184917, A	1121	72.8	2.6	601	4	US-09-949-016-127061	Sequence 127061, A
c1049	73.8	2.6	601	4	US-09-949-016-185072	Sequence 185072, A	1122	72.8	2.6	601	4	US-09-949-016-127061	Sequence 127061, A

c1123	72.8	2.6	601	4	US-09-949-016-149677	Sequence 149677,	1196	72.2	2.5	601	4	US-09-949-016-55173	Sequence 55173, A
1124	72.8	2.6	601	4	US-09-949-016-184898	Sequence 184898,	1197	72.2	2.5	601	4	US-09-949-016-55174	Sequence 55174, A
1125	72.8	2.6	601	4	US-09-949-016-185053	Sequence 185053,	1198	72.2	2.5	601	4	US-09-949-016-122967	Sequence 122967, A
1126	72.8	2.6	1534	1	US-08-300-903A-6	Sequence 6, Appli	1199	72.2	2.5	601	4	US-09-949-016-123061	Sequence 123061, A
1127	72.8	2.6	1534	4	US-08-988-197-6	Sequence 6, Appli	1200	72.2	2.5	601	4	US-09-949-016-123155	Sequence 123155, A
1128	72.8	2.6	1534	4	US-10-385-072-6	Sequence 6, Appli	1201	72.2	2.5	601	4	US-09-949-016-123249	Sequence 123249, A
1129	72.8	2.6	1976	4	US-09-920-759-10	Sequence 10, Appli	1202	72.2	2.5	601	4	US-09-949-016-123343	Sequence 123343, A
1130	72.8	2.6	2291	4	US-09-220-132-114	Sequence 11, App	1203	72.2	2.5	601	4	US-09-949-016-123385	Sequence 123385, A
1131	72.8	2.6	2291	4	US-09-814-915A-95	Sequence 95, Appl	1204	72.2	2.5	601	4	US-09-949-016-123427	Sequence 123427, A
1132	72.8	2.6	8920	2	US-08-446-855A-1	Sequence 1, Appli	1205	72.2	2.5	601	4	US-09-949-016-123469	Sequence 123469, A
1133	72.8	2.6	8920	3	US-09-150-741-1	Sequence 1, Appli	1206	72.2	2.5	601	4	US-09-949-016-123511	Sequence 123511, A
1134	72.8	2.6	14554	4	US-09-949-016-15908	Sequence 15908, A	1207	72.2	2.5	601	4	US-09-949-016-123553	Sequence 123553, A
1135	72.8	2.6	23319	4	US-09-949-016-18407	Sequence 14007, A	1208	72.2	2.5	601	4	US-09-949-016-123595	Sequence 123595, A
c1136	72.8	2.6	53336	4	US-09-949-016-12500	Sequence 12500, A	1209	72.2	2.5	601	4	US-09-949-016-123637	Sequence 123637, A
c1137	72.8	2.6	53337	4	US-09-949-016-16092	Sequence 16092, A	1210	72.2	2.5	601	4	US-09-949-016-123679	Sequence 123679, A
c1138	72.8	2.6	56326	4	US-09-949-016-16468	Sequence 16468, A	1211	72.2	2.5	601	4	US-09-949-016-123721	Sequence 123721, A
1139	72.8	2.6	67429	4	US-09-949-016-11804	Sequence 11804, A	1212	72.2	2.5	601	4	US-09-949-016-123763	Sequence 123763, A
1140	72.8	2.6	71119	4	US-09-949-016-13358	Sequence 13358, A	c1213	72.2	2.5	974	4	US-09-270-767-14699	Sequence 14699, A
c1141	72.8	2.6	89892	4	US-09-949-016-13667	Sequence 13667, A	1214	72.2	2.5	1662	4	US-09-248-796A-3485	Sequence 2485, Ap
1142	72.8	2.6	312474	4	US-09-949-016-17434	Sequence 17434, A	1215	72.2	2.5	3238	3	US-08-123-934A-5	Sequence 5, Appli
1143	72.6	2.6	73	4	US-09-621-976-14729	Sequence 14729, A	1216	72.2	2.5	3238	4	PCT-US94-10080-5	Sequence 5, Appli
1144	72.6	2.6	601	4	US-09-949-016-48516	Sequence 48516, A	1217	72.2	2.5	3238	5	US-09-949-016-13342	Sequence 13342, A
1145	72.6	2.6	601	4	US-09-949-016-48521	Sequence 48521, A	1218	72.2	2.5	6029	4	US-09-949-016-13342	Sequence 13342, A
c1146	72.6	2.6	601	4	US-09-949-016-13348	Sequence 13348, Ap	1219	72.2	2.5	13093	4	US-09-621-976-10145	Sequence 10145, A
1147	72.6	2.6	787	4	US-09-621-976-1878	Sequence 1878, Ap	1220	72	2.5	72	4	US-09-621-976-10145	Sequence 10145, A
1148	72.6	2.6	2481	2	US-08-630-118A-1	Sequence 1, Appli	1221	72	2.5	72	4	US-09-621-976-14815	Sequence 14815, A
1149	72.6	2.6	2481	2	US-08-838-399-1	Sequence 1, Appli	1222	72	2.5	72	4	US-09-621-976-14842	Sequence 14842, A
1150	72.6	2.6	2481	3	US-09-325-839-1	Sequence 1, Appli	c1223	72	2.5	101	3	US-09-404-879A-293	Sequence 293, App
1151	72.6	2.6	2481	3	US-09-327-035-1	Sequence 1, Appli	c1224	72	2.5	101	4	US-09-338-933-293	Sequence 293, App
1152	72.6	2.6	2604	2	US-08-630-118A-3	Sequence 3, Appli	c1225	72	2.5	101	4	US-09-215-681-293	Sequence 293, App
1153	72.6	2.6	2604	2	US-08-838-399-3	Sequence 3, Appli	c1226	72	2.5	101	4	US-09-216-003A-293	Sequence 293, App
1154	72.6	2.6	2604	3	US-09-235-839-3	Sequence 3, Appli	c1227	72	2.5	101	4	US-09-667-857-293	Sequence 293, App
1155	72.6	2.6	2604	3	US-09-327-035-3	Sequence 3, Appli	1228	72	2.5	183	4	US-09-621-976-13606	Sequence 13606, A
1156	72.6	2.6	34372	4	US-09-949-016-13098	Sequence 13098, A	1229	72	2.5	358	4	US-09-621-976-997	Sequence 927, App
1157	72.6	2.6	34875	4	US-09-949-016-13099	Sequence 13099, A	c1230	72	2.5	509	3	US-09-030-607-202	Sequence 202, App
c1158	72.6	2.6	58768	4	US-09-949-016-13175	Sequence 13175, A	c1231	72	2.5	509	3	US-09-433-313-202	Sequence 202, App
c1159	72.6	2.6	152070	4	US-09-949-016-15402	Sequence 15402, A	c1232	72	2.5	509	3	US-09-352-616A-202	Sequence 202, App
c1160	72.6	2.6	236474	4	US-09-949-016-13418	Sequence 13418, A	c1233	72	2.5	509	3	US-09-232-149A-202	Sequence 202, App
1161	72.4	2.5	601	4	US-09-949-016-79789	Sequence 79789, A	c1234	72	2.5	509	4	US-09-159-812-202	Sequence 202, App
c1162	72.4	2.5	601	4	US-09-949-016-89635	Sequence 89635, A	c1235	72	2.5	509	4	US-09-636-215-202	Sequence 202, App
c1163	72.4	2.5	601	4	US-09-949-016-89636	Sequence 89636, A	c1236	72	2.5	509	4	US-09-685-166A-202	Sequence 202, App
c1164	72.4	2.5	601	4	US-09-949-016-126417	Sequence 126417, A	c1237	72	2.5	509	4	US-09-115-453-202	Sequence 202, App
c1165	72.4	2.5	601	4	US-09-949-016-127053	Sequence 127053, A	c1238	72	2.5	509	4	US-09-688-489-202	Sequence 202, App
c1166	72.4	2.5	601	4	US-09-949-016-127055	Sequence 127055, A	c1239	72	2.5	509	4	US-09-679-426-202	Sequence 202, App
1167	72.4	2.5	601	4	US-09-949-016-161232	Sequence 161232, A	c1240	72	2.5	509	4	US-09-759-143-202	Sequence 202, App
c1168	72.4	2.5	601	4	US-09-949-016-173108	Sequence 173108, A	c1241	72	2.5	509	4	US-09-651-236-202	Sequence 202, App
1169	72.4	2.5	601	4	US-09-949-016-184918	Sequence 184918, A	1242	72	2.5	601	4	US-09-949-016-32214	Sequence 32214, A
1170	72.4	2.5	601	4	US-09-949-016-185073	Sequence 185073, A	1243	72	2.5	601	4	US-09-949-016-32215	Sequence 32215, A
1171	72.4	2.5	991	3	US-08-924-747-25	Sequence 25, Appli	1244	72	2.5	601	4	US-09-949-016-32216	Sequence 32216, A
1172	72.4	2.5	991	3	US-09-247-373B-25	Sequence 25, Appli	1245	72	2.5	601	4	US-09-949-016-108014	Sequence 108014, A
1173	72.4	2.5	991	3	US-09-296-715-25	Sequence 25, Appli	1246	72	2.5	601	4	US-09-949-016-108015	Sequence 108015, A
1174	72.4	2.5	1398	4	US-09-270-767-4082	Sequence 4082, Ap	1247	72	2.5	601	4	US-09-949-016-108016	Sequence 108016, A
1175	72.4	2.5	1398	4	US-09-270-767-13364	Sequence 13364, A	c1248	72	2.5	601	4	US-09-949-016-126415	Sequence 126415, A
1176	72.4	2.5	2187	3	US-09-127-219B-2	Sequence 2, Appli	1249	72	2.5	2158	1	US-07-602-608-1	Sequence 1, Appli
1177	72.4	2.5	15575	4	US-09-949-016-12634	Sequence 12634, A	1250	72	2.5	2158	1	US-08-261-578-1	Sequence 1, Appli
1178	72.4	2.5	15575	4	US-09-949-016-16568	Sequence 16568, A	1251	72	2.5	13118	4	US-09-949-016-14721	Sequence 14721, A
1179	72.4	2.5	20721	4	US-09-949-016-16257	Sequence 16257, A	1252	72	2.5	13648	4	US-09-949-016-12470	Sequence 12470, A
c1180	72.4	2.5	23927	4	US-09-949-016-14284	Sequence 14284, A	c1253	72	2.5	63247	4	US-09-949-016-16809	Sequence 16809, A
c1181	72.4	2.5	45484	4	US-09-949-016-12967	Sequence 12967, A	1254	71.8	2.5	146	4	US-09-621-976-16686	Sequence 16686, A
c1182	72.4	2.5	61913	4	US-09-949-016-15338	Sequence 15338, A	1255	71.8	2.5	536	1	US-08-341-568-1	Sequence 1, Appli
c1183	72.4	2.5	61922	4	US-09-949-016-11772	Sequence 11772, A	1256	71.8	2.5	536	2	US-08-911-020-1	Sequence 1, Appli
c1184	72.4	2.5	90472	4	US-09-949-016-14038	Sequence 14038, A	1257	71.8	2.5	601	4	US-09-949-016-122969	Sequence 122969, A
1185	72.2	2.5	146	4	US-09-621-976-16695	Sequence 16695, A	1258	71.8	2.5	601	4	US-09-949-016-123063	Sequence 123063, A
1186	72.2	2.5	243	1	US-07-922-723A-9	Sequence 9, Appli	1259	71.8	2.5	601	4	US-09-949-016-123157	Sequence 123157, A
1187	72.2	2.5	243	1	US-07-799-828C-9	Sequence 9, Appli	1260	71.8	2.5	601	4	US-09-949-016-123251	Sequence 123251, A
1188	72.2	2.5	243	1	US-08-074-275-9	Sequence 9, Appli	1261	71.8	2.5	601	4	US-09-949-016-123345	Sequence 123345, A
1189	72.2	2.5	243	1	US-08-480-366-9	Sequence 9, Appli	1262	71.8	2.5	601	4	US-09-949-016-123387	Sequence 123387, A
1190	72.2	2.5	243	2	US-07-952-277A-9	Sequence 9, Appli	1263	71.8	2.5	601	4	US-09-949-016-123429	Sequence 123429, A
1191	72.2	2.5	601	4	US-09-949-016-25851	Sequence 25851, A	1264	71.8	2.5	601	4	US-09-949-016-123471	Sequence 123471, A
1192	72.2	2.5	601	4	US-09-949-016-25852	Sequence 25852, A	1265	71.8	2.5	601	4	US-09-949-016-123513	Sequence 123513, A
1193	72.2	2.5	601	4	US-09-949-016-48517	Sequence 48517, A	1266	71.8	2.5	601	4	US-09-949-016-123555	Sequence 123555, A
1194	72.2	2.5	601	4	US-09-949-016-48518	Sequence 48518, A	1267	71.8	2.5	601	4	US-09-949-016-123597	Sequence 123597, A
1195	72.2	2.5	601	4	US-09-949-016-48519	Sequence 48519, A	1268	71.8	2.5	601	4	US-09-949-016-123639	Sequence 123639, A

1269	71.8	2.5	601	4	US-09-949-016-123681,	Sequence 123681,	1342	71.4	2.5	278866	4	US-09-949-016-13924	Sequence 13924, A
1270	71.8	2.5	601	4	US-09-949-016-123723	Sequence 123723,	1343	71.4	2.5	278866	4	US-09-949-016-13925	Sequence 13925, A
1271	71.8	2.5	601	4	US-09-949-016-123765	Sequence 123765,	1344	71.4	2.5	278866	4	US-09-949-016-13926	Sequence 13926, A
c1272	71.8	2.5	601	4	US-09-949-016-182882	Sequence 128882,	1345	71.4	2.5	278866	4	US-09-949-016-14699	Sequence 14699, A
1273	71.8	2.5	732	3	US-09-149-476-66	Sequence 66, Appl	1346	71.4	2.5	278866	4	US-09-949-016-14700	Sequence 14700, A
1274	71.8	2.5	1844	4	US-10-003-392-7	Sequence 7, Appl	1347	71.4	2.5	278866	4	US-09-949-016-14701	Sequence 14701, A
1275	71.8	2.5	55195	4	US-09-949-016-15854	Sequence 15854, A	1348	71.4	2.5	278866	4	US-09-949-016-14702	Sequence 14702, A
1276	71.8	2.5	15942	4	US-09-949-016-12227	Sequence 12227, A	1349	71.4	2.5	278866	4	US-09-949-016-14703	Sequence 14703, A
1277	71.8	2.5	15950	4	US-09-949-016-15946	Sequence 12946, A	1350	71.2	2.5	72	4	US-09-621-976-9837	Sequence 9837, Ap
1278	71.6	2.5	72	4	US-09-621-976-15064	Sequence 15064, A	1351	71.2	2.5	145	4	US-09-621-976-16691	Sequence 16691, A
1279	71.6	2.5	253	4	US-09-621-976-12799	Sequence 12799, A	1352	71.2	2.5	261	4	US-09-248-796A-12701	Sequence 12701, A
1280	71.6	2.5	601	4	US-09-949-016-126130	Sequence 126130,	c1353	71.2	2.5	467	2	US-08-841-349-18	Sequence 18, Appl
1281	71.6	2.5	601	4	US-09-949-016-126131	Sequence 126131,	c1354	71.2	2.5	467	4	US-09-431-104A-18	Sequence 18, Appl
1282	71.6	2.5	601	4	US-09-949-016-126132	Sequence 126132,	1355	71.2	2.5	601	4	US-09-949-016-126134	Sequence 126134, A
1283	71.6	2.5	601	4	US-09-949-016-126133	Sequence 126133,	1356	71.2	2.5	601	4	US-09-949-016-126135	Sequence 126135, A
1284	71.6	2.5	601	4	US-09-949-016-126137	Sequence 126137,	1357	71.2	2.5	601	4	US-09-949-016-126136	Sequence 126136, A
1285	71.6	2.5	1485	3	US-09-372-422A-39	Sequence 39, Appl	1358	71.2	2.5	3212	3	US-08-697-954-1	Sequence 1, Appl
1286	71.6	2.5	1810	4	US-09-800-729-73	Sequence 73, Appl	c1359	71.2	2.5	3212	4	US-09-949-016-16941	Sequence 16941, A
1287	71.6	2.5	1811	4	US-09-800-729-77	Sequence 77, Appl	c1360	71.2	2.5	27794	4	US-09-949-016-15133	Sequence 15133, A
1288	71.6	2.5	1813	5	PCT-US94-12883-3	Sequence 3, Appl	1361	71.2	2.5	37254	4	US-09-949-016-15973	Sequence 15973, A
1289	71.6	2.5	2679	4	US-09-684-579-2	Sequence 2, Appl	1362	71	2.5	71	4	US-09-621-976-14905	Sequence 14905, A
1290	71.6	2.5	4239	4	US-09-815-048-1	Sequence 1, Appl	1363	71	2.5	1965	4	US-09-482-273-27	Sequence 27, Appl
c1291	71.6	2.5	5340	4	US-09-627-122-21	Sequence 21, Appl	1364	71	2.5	2964	4	US-09-578-063-25	Sequence 25, Appl
c1292	71.6	2.5	29121	4	US-09-949-016-11748	Sequence 11748, A	c1365	71	2.5	12951	4	US-09-949-016-14075	Sequence 14075, A
c1293	71.6	2.5	29122	4	US-09-949-016-13591	Sequence 13591, A	1366	71	2.5	101349	4	US-09-949-016-17433	Sequence 17433, A
c1294	71.6	2.5	35007	4	US-09-949-016-15330	Sequence 15330, A	1367	70.8	2.5	234	4	US-09-248-796A-10692	Sequence 10692, A
c1295	71.6	2.5	44244	4	US-09-949-016-11743	Sequence 11743, A	c1368	70.8	2.5	388	2	US-08-623-906A-13	Sequence 13, Appl
c1296	71.6	2.5	44245	4	US-09-949-016-13579	Sequence 13579, A	1369	70.8	2.5	490	4	US-09-270-767-10524	Sequence 10524, A
c1297	71.6	2.5	140224	4	US-09-949-016-17002	Sequence 17002, A	c1370	70.8	2.5	553	4	US-09-270-767-11139	Sequence 11139, A
1298	71.4	2.5	80	1	US-07-920-281C-25	Sequence 25, Appl	c1371	70.8	2.5	601	4	US-09-949-016-105488	Sequence 105488, A
1299	71.4	2.5	80	3	US-08-466-277-25	Sequence 25, Appl	1372	70.8	2.5	601	4	US-09-949-016-139454	Sequence 139454, A
1300	71.4	2.5	80	4	US-09-688-842-25	Sequence 25, Appl	1373	70.8	2.5	705	4	US-09-270-767-5061	Sequence 5061, Ap
1301	71.4	2.5	601	4	US-09-949-016-47328	Sequence 47328, A	1374	70.8	2.5	705	4	US-09-270-767-20343	Sequence 20343, A
c1302	71.4	2.5	601	4	US-09-949-016-193437	Sequence 193437,	1375	70.8	2.5	2389	4	US-09-799-875-7	Sequence 7, Appl
c1303	71.4	2.5	601	4	US-09-949-016-199458	Sequence 199458,	1376	70.8	2.5	6078	3	US-09-173-914-1	Sequence 1, Appl
c1304	71.4	2.5	601	4	US-09-949-016-199461	Sequence 199461,	1377	70.8	2.5	6200	3	US-09-439-923-1	Sequence 1, Appl
1305	71.4	2.5	980	3	US-09-171-209-8	Sequence 8, Appl	1378	70.8	2.5	6200	4	US-09-711-202A-1	Sequence 1, Appl
1306	71.4	2.5	1138	4	US-09-800-729-44	Sequence 44, Appl	1379	70.8	2.5	6200	4	US-09-711-205A-1	Sequence 1, Appl
1307	71.4	2.5	1578	3	US-09-416-050A-1	Sequence 1, Appl	c1380	70.8	2.5	117001	4	US-09-949-016-15684	Sequence 15684, A
1308	71.4	2.5	1578	3	US-09-664-800-1	Sequence 1, Appl	c1381	70.8	2.5	129899	4	US-09-949-016-14684	Sequence 14684, A
1309	71.4	2.5	1578	3	US-09-665-309-1	Sequence 1, Appl	c1382	70.8	2.5	148156	4	US-09-949-016-11776	Sequence 11776, A
1310	71.4	2.5	1578	3	US-09-661-569-1	Sequence 1, Appl	c1383	70.8	2.5	301828	4	US-09-949-016-13969	Sequence 13969, A
1311	71.4	2.5	1898	1	US-08-342-411A-1	Sequence 1, Appl	1384	70.6	2.5	261	4	US-09-248-796A-8502	Sequence 8502, Ap
1312	71.4	2.5	2381	1	US-08-021-608D-9	Sequence 9, Appl	1385	70.6	2.5	412	3	US-09-018-584A-22	Sequence 22, Appl
1313	71.4	2.5	2381	1	US-08-726-160-9	Sequence 9, Appl	1386	70.6	2.5	412	4	US-09-784-423-22	Sequence 22, Appl
1314	71.4	2.5	2381	5	PCT-US94-01782-9	Sequence 9, Appl	c1387	70.6	2.5	517	4	US-09-270-767-13688	Sequence 13688, A
1315	71.4	2.5	2384	1	US-08-021-608D-1	Sequence 1, Appl	1388	70.6	2.5	601	4	US-09-949-016-122965	Sequence 122965, A
1316	71.4	2.5	2384	1	US-08-726-160-1	Sequence 1, Appl	1389	70.6	2.5	601	4	US-09-949-016-122966	Sequence 122966, A
1317	71.4	2.5	2384	5	PCT-US94-01782-1	Sequence 1, Appl	1390	70.6	2.5	601	4	US-09-949-016-123059	Sequence 123059, A
1318	71.4	2.5	3871	2	US-08-599-455B-3	Sequence 3, Appl	1391	70.6	2.5	601	4	US-09-949-016-123060	Sequence 123060, A
1319	71.4	2.5	3871	3	US-09-069-781B-3	Sequence 3, Appl	1392	70.6	2.5	601	4	US-09-949-016-123153	Sequence 123153, A
1320	71.4	2.5	3871	3	US-09-137-132-3	Sequence 3, Appl	1393	70.6	2.5	601	4	US-09-949-016-123154	Sequence 123154, A
1321	71.4	2.5	3871	3	US-08-864-564A-3	Sequence 3, Appl	1394	70.6	2.5	601	4	US-09-949-016-123247	Sequence 123247, A
1322	71.4	2.5	3871	3	US-09-094-410-3	Sequence 3, Appl	1395	70.6	2.5	601	4	US-09-949-016-123248	Sequence 123248, A
1323	71.4	2.5	3871	4	US-08-708-123D-3	Sequence 3, Appl	1396	70.6	2.5	601	4	US-09-949-016-123341	Sequence 123341, A
1324	71.4	2.5	3871	4	US-08-583-153A-3	Sequence 3, Appl	1397	70.6	2.5	601	4	US-09-949-016-123342	Sequence 123342, A
1325	71.4	2.5	3871	4	US-08-570-142D-3	Sequence 3, Appl	1398	70.6	2.5	601	4	US-09-949-016-123383	Sequence 123383, A
1326	71.4	2.5	3871	4	US-08-638-524B-3	Sequence 3, Appl	1399	70.6	2.5	601	4	US-09-949-016-123384	Sequence 123384, A
c1327	71.4	2.5	22497	4	US-09-949-016-13511	Sequence 13511, A	1400	70.6	2.5	601	4	US-09-949-016-123425	Sequence 123425, A
1328	71.4	2.5	49052	4	US-09-949-016-13203	Sequence 12203, A	1401	70.6	2.5	601	4	US-09-949-016-123426	Sequence 123426, A
1329	71.4	2.5	58407	4	US-08-916-421B-2	Sequence 2, Appl	1402	70.6	2.5	601	4	US-09-949-016-123467	Sequence 123467, A
1330	71.4	2.5	58407	4	US-09-692-570-2	Sequence 2, Appl	1403	70.6	2.5	601	4	US-09-949-016-123509	Sequence 123509, A
c1331	71.4	2.5	80178	4	US-09-949-016-17369	Sequence 17369, A	1404	70.6	2.5	601	4	US-09-949-016-123510	Sequence 123510, A
1332	71.4	2.5	80246	3	US-09-078-294-4	Sequence 4, Appl	1405	70.6	2.5	601	4	US-09-949-016-123551	Sequence 123551, A
1333	71.4	2.5	80595	3	US-09-078-294-3	Sequence 3, Appl	1406	70.6	2.5	601	4	US-09-949-016-123552	Sequence 123552, A
c1334	71.4	2.5	83178	4	US-09-949-016-14606	Sequence 14606, A	1407	70.6	2.5	601	4	US-09-949-016-123593	Sequence 123593, A
1335	71.4	2.5	236964	4	US-09-949-016-15753	Sequence 15753, A	1408	70.6	2.5	601	4	US-09-949-016-123594	Sequence 123594, A
c1336	71.4	2.5	251769	4	US-09-949-016-13185	Sequence 13185, A	1409	70.6	2.5	601	4	US-09-949-016-123635	Sequence 123635, A
c1337	71.4	2.5	251769	4	US-09-949-016-13186	Sequence 13186, A	1410	70.6	2.5	601	4	US-09-949-016-123636	Sequence 123636, A
c1338	71.4	2.5	266748	4	US-09-949-016-13187	Sequence 13187, A	1411	70.6	2.5	601	4	US-09-949-016-123677	Sequence 123677, A
c1339	71.4	2.5	266748	4	US-09-949-016-13188	Sequence 13188, A	1412	70.6	2.5	601	4	US-09-949-016-123678	Sequence 123678, A
1340	71.4	2.5	278866	4	US-09-949-016-13922	Sequence 13922, A	1413	70.6	2.5	601	4	US-09-949-016-123719	Sequence 123719, A
1341	71.4	2.5	278866	4	US-09-949-016-13923	Sequence 13923, A	1414	70.6	2.5	601	4	US-09-949-016-123719	Sequence 123719, A

1415	70.6	2.5	601	4	US-09-949-016-132720	Sequence 123720,
1416	70.6	2.5	601	4	US-09-949-016-123761	Sequence 123761,
1417	70.6	2.5	601	4	US-09-949-016-123762	Sequence 123762,
1418	70.6	2.5	601	4	US-09-949-016-167541	Sequence 167541,
1419	70.6	2.5	601	4	US-09-949-016-167542	Sequence 167542,
1420	70.6	2.5	601	4	US-09-949-016-167543	Sequence 167543,
1421	70.6	2.5	601	4	US-09-949-016-167648	Sequence 167648,
1422	70.6	2.5	601	4	US-09-949-016-167649	Sequence 167649,
1423	70.6	2.5	601	4	US-09-949-016-167650	Sequence 167650,
1424	70.6	2.5	992	4	US-09-270-767-14599	Sequence 14599, A
1425	70.6	2.5	1359	3	US-09-387-574-11	Sequence 11, Appl
1426	70.6	2.5	1359	3	US-09-668-096-11	Sequence 9, Appl
1427	70.6	2.5	1660	4	US-09-722-971-9	Sequence 15217, A
1428	70.6	2.5	32379	4	US-09-949-016-15217	Sequence 15218, A
1429	70.6	2.5	32379	4	US-09-949-016-15218	Sequence 15219, A
1430	70.6	2.5	32379	4	US-09-949-016-15219	Sequence 15220, A
1431	70.6	2.5	32379	4	US-09-949-016-15220	Sequence 15221, A
1432	70.6	2.5	32379	4	US-09-949-016-15221	Sequence 15222, A
1433	70.6	2.5	32379	4	US-09-949-016-15222	Sequence 15223, A
1434	70.6	2.5	32379	4	US-09-949-016-15223	Sequence 15224, A
1435	70.6	2.5	32379	4	US-09-949-016-15224	Sequence 15225, A
1436	70.6	2.5	32379	4	US-09-949-016-15225	Sequence 15226, A
1437	70.6	2.5	32379	4	US-09-949-016-15226	Sequence 15227, A
1438	70.6	2.5	34539	4	US-09-949-016-12226	Sequence 13156, A
1439	70.6	2.5	34540	4	US-09-949-016-13156	Sequence 12326, A
1440	70.6	2.5	37948	3	US-09-251-645-11	Sequence 11, Appl
1441	70.6	2.5	45456	3	US-09-146-053-6	Sequence 6, Appl
1442	70.6	2.5	64377	4	US-09-949-016-15212	Sequence 15212, A
1443	70.6	2.5	64377	4	US-09-949-016-15213	Sequence 15213, A
1444	70.6	2.5	64377	4	US-09-949-016-15214	Sequence 15214, A
1445	70.6	2.5	64377	4	US-09-949-016-15214	Sequence 15215, A
1446	70.6	2.5	64377	4	US-09-949-016-15216	Sequence 15216, A
1447	70.6	2.5	78157	4	US-09-949-016-16466	Sequence 16466, A
1448	70.6	2.5	78157	4	US-09-949-016-16467	Sequence 16467, A
1449	70.6	2.5	84571	4	US-09-949-016-17420	Sequence 17420, A
1450	70.6	2.5	154023	4	US-09-949-016-17057	Sequence 17057, A
1451	70.4	2.5	142	4	US-09-621-976-10801	Sequence 10801, A
1452	70.4	2.5	145	4	US-09-621-976-16688	Sequence 16688, A
1453	70.4	2.5	279	2	US-08-623-906A-3	Sequence 3, Appl
1454	70.4	2.5	649	4	US-09-468-253B-7	Sequence 7, Appl
1455	70.4	2.5	801	4	US-10-039-659A-5	Sequence 5, Appl
1456	70.4	2.5	1196	4	US-09-065-040-2	Sequence 2, Appl
1457	70.4	2.5	1842	4	US-09-482-273-90	Sequence 90, Appl
1458	70.4	2.5	43117	4	US-09-949-016-17589	Sequence 17589, A
1459	70.4	2.5	95318	4	US-09-949-016-11784	Sequence 11784, A
1460	70.4	2.5	95318	4	US-09-949-016-13998	Sequence 13998, A
1461	70.2	2.5	236	3	US-09-889-595-8	Sequence 8, Appl
1462	70.2	2.5	236	4	US-09-889-595-8	Sequence 8, Appl
1463	70.2	2.5	601	4	US-09-949-016-113694	Sequence 113694,
1464	70.2	2.5	601	4	US-09-949-016-122968	Sequence 122968,
1465	70.2	2.5	601	4	US-09-949-016-123062	Sequence 123062,
1466	70.2	2.5	601	4	US-09-949-016-123156	Sequence 123156,
1467	70.2	2.5	601	4	US-09-949-016-123250	Sequence 123250,
1468	70.2	2.5	601	4	US-09-949-016-123344	Sequence 123344,
1469	70.2	2.5	601	4	US-09-949-016-123386	Sequence 123386,
1470	70.2	2.5	601	4	US-09-949-016-123428	Sequence 123428,
1471	70.2	2.5	601	4	US-09-949-016-123470	Sequence 123470,
1472	70.2	2.5	601	4	US-09-949-016-123512	Sequence 123512,
1473	70.2	2.5	601	4	US-09-949-016-123554	Sequence 123554,
1474	70.2	2.5	601	4	US-09-949-016-123596	Sequence 123596,
1475	70.2	2.5	601	4	US-09-949-016-123638	Sequence 123638,
1476	70.2	2.5	601	4	US-09-949-016-123680	Sequence 123680,
1477	70.2	2.5	601	4	US-09-949-016-123722	Sequence 123722,
1478	70.2	2.5	601	4	US-09-949-016-123764	Sequence 123764,
1479	70.2	2.5	647	4	US-09-495-050A-54	Sequence 54, Appl
1480	70.2	2.5	953	4	US-09-270-767-11290	Sequence 11290, A
1481	70.2	2.5	1446	3	US-09-270-767-11708	Sequence 11708, A
1482	70.2	2.5	5058	3	US-09-889-595-1	Sequence 1, Appl
1483	70.2	2.5	5058	4	US-09-889-595-1	Sequence 1, Appl
1484	70.2	2.5	5225	4	US-09-949-016-16351	Sequence 16351, A
1485	70.2	2.5	9281	4	US-09-949-016-14660	Sequence 14660, A
1486	70.2	2.5	283538	4	US-09-949-016-13506	Sequence 13506, A
1487	70	2.5	306	4	US-09-621-976-16035	Sequence 16035, A
1488	70	2.5	306	4	US-09-621-976-16057	Sequence 16057, A
1489	70	2.5	371	4	US-09-621-976-19223	Sequence 19223, A
1490	70	2.5	601	4	US-09-949-016-163796	Sequence 163796,
1491	70	2.5	607	4	US-09-809-545A-19	Sequence 19, Appl
1492	70	2.5	1579	4	US-09-403-463A-5	Sequence 5, Appl
1493	70	2.5	1963	4	US-09-482-273-91	Sequence 91, Appl
1494	70	2.5	2483	4	US-09-203-258-68	Sequence 68, Appl
1495	70	2.5	260286	4	US-09-949-016-17037	Sequence 17037, A
1496	70	2.5	260293	4	US-09-949-016-12106	Sequence 12106, A
1497	70	2.5	373182	4	US-09-949-016-17371	Sequence 17371, A
1498	70	2.5	373694	4	US-09-949-016-12062	Sequence 12062, A
1499	69.8	2.5	315	4	US-09-621-976-16028	Sequence 16028, A
1500	69.8	2.5	341	4	US-09-621-976-16135	Sequence 16135, A

ALIGNMENTS

RESULT 1

US-09-280-116-104
; Sequence 104, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-34, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
; LENGTH: 2886
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
; NAME/KEY: misc feature
; LOCATION: (1)..(2886)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-104

Query Match 79.4%; Score 2259.4; DB 3; Length 2886;
Best Local Similarity 96.9%; Pred. No. 0;
Matches 2689; Conservative 0; Mismatches 41; Indels 45; Gaps 36;

QY	1	CGCTCGGCGACCGCGGCAAGATGGAGTGGGTTGCTGGACGCA-GTTGGGSGCTCA	59
DB	110	CGCTCGGCGACCGCGGCGGCAAGATGGAGTGGGTTGCTGGACGCGACGTTGGGGGCTCA	169
QY	60	CTTTTCTTCAGTCTCTTCATCTCGTCTTGTCCCAAGAGATACACAGTCATTATGAAG	119
DB	170	CTTTTCTTCAGTCTCTTCATCTCGTCTTGTCCCAAGAGATACACAGTCATTATGAAG	229
QY	120	CTGTCCTTGGAGCAGAGTGGGAATCATGTGTGGGAGTGTGTGAATATGATCATGATTG	179
DB	230	CTGTCCTTGGAGCAGAGTGGGAATCATGTGTGGGAGTGTGTGAATATGATCATGATTG	289
QY	180	AGTG-CGTCTCCCGGGAAGGGAAGTCTGGGTTATACCATCCCTTGTGTCAGGAGT	238
DB	290	AGTCCGCTCTCCCGGGAAGGGAAGTCTGGGTTATACCATCCCTTGTGTCAGGAGT	349
QY	239	GAGGAGATGAGTGTGACTCTCTGCTGATCAACCCAGGTTGTACCATCTTTGAAAACTGC	298
DB	350	GAGGAGATGAGTGTGACTCTCTGCTGATCAACCCAGGTTGTACCATCTTTGAAAACTGC	409
QY	299	AAGAGTCCGAAATGGCTCATGCGGGGG--TACCTTGGATGACTT--CTATGTGAAGGG	354
DB	410	AAGAGTCCGAAATGGCTCATGCGGGGGTTACCTTGGATGACTTCTATGTGAAGGG	469
QY	355	GTTCTAC-TGTGCAGAGTCCGAGCAGCTGGTAGCGA--GGAGACTGCATGC--GATGT	409
DB	470	GTTCTACTTGTGCAGAGTCCGAGCAGCTGGTAGCGAANGAGGACTGCATGCCGATGTT	529

QY 410 GCCAGGTTCTG-CGAGCCCAAGGGTCAGATTTTG--TTGGAAAGCTATCCCC--TAAAT 466
Db 530 GCCAGGTTCTGCCAAACCCCAAGGGTCAGATTTTGTTTGGAAAGCTATCCCCTTAAAT 589
QY 467 GCTCAC-TGTGAATGGACCATTCATGCTAAACCTGGGTTTGTATCCAACTAAAGATTTGT 525
Db 590 GCTCACTTGTGAATGGACCATTCATGCTAAACCTGGGTTTGTATCCAACTAAAGATTTGT 649
QY 526 CATGTTGAGTCTGGAGTTGACTACATGTCAGATGATGACTATGTTGAGGTTCTGATGG 585
Db 650 CATGTTGAGCTGGAGTTGACTACATGTCAGATGATGACTATGTTGAGGTTCTGATGG 709
QY 586 AGACAA-CGGCGATGGCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTA 644
Db 710 AGACAAACCGGATGGCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTA 769
QY 645 TCCAGAGCATAGATTCCT---CACCTCCACGTCCTCTCCACTCC--GATGGCTCCAAAGAT 700
Db 770 TCCAGAGCATAGATTCCTCCACTCCACGTCCTCTCCACTCCCGATGGCTCCAAAGAT 829
QY 701 TTTGACGTTTCCATGGCAATTTATGAGGAGATCAAGCATGCTCTCATCCCTTTGTTTC 760
Db 830 TTTGACGTTTCCATGGCAATTTATGAGGAGATCAAGCATGCTCTCATCCCTTTGTTTC 889
QY 761 CATGACGGCAGCTGCGTCTTACAAAGCTGGATCTTACAGTGTGCTGTTGGCAGGC 820
Db 890 CATGACGGCAGCTGCGTCTTACAAAGCTGGATCTTACAGTGTGCTGTTGGCAGGC 949
QY 821 -TATACTGGGACGCTGTGAAAATCTCTTGAAGAAAGAACTGCTCAGACCTCGGGGG 879
Db 950 TTAATACTGGGACGCTGTGAAAATCTCTTGAAGAAAGAACTGCTCAGACCTCGGGGG 1009
QY 880 CCCAGTCAATGGGTACCGAAATTAACAGGGGGCCCTGGGCTTTATCAAGCGACGCATGC 939
Db 1010 CCCAGTCAATGGGTACCGAAATTAACAGGGGGCCCTGGGCTTTATCAAGCGACGCATGC 1069
QY 940 TAAATTTGGCACCGTGTCTTTCTTTTGTAAACAACTCCTATGTTCTTAGTGGAATGA 999
Db 1070 TAAATTTGGCACCGTGTCTTTCTTTTGTAAACAACTCCTATGTTCTTAGTGGAATGA 1129
QY 1000 GAAAAGAACTTCCAGCAGAAATGGAGAGTGGTCAGGGAAACAGCCCATCTGCTATAAAGC 1059
Db 1130 GAAAGAACTTCCAGCAGAAATGGAGAGTGGTCAGGGAAACAGCCCATCTGCTATAAAGC 1189
QY 1060 CTGCCGAGAACCAAGATTTACAGCTGTGTGAGAGAGAGTTCCTTCGATCGAGTTCA 1119
Db 1190 CTGCCGAGAACCAAGATTTACAGCTGTGTGAGAGAGAGTTCCTTCGATCGAGTTCA 1249
QY 1120 GTCAAGGGAGACA-CCATTTACACAGCTATATCTCAGCGGCTTCAGCAGCAGAACT-- 1176
Db 1250 GTCAAGGGAGACACCCAAATTCACCAAGCTATATCTCAGCGGCTTCAGCAGCAGAACTTG 1309
QY 1177 GCAGAGTGCCTTACCAAGAACCCAGCCCTTCCCTTTGGAGATC--TGCCCATGGGATACC 1235
Db 1310 CAAGAGTGCCTTACCAAGAACCCAGCCCTTCCCTTTGGAGATCTTGCCCATGGGATACC 1369
QY 1236 AACATC-TGCATACCCAGCTCCAGTATGATGATCTCAACCTTTCTACCGCCGCTGGGC 1294
Db 1370 AACATCTTGCATACCCAGCTCCAGTATGATGATCTCAACCTTTCTACCGCCGCTGGGC 1429
QY 1295 AGCAGCA-CGAGGACATGCTCAGGACTGGGAAGTGGAGTGGGC--GGGCACCATCTTGCA 1352
Db 1430 AGCAGCACCGAGGACATGTTTGGAGACTGGGAAGTGGAGTGGGGGGGACCATCTTGCA 1489
QY 1353 TCCCTATCTCGGGGAAAATTGAGAACATCACTGCTCCAAAGACCCAAAGGTTGCGCTGGC 1412
Db 1490 TCCCTATCTCGGGGAAAATTGAGAACATCACTGCTCCAAAGACCCAAAGGTTGCGCTGGC 1549
QY 1413 CTTGGCAGCAGCCATCTTACAGAGGACAGCGGGGTGATGACGGCAGCCTACACAAGG 1472
Db 1550 CTTGGCAGCAGCCATCTTACAGAGGACAGCGGGGTGATGACGGCAGCCTACACAAGG 1609

QY 1473 GAGCGTGTCTCTAGTCTGCAG-CGGTGCCCTGTGTGAATGAGCGCAC--TGTTGTTGGTGGC 1530
Db 1610 GAGCGTGTCTCTAGTCTGCAGCGGTGCCCTGTGTGAATGAGCGCACTTGTGTTGGTGGC 1669
QY 1531 TGCCCACTGTGTACTGACCTTGGGGAAGGTCACTATGATCAAGACAGCAGACCTGAAAGT 1590
Db 1670 TGCCCACTGTGTACTGACCTTGGGGAAGGTCACTATGATCAAGACAGCAGACCTGAAAGT 1729
QY 1591 TGTTTTGGGGAATTTCTACCGGGATGATGACC--GGGATGAGAAGACCATCCAGAGCCTTAC 1649
Db 1730 TGTTTTGGGGAATTTCTACCGGGATGATGACCGGGATGAGAAGACCATCCAGAGCCTTAC 1789
QY 1650 AGATTTCTGCTATCATTTCTGCATCCCAACTATGACCCCATCTCTGTTGATGCTGACATCG 1709
Db 1790 AGATTTCTGCTATCATTTCTGCATCCCAACTATGACCCCATCTCTGTTGATGCTGACATCG 1849
QY 1710 CCATCTGAAAGTCTTAGCAAGGCCCTGTATCAGCACCCGAGTCCAGCCCATCTGCTCTCG 1769
Db 1850 CCATCTGAAAGTCTTAGCAAGGCCCTGTATCAGCACCCGAGTCCAGCCCATCTGCTCTCG 1909
QY 1770 CTGCCAGTCCGGATCTCAGCACTTCTTCCAGGAGTCCACATC--ACTGTGGCTGGCTGG 1828
Db 1910 CTGCCAGTCCGGATCTCAGCACTTCTTCCAGGAGTCCACATCAGACTGTGGCTGGCTGG 1969
QY 1829 AATGTCCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAAACGACACACTGCGCTCTGGGGTG 1888
Db 1970 AATGTCCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAAACGACACACTGCGCTCTGGGGTG 2029
QY 1889 GTCACTGTGTGGACTCGCTGCTGTGTGAGG--AGCAGCATGA--GGACCATGGCATCCCG 1946
Db 2030 GTCACTGTGTGGACTCGCTGCTGTGTGAGGAAGCAACATGAGGGACCATGGCATCCCG 2089
QY 1947 T-GAGTGTCACTGATAACATGTTCTGTCGCGAGTGGGAACCCACATGCCCTTCTGATATC 2005
Db 2090 TGGAGTGTCACTGATAACATGTTCTGTCGAGCTGGGAACCCACATGCCCTTCTGATATC 2149
QY 2006 TGCACTGCAGAGACAGGAGGCATCGCGCTGTGTCTTCCCGGGACGAGCATCTCTGAG 2065
Db 2150 TGCACTGCAGAGACAGGAGGCATCGCGCTGTGTCTTCCCGGGACGAGCATCTCTGAG 2209
QY 2066 CCACCTGGCATCTGATGGGACTGTC--AGCTGAGC--TATGATAAACATGCGACCCAC 2122
Db 2210 CCACCTGGCATTTGATGGGAACTGTGTCAGAGCTGGAGCTTATGATAAAACATGCGACCCAC 2269
QY 2123 AGGCTCTCCACTGCTTCCAAAGTGTGCTCTTTT-AAAGACTGGATTGAAGAAATAT 2181
Db 2270 AGGCTCTCCACTGCTTCCAAAGTGTGCTCTTTTAAAGACTGGATTGAAGAAATAT 2329
QY 2182 GAAATGAACCATGCTCATGCACTCTCTGAG--AAGTGTGTTTCTGTATATCCGCTGTACGTTG 2240
Db 2330 GAAATGAACCATGCTCATGCACTCTCTGAGAAAGTGTTCCTGTATATCCGCTGTACGTTG 2389
QY 2241 TGTCAATTCGTTGAAGACGTGTGGGCTGAAAGTGTGATTTGGCTGTGAACTTGGCTGTGTC 2300
Db 2390 TGTCAATTCGTTGAAGACGTGTGGGCTGAAAGTGTGATTTGGGCTGTGAACTTGGCTGTGTC 2449
QY 2301 GAGGCTTCTGACTTTCAGGACAAACCTCAGTGAAGGTTGACTAGACCTCCATTTGCTGTGT 2360
Db 2450 GAGGCTTCTGACTTTCAGGACAAACCTCAGTGAAGGTTGAGTAGACCTCCATTTGCTGTGT 2509
QY 2361 AGGCTGATGCCCGCTCCACTACTAGGACAGCCAAATTTGGAAGATGCCAGGGCTTGAAGAA 2420
Db 2510 AGGCTGATGCCCGCTCCACTACTAGGACAGCCAAATTTGGAAGATGCCAGGGCTTGAAGAA 2569
QY 2421 GTAAAGTTTC-TTCAAAGAGACCATATACAAAACCTCTCCACTCCACTGACCTGTGGTCTC 2479
Db 2570 GTAAAGTTTCGTTCAAAGAGACCATATACAAAACCTCTCCACTCCACTGACCTGTGGTCTC 2629
QY 2480 TTTCCCACTTTTCACTTATACGAATGCCATGAGTTGACCGAGGAGATCTGGGCTTCTCAT 2539
Db 2630 TTTCCCACTTTTCACTTATACGAATGCCATGAGTTGACCGAGGAGATCTGGGCTTCTCAT 2689
QY 2540 GAGGGCCCTTTTGGGCTCTCAAGATTTCTAGAGA-GCTGCTGTGGGACAGCCGAGGCGAG 2598


```
Db 2690 GAGGCCCTTTTGGGCTCTCAAGTTCTAGAGCGCTGCTGTGGACAGCCAGGGCAG 2749
Qy 2599 CAGAGCTGGGA--TGTGGTGCATGCTTTGTGTACATGCCACAGTAC-AGTCTGGTCT 2655
Db 2750 CAGAGCTGGGAATTTGTGGTGCATGCTTTGTGTACATGCCACAGTACAAGTCTGGTCT 2809
Qy 2656 TTTCTTCCCATCTCTGTGTACACATTTTAATAAATAAGGTTGGCTTCTGAATACAA 2715
Db 2810 TTTCTTCCCATCTCTGTGTACACATTTTAATAAATAAGGTTGGCTTCTGTACTCAA 2869
Qy 2716 AAAAAAAAAAAAAA 2730
Db 2870 AAAAAAAAAAAAAA 2884

RESULT 2
US-10-067-422-2
; Sequence 2, Application US/10067422
; Patent No. 6743613
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and
; FILE REFERENCE: PT004P1
; CURRENT APPLICATION NUMBER: US/10/067,422
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/685,899
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: PCT/US00/09028
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/152,933
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/147,020
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/131,672
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/130,693
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2259
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-067-422-2

Query Match 75.3%; Score 2142.2; DB 4; Length 2259;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 2205; Conservative 0; Mismatches 3; Indels 51; Gaps 1;

Qy 527 ATGTTGAGTCTGGAGTTTGACTATGATGTCAGATGATGATGTTGAGGTTCTGTATGGA 586
Db 1 ATGTTGAGTCTGGAGTTTGACTATGATGTCAGATGATGATGTTGAGGTTCTGTATGGA 60
Qy 587 GACAAACCGGATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGCCAGCTCTATC 646
Db 61 GACAAACCGGATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGCCAGCTCTATC 120
Qy 647 CAGAGCATAGGATCTCACTCAAGTCTCTTCCACTCCGATGGCTCCAGAAATTTGAC 706
Db 121 CAGAGCATAGGATCTCACTCAAGTCTCTTCCACTCCGATGGCTCCAGAAATTTGAC 180
Qy 707 GGTTCATGCAATTTATGAGGAGATCACAGATGCTCTCATCCCTTGTTCATGAC 766
Db 181 GGTTCATGCAATTTATGAGGAGATCACAGATGCTCTCATCCCTTGTTCATGAC 240
Qy 767 GGCAGTGGCTCTTGACAGGCTGGATCTTCAAGTGTGCTGTGGCAGGCTATATCT 826
Db 241 GGCAGTGGCTCTTGACAGGCTGGATCTTCAAGTGTGCTGTGGCAGGCTATATCT 300
Qy 827 GGGCAGCGCTGTGAAATC----- 845
```

```
Db 301 GGGCAGCGCTGTGAAATCTTCTCGAGGCTGGGAAGTCCAAGATCAAGCGCTCAGAAGAT 360
Qy 846 -----TCCTTTGAAAGAAAGAACTGCTCAGACCTCTGGGGGCCAGTCAATGGGTAC 895
Db 361 TCATTTGTCTGCTCTTTGAAAGAAAGAACTGCTCAGACCTCTGGGGGCCAGTCAATGGGTAC 420
Qy 896 CAGAAATAACAGGGGGCCCTGGGCTTATCAACGAGCGCCATCTGCTAATAATTCGCACCGG 955
Db 421 CAGAAATAACAGGGGGCCCTGGGCTTATCAACGAGCGCCATCTGCTAATAATTCGCACCGG 480
Qy 956 GTGTCTTTCTTTTGTAAACAATCTCTATGTTCTTAGTGGCAATGAGAAAGAACTTGCACAG 1015
Db 481 GTGTCTTTCTTTTGTAAACAATCTCTATGTTCTTAGTGGCAATGAGAAAGAACTTGCACAG 540
Qy 1016 CAGAAATGAGAGTGTCTAGGGGAAAACAGCCCATCTGCATAAAAGCTGCCGAGAACAAAG 1075
Db 541 CAGAAATGAGAGTGTCTAGGGGAAAACAGCCCATCTGCATAAAAGCTGCCGAGAACAAAG 600
Qy 1076 ATTTTCAGACCTGGTGAAGAGAGGTTCTTCCGATGCGAGGTTTCACTCAAGGAGACACCA 1135
Db 601 ATTTTCAGACCTGGTGAAGAGAGGTTCTTCCGATGCGAGGTTTCACTCAAGGAGACACCA 660
Qy 1136 TTACACCACTATCTCTAGCGGCCCTTTCAGCAAGCAGAAACTGCAGAGTCCCTCTACCAAG 1195
Db 661 TTACACCACTATCTCTAGCGGCCCTTTCAGCAAGCAGAAACTGCAGAGTCCCTCTACCAAG 720
Qy 1196 AAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTC 1255
Db 721 AAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTC 780
Qy 1256 CAGTATGATGCTCTCAACCTTCTACCGCCGCTTGGCAGCAGCAGGAGGACATGCTCTG 1315
Db 781 CAGTATGATGCTCTCAACCTTCTACCGCCGCTTGGCAGCAGCAGGAGGACATGCTCTG 840
Qy 1316 AGGACTGCGAAGTGGAGTGGCGGCGCACCATCTGCATCCCTATCTCGGGGAAAATTGAG 1375
Db 841 AGGACTGCGAAGTGGAGTGGCGGCGCACCATCTGCATCCCTATCTCGGGGAAAATTGAG 900
Qy 1376 AACATCACTGTCTCCAAAGACCCAAAGGTTGGCTGGCGTGGCAGCAGCAGCCTACACAG 1435
Db 901 AACATCACTGTCTCCAAAGACCCAAAGGTTGGCTGGCGTGGCAGCAGCAGCCTACACAG 960
Qy 1436 AGGACACGCGGGTGCATGACGGGAGCCTACACAGGAGGCGTGGTCTTAGTCTGCAGC 1495
Db 961 AGGACACGCGGGTGCATGACGGGAGCCTACACAGGAGGCGTGGTCTTAGTCTGCAGC 1020
Qy 1496 GGTGCGCTGTGTAATGAGCGCACTGTGTGGTGGCTGCCCATCTGTGTACTGACCTGGGG 1555
Db 1021 GGTGCGCTGTGTAATGAGCGCACTGTGTGGTGGCTGCCCATCTGTGTACTGACCTGGGG 1080
Qy 1556 AAGGTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTTGGGAAAATTTCTACCGGAT 1615
Db 1081 AAGGTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTTGGGAAAATTTCTACCGGAT 1140
Qy 1616 GATGACCGGGATGAGAAACCATTCAGAGCCTACAGATTTCTGCTATCATTTCTGCATCC 1675
Db 1141 GATGACCGGGATGAGAAACCATTCAGAGCCTACAGATTTCTGCTATCATTTCTGCATCC 1200
Qy 1676 AACTATGACCCCATCTGCTTGTGATGCTGACATCGCCATCTCAAGCTCTAGACAAAGGC 1735
Db 1201 AACTATGACCCCATCTGCTTGTGATGCTGACATCGCCATCTCAAGCTCTAGACAAAGGC 1260
Qy 1736 CGTATCAGACCCGAGTCCAGCCCATCTGCTCTGCTGCGCAGTCCGGGATCTCAGACATTC 1795
Db 1261 CGTATCAGACCCGAGTCCAGCCCATCTGCTCTGCTGCGCAGTCCGGGATCTCAGACATTC 1320
Qy 1796 TTCCAGAGTCCCATCATCATGCTGTGCTGGTGGATGTCCTGGCAGACGTGAGGAGCCCT 1855
Db 1321 TTCCAGAGTCCCATCATCATGCTGTGCTGGTGGATGTCCTGGCAGACGTGAGGAGCCCT 1380
Qy 1856 GGCCTTCAGAACGACACACTGCGCTCTGGGGTGGTTCAGTGTGGTGCATCGCTGCTGTCT 1915
Db 1381 GGCCTTCAGAACGACACACTGCGCTCTGGGGTGGTTCAGTGTGGTGCATCGCTGCTGTCT 1440
```

```
QY 1916 GAGGAGCAGCATGAGGACCATGGCATCCAGTGAAGTGTACATGATAAATGTTCTGTGCC 1975
Db 1441 GAGGAGCAGCATGAGGACCATGGCATCCAGTGAAGTGTACATGATAAATGTTCTGTGCC 1500
QY 1976 AGCTGGGAACCCACATCGCCCTTCTGATATCTGCACTGACAGACAGGAGGCATCCGGCT 2035
Db 1501 AGCTGGGAACCCACATCGCCCTTCTGATATCTGCACTGACAGACAGGAGGCATCCGGCT 1560
QY 2036 GTGTCTTCCCGGACGAGCATCTCTGAGCCACGCTGGCATCTGATGGACATGTCTAGC 2095
Db 1561 GTGTCTTCCCGGACGAGCATCTCTGAGCCACGCTGGCATCTGATGGACATGTCTAGC 1620
QY 2096 TGGACATATGATAAACAATGACGACACAGGCTCTCCACTGCTTCCACCAAGTGTGCT 2155
Db 1621 TGGACATATGATAAACAATGACGACACAGGCTCTCCACTGCTTCCACCAAGTGTGCT 1680
QY 2156 TTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCTTGAAGAAT 2215
Db 1681 TTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCTTGAAGAAT 1740
QY 2216 GTTCTGTATATCCGTCTGTACGTGTGTCATTTGCGTGAAGCAGTGTGGCCTGAAATGTG 2275
Db 1741 GTTCTGTATATCCGTCTGTACGTGTGTCATTTGCGTGAAGCAGTGTGGCCTGAAATGTG 1800
QY 2276 ATTTGGCCTGTGAATCTGGCTGTGCGAGGCTTCTGACTTCAGGACAAAACCTCAGTGA 2335
Db 1801 ATTTGGCCTGTGAATCTGGCTGTGCGAGGCTTCTGACTTCAGGACAAAACCTCAGTGA 1860
QY 2336 GGGTCAGTAGACCTCATTTGCTGTAGGCTGTGCGGCTGATGCGCTCACTACTAGGACGCCAAT 2395
Db 1861 GGGTCAGTAGACCTCATTTGCTGTAGGCTGTGCGGCTGATGCGCTCACTACTAGGACGCCAAT 1920
QY 2396 TGGAAAGATGCCAGGGCTTGCAGAAAGTAAATTTCTTCAAAGAAAGACCATATACAAAACCT 2455
Db 1921 TGGAAAGATGCCAGGGCTTGCAGAAAGTAAATTTCTTCAAAGAAAGACCATATACAAAACCT 1980
QY 2456 CTCACATCCAGTCTGGTGTCTTCCCAACTTTTCAGTTATACGAATGCCATCAGCTT 2515
Db 1981 CTCACATCCAGTCTGGTGTCTTCCCAACTTTTCAGTTATACGAATGCCATCAGCTT 2040
QY 2516 GACCAAGGAAGATCTGGGCTTCATGAGGCCCTTTTGAGGCTCTCAAGTTCTAGAGAGCT 2575
Db 2041 GACCAAGGAAGATCTGGGCTTCATGAGGCCCTTTTGAGGCTCTCAAGTTCTAGAGAGCT 2100
QY 2576 GCCTGTGGACAGCCCGAGGACAGAGCTGGGATGTGGTGATGCTTTTGTGTACATGG 2635
Db 2101 GCCTGTGGACAGCCCGAGGACAGAGCTGGGATGTGGTGATGCTTTTGTGTACATGG 2160
QY 2636 CCACAGTACAGTCTGGTCTTTTCCCTTCCCAATCTCTTGTACACATTTTAATAAATAAG 2695
Db 2161 CCACAGTACAGTCTGGTCTTTTCCCTTCCCAATCTCTTGTACACATTTTAATAAATAAG 2220
QY 2696 GGTTCGCTTCTGAATCTACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2734
Db 2221 GGTTCGCTTCTGAATCTACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2259
```

```
RESULT 3
US-09-620-312D-969
; Sequence 969, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
```

```
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784C1P2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 969
; LENGTH: 2144
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (528)..(1607)
US-09-620-312D-969
```

```
Query Match 69.9%; Score 1988.4; DB 4; Length 2144;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 2056; Conservative 0; Mismatches 11; Indels 51; Gaps 1;

QY 659 TCCTCACTCCACGTCCTCTTCCACTCCGATCGCTCCAGAAATTTTGACGGTTTCCATGCC 718
Db 27 TCCCGGGTCGACCCACGCGTCGCTCCGATGCTCCAGAAATTTTGACGGTTTCCATGCC 86
QY 719 ATTTATGAGGAGATCACAGCATGCTCTCATCCCCCTGTTTCCATGACGGCACGTCGCTC 778
Db 87 ATTTATGAGGAGATCACAGCATGCTCTCATCCCCCTGTTTCCATGACGGCACGTCGCTC 146
QY 779 CTTGCAAGGCTGGATCTTTACAAGTGTGCTGCTTGGCAGGCTATATCGGCGAGGCTGT 838
Db 147 CTTGCAAGGCTGGATCTTTACAAGTGTGCTGCTTGGCAGGCTATATCTGGCGAGGCTGT 206
QY 839 GAAATTC-----TC 847
Db 207 GAAATTCCTTCTGAGGCTGGGAAATCCAGATCAAGGCGTCAAGAGATTCATTGTCTGTC 266
QY 848 CTTGAAGAAAGAAACTGCTCAGACCTCGGGGCCCAAGTCAATGGGTACCGAGAAATAACA 907
Db 267 CTTGAAGAAAGAAACTGCTCAGACCTCGGGGCCCAAGTCAATGGGTACCGAGAAATAACA 326
QY 908 GGGGCCCTTGGGCTTATCAACGACGCGCATGTCTAAAATTTGGCAACCGTGTGTCTTTT 967
Db 327 GGGGCCCTTGGGCTTATCAACGACGCGCATGTCTAAAATTTGGCAACCGTGTGTCTTTT 386
QY 968 TGTAACTCTATGTTCTTAGTGGCAATGAGAAAGAACTTGCAGCAGAGATCGAGAG 1027
Db 387 TGTAACTCTATGTTCTTAGTGGCAATGAGAAAGAACTTGCAGCAGAGATCGAGAG 446
QY 1028 TGGTCAGGGAACACGCCCATCTGCTATAAAGCTCCCGAGAACCAAGATTTTCAGACCTG 1087
Db 447 TGGTCAGGGAACACGCCCATCTGCTATAAAGCTCCCGAGAACCAAGATTTTCAGACCTG 506
QY 1088 GTGAGAGGAGAGTCTTCCGATGAGGTTTCAAGTCAAGGAGACACCATATACACAGCTA 1147
Db 507 GTGAGAGGAGAGTCTTCCGATGAGGTTTCAAGTCAAGGAGACACCATATACACAGCTA 566
QY 1148 TACTCAGGGCCTTCAGCAAGCAGAACTGACAGTGGCCCTTACCAAGAGCAGGCCCTT 1207
Db 567 TACTCAGGGCCTTCAGCAAGCAGAACTGACAGTGGCCCTTACCAAGAGCAGGCCCTT 626
QY 1208 CCTTTTGGAGATCTGCCCATGGATACCAACATCTGTACATCCAGCTCCAGTATGAGTGC 1267
```


Best Local Similarity 97.0%; Pred. No. 0; Matches 2053; Conservative 0; Mismatches 12; Indels 51; Gaps 1;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
QY	659	TCCTCACTCCAGTCTCTCTTCACATCCAGTGGCTCCAGAAATTTTGA	CGGTTTTCATGCC	718																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	27	TCCCGGTCGACCCAGGCTCCGCTCCGATGGCTCCAGAAATTTTGA	CGGTTTTCATGCC	86																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	719	ATTTATGAGGAGATCACAGCATGCTCTCATCCCTTTTCCATGACGG	CACTGGCTC	778																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	87	ATTTATGAGGAGATCACAGCATGCTCTCATCCCTTTTCCATGACGG	CACTGGCTC	146																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	779	CTTGACAGGCTGGATCTTACAGTGTGCTGCTTGGCAGGCTATATCT	GGCAGCGCTGT	838																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	147	CTTGACAGGCTGGATCTTACAGTGTGCTGCTTGGCAGGCTATATCT	GGCAGCGCTGT	206																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	839	GA	AAATC-----TC	847																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	207	GA	AAATCTTCTCGAGGCTGGGAAGTCCAAAGATCAAGGCGTCAGAAG	ATTCATTTCTGTCTC	266																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
QY	848	CTTGAGAAAGAAATCTGTCTCAGACCCCTGGGGCCCACTCAATGGG	TACCAAGAAATAACA	907																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	267	CTTGAGAAAGAAATCTGTCTCAGACCCCTGGGGCCCACTCAATGG	TACCAAGAAATAACA	326																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	908	GGGGCCCTGGGCTTATCAACGGACGCCATGCTAAATTTGGCA	CCGTGTCTTTCTTT	967																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	327	GGGGCCCTGGGCTTATCAACGGACGCCATGCTAAATTTGGCA	CCGTGTCTTTCTTT	386																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	968	TGTATCAACTCTATGTCTTAGTGGCAATGAGAAAGAACTTCCG	ACAGCATGGAGAG	1027																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	387	TGTATCAACTCTATGTCTTAGTGGCAATGAGAAAGAACTTCCG	ACAGCATGGAGAG	446																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	1028	TGGTCAGGAAACAGCCCATCTGCATAAAGCTGCCAGAAACCA	AAAGATTTTCAGACCTG	1087																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	447	TGGTCAGGAAACAGCCCATCTGCATAAAGCTGCCAGAAACCA	AAAGATTTTCAGACCTG	506																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	1088	GTGAGAAAGAGATTTCTTCCGATGAGGTTTCAGTCAAGGGAGA	CAACATTAACACGCTA	1147																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	507	GTGAGAAAGAGATTTCTTCCGATGAGGTTTCAGTCAAGGGAGA	CAACATTAACACGCTA	566																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	1148	TACTCAGCGGCTTCAGCAAGCAAGAACTGCAGAGTGCCCTTAC	CAAGAACCCAGCCCTT	1207																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	567	TACTCAGCGGCTTCAGCAAGCAAGAACTGCAGAGTGCCCTTAC	CAAGAACCCAGCCCTT	626																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	1208	CCCTTTGGAGATCTGCCATGGGATACCAACATCTGCATACCC	AGCTCCAGTATGATGC	1267																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	627	CCCTTTGGAGATCTGCCATGGGATACCAACATCTGCATACCC	AGCTCCAGTATGATGC	686																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	1268	ATCTCACCTTCTACCGCGCTGGGCAAGCAGCAGGAGCAATGT	CTGAGGACTTGGGAAG	1327																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	687	ATCTCACCTTCTACCGCGCTGGGCAAGCAGCAGGAGCAATGT	CTGAGGACTTGGGAAG	746																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	1328	TGGAGTGGCGGGCAACATCTTCGATTCCTATCTCGGGGAAAT	TTGAGAACATCACTGCT	1387																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	747	TGGAGTGGCGGGCAACATCTTCGATTCCTATCTCGGGGAAAT	TTGAGAACATCACTGCT	806																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	1388	CCAAAGACCCAAAGGTTGCGCTGGCCGTGGCAGGCAGCCATCT	ACAGGAGACCAAGCGG	1447																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	807	CCAAAGACCCAAAGGTTGCGCTGGCCGTGGCAGGCAGCCATCT	ACAGGAGACCAAGCGG	866																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	1448	GTGCATGAGCGGACGCTCAACAAGGGAGCGTGGTTCTTAGTCT	GCAGCGGTGCCCTGGTG	1507																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	867	GTGCATGAGCGGACGCTCAACAAGGGAGCGTGGTTCTTAGTCT	GCAGCGGTGCCCTGGTG	926																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	1508	AATGAGCGCATGTGTGTGTGCTGCCCATCTGTGTATTCTGAC	CTTGGGGAAGGTCAACATG	1567																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	927	AATGAGCGCATGTGTGTGTGCTGCCCATCTGTGTATTCTGAC	CTTGGGGAAGGTCAACATG	986																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	1568	ATCAAGACAGCAGACTGGAAGTCTTTTGGGGAATTTCTACCG	GGATGATGACCGGGAT	1627																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	987	ATCAAGACAGCAGACTGGAAGTCTTTTGGGGAATTTCTACCG	GGATGATGACCGGGAT	1046																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	1628	GAGNAGACCATCCAGAGCCCTACAGATTTCTGTATCATTTCT	GTGATCTTCCCAACTATGACCCC	1687																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					</

```
RESULT 5
US-09-280-116-179
; Sequence 179, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 179
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: aticlin/m 12a metalloproteases
US-09-280-116-179

Query Match      16.8%; Score 479.4; DB 3; Length 505;
Best Local Similarity 99.4%; Pred. No. 8.4e-103; Indels 2; Gaps 2;
Matches 502; Conservative 0; Mismatches 1;

Qy 331 CTTGATGACCTTCTATGTGAAGGGGTTCTACTGTGCAGAGTCCCGAGCGGCTGTACGG 390
Db      |||||||
Qy 391 AGGAGACTGCATGCGATGTGGCAGGTTCTGAGAGCCCAAGGTCAGATTTGTTGGA 450
Db      |||||||
Qy 61  AGGAGACTGCATGCGATGTGGCAGGTTCTGAGAGCCCAAGGTCAGATTTGTTGGA 120
Db      |||||||
Qy 451 AAGCTATCCCTAAATGCTCACTGTAATGACCAATTCATGTAACCTGGGTTGTCTAT 510
Db      |||||||
Qy 121 AAGCTATCCCTAAATGCTCACTGTAATGACCAATTCATGTAACCTGGGTTGTCTAT 180
Db      |||||||
Qy 511 CCAACTAAGATTTGTCTAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGT 570
Db      |||||||
Qy 181 CCAACTAAGATTTGTCTAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGT 240
Db      |||||||
Qy 571 TGAGTTTCGTATGAGAGACAACCGCGATGGCCAGATCATCAAGCGTGTCTGTGGCAAGA 630
Db      |||||||
Qy 241 TGAGTTTCGTATGAGAGACAACCGCGATGGCCAGATCATCAAGCGTGTCTGTGGCAAGA 300
Db      |||||||
Qy 631 GCGGCCAGCTCCTATCCAGAGATAGGATCCTCACTCCAGCTCTTCCACTCCGATGG 690
Db      |||||||
Qy 301 GCGGCCAGCTCCTATCCAGAGATAGGATCCTCACTCCAGCTCTTCCACTCCGATGG 360
Db      |||||||
Qy 691 CTCCAAGATTTTGACGGTTTCCATGCCATTTATGAGGAGATCAGCATGTCTCTCATC 750
Db      |||||||
Qy 361 CTCCAAGATTTTGACGGTTTCCATGCCATTTATGAGGAGATCAGCATGTCTCTCATC 420
Db      |||||||
Qy 751 CCCTTGTTCATGACGCGACGTCGTCTCTTGACAAGGCTGATCTTAC-AAGTGTGCT 809
Db      |||||||
Qy 421 CCCTTGTTCATGACGCGACGTCGTCTCTTGACAAGGCTGATCTTACAAAGTGTGCT 480
Db      |||||||
Qy 810 GCTTGGCAGGCTATCTGGGCGCG 834
Db      |||||||
Qy 481 GCTTGGCAGGCTATCTGGGCGCG 505
Db      |||||||

RESULT 6
US-09-835-811-1
; Sequence 1, Application US/09835811
; Patent No. 6482936
; GENERAL INFORMATION:
; APPLICANT: HU, Song et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS
; OTHER INFORMATION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: CL0012228
```

```
; CURRENT APPLICATION NUMBER: US/09/835,811
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Human
US-09-835-811-1

Query Match      4.9%; Score 140.8; DB 4; Length 1696;
Best Local Similarity 87.5%; Pred. No. 4.9e-23; Indels 0; Gaps 0;
Matches 154; Conservative 0; Mismatches 22;

Qy 2671 CTTGTACACATTTTAATAAAATAAGGGTTGGCTTCTGAACTACAAAAA 2730
Db      |||||||
Qy 1473 CTTGTCCCTCCCAAGATTAAAGGATCACTGTATAGATTAAAAA 1532
Db      |||||||
Qy 2731 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2790
Db      |||||||
Qy 1533 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1592
Db      |||||||
Qy 2791 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2846
Db      |||||||
Qy 1593 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1648
Db      |||||||

RESULT 7
US-08-628-417-6
; Sequence 6, Application US/08628417
; Patent No. 5627054
; GENERAL INFORMATION:
; APPLICANT: GILLESPIE, DAVID
; TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
; ADDRESS: DEFENSE COMMAND
; STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
; CITY: ABERDEEN PROVING GROUND
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/628,417
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BIFFONI, ULYSSES J
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 398-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligodeoxynucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-628-417-6

Query Match      4.9%; Score 140; DB 1; Length 240;
Best Local Similarity 86.1%; Pred. No. 2.8e-23;
```

Matches 155; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

```
QY 2667 ATCTCTGTACACATTTTAAATAAGGTTGGCTTCTGAACACACAAAAA 2726
DB 19 AACTTTAGAAATAATTTTACTAAAAA 78
QY 2727 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2786
DB 79 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 138
QY 2787 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2846
DB 139 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 198
```

RESULT 8

US-09-640-173-53/c
; Sequence 53, Application US/09640173
; Patent No. 6613515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 210121.484C2
; CURRENT APPLICATION NUMBER: US/09/640,173
; CURRENT FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G

US-09-640-173-53

Query Match 4.9%; Score 138.4; DB 4; Length 396;
Best Local Similarity 79.3%; Pred. No. 8.5e-23;
Matches 157; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

```
QY 2649 TGGTCCTTTCTCCCATCTCTGTACACATTTTAAATAAGGTTGGCTTCTGA 2708
DB 280 TTTTATNTTTCTTTCTTTTNTGAAATTAANAAGGNAANAANAANNTAA 221
QY 2709 ACTACAAAAA 2768
DB 220 AAAAAA 161
QY 2769 AAAAAA 2828
DB 160 AAAAAA 101
QY 2829 AAAAAA 2846
DB 100 AAAAAA 83
```

RESULT 9

US-09-713-550-53/c
; Sequence 53, Application US/09713550
; Patent No. 6617109
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G

US-09-713-550-53

Query Match 4.9%; Score 138.4; DB 4; Length 396;
Best Local Similarity 79.3%; Pred. No. 8.5e-23;
Matches 157; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

```
QY 2649 TGGTCCTTTCTCCCATCTCTGTACACATTTTAAATAAGGTTGGCTTCTGA 2708
DB 280 TTTTATNTTTCTTTCTTTTNTGAAATTAANAAGGNAANAANAANNTAA 221
QY 2709 ACTACAAAAA 2768
DB 220 AAAAAA 161
QY 2769 AAAAAA 2828
DB 160 AAAAAA 101
QY 2829 AAAAAA 2846
DB 100 AAAAAA 83
```

RESULT 10

US-09-825-294-53/c
; Sequence 53, Application US/09825294
; Patent No. 6710170
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G

US-09-825-294-53

Query Match 4.9%; Score 138.4; DB 4; Length 396;
Best Local Similarity 79.3%; Pred. No. 8.5e-23;
Matches 157; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

```
QY 2649 TGGTCCTTTCTCCCATCTCTGTACACATTTTAAATAAGGTTGGCTTCTGA 2708
DB 280 TTTTATNTTTCTTTCTTTTNTGAAATTAANAAGGNAANAANAANNTAA 221
QY 2709 ACTACAAAAA 2768
DB 220 AAAAAA 161
QY 2769 AAAAAA 2828
DB 160 AAAAAA 101
```

QY	2829	AAAAAAAAAAAAAAAAAAAA	2846
Db	100	AAAAAAAAAAAAAAAAAAAA	83
RESULT 11			
US-09-970-966-53/c			
; Sequence 53, Application US/09970966			
; Patent No. 6720146			
; GENERAL INFORMATION:			
; APPLICANT: Stolk, John A.			
; APPLICANT: Molesch, David Alan			
; APPLICANT: Fling, Steven P.			
; APPLICANT: Xu, Jiangchun			
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER			
; FILE REFERENCE: 210121.484C6			
; CURRENT APPLICATION NUMBER: US/09/970,966			
; CURRENT FILING DATE: 2001-10-02			
; NUMBER OF SEQ ID NOS: 215			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 53			
; LENGTH: 396			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc feature			
; LOCATION: 224, 225, 228, 235, 240, 246, 257, 266, 274, 279, 281, 282,			
; LOCATION: 283, 285, 287, 288, 290, 291, 292, 293, 294, 295, 296, 297,			
; LOCATION: 300, 301, 303, 307, 311, 313, 314, 317, 318, 319, 320, 321,			
; LOCATION: 323, 324, 328, 329, 330, 336, 337, 338, 339, 340, 341			
; OTHER INFORMATION: n = A,T,C or G			
; NAME/KEY: misc feature			
; LOCATION: 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 356,			
; LOCATION: 357, 358, 359, 362, 363, 364, 365, 366, 367, 373, 380, 381,			
; LOCATION: 382, 385, 387, 388, 389, 390, 392			
; OTHER INFORMATION: n = A,T,C or G			
US-09-970-966-53			
Query Match			
Best Local Similarity 4.9%; Score 138.4; DB 4; Length 396;			
Matches 157; Conservative 0; Mismatches 41; Indels 0; Gaps 0;			
QY	2649	TGTCCTCTTTCTCCCATCTCTTGTCACACATTTTATAAATAAGGGTTGGCTTCTGA	2708
Db	280	TNTATNTTTCTTCTTTCTTTTNGAATTAAGNAAAGNAAANAAANAAANNTAA	221
QY	2709	ACTACAAAAA	2768
Db	220	AA	161
QY	2769	AA	2828
Db	160	AA	101
QY	2829	AAAAAAAAAAAAAAAAAAAA	2846
Db	100	AAAAAAAAAAAAAAAAAAAA	83
RESULT 12			
US-09-370-838-151			
; Sequence 151, Application US/09370838			
; Patent No. 644425			
; GENERAL INFORMATION:			
; APPLICANT: Reed, Steven G.			
; APPLICANT: Lodes, Michael J.			
; APPLICANT: Mohamath, Roadoh			
; APPLICANT: Secrist, Heather			
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF			
; FILE REFERENCE: 210121.475C1			
; CURRENT APPLICATION NUMBER: US/09/854,133			
; CURRENT FILING DATE: 2001-05-11			
; NUMBER OF SEQ ID NOS: 735			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 151			
; LENGTH: 3275			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-09-854-133-151			
Query Match			
Best Local Similarity 4.9%; Score 138.2; DB 4; Length 3275;			
Matches 146; Conservative 0; Mismatches 13; Indels 0; Gaps 0;			
QY	2688	AAATAAGGGTTGGCTTCTGAACCTACAA	2747
Db	3111	AATAAAGTTACATGCA	3170
QY	2748	AA	2807
Db	3171	AA	3230
QY	2808	AA	2846
Db	3231	AA	3269
RESULT 13			
US-09-854-133-151			
; Sequence 151, Application US/09854133			
; Patent No. 6759508			
; GENERAL INFORMATION:			
; APPLICANT: Lodes, Michael J.			
; APPLICANT: Mohamath, Roadoh			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: Benson, Darin R.			
; APPLICANT: Secrist, Heather			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR			
; FILE REFERENCE: 210121.475C10			
; CURRENT APPLICATION NUMBER: US/09/854,133			
; CURRENT FILING DATE: 2001-05-11			
; NUMBER OF SEQ ID NOS: 735			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 151			
; LENGTH: 3275			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-09-854-133-151			
Query Match			
Best Local Similarity 4.9%; Score 138.2; DB 4; Length 3275;			
Matches 146; Conservative 0; Mismatches 13; Indels 0; Gaps 0;			
QY	2688	AAATAAGGGTTGGCTTCTGAACCTACAA	2747
Db	3111	AATAAAGTTACATGCA	3170
QY	2748	AA	2807
Db	3171	AA	3230
QY	2808	AA	2846
Db	3231	AA	3269
RESULT 14			
US-09-797-906-1			
; Sequence 1, Application US/09797906			
; Patent No. 6329188			

GENERAL INFORMATION:
; APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
; TITLE OF INVENTION: ISOLATED HUMAN PROTEINASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001151CIP
; CURRENT APPLICATION NUMBER: US/09/797,906
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Human
US-09-797-906-1

Query Match 4.8%; Score 137.8; DB 3; Length 1798;
Best Local Similarity 95.3%; Pred. No. 2.6e-22;
Matches 142; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2698 TTGGCTTCTGAACTACAAAAA 2757
DB 1635 TTGGCAGTGGAAAAA 1694
QY 2758 AAAAAA 2817
DB 1695 AAAAAA 1754
QY 2818 AAAAAA 2846
DB 1755 AAAAAA 1783

RESULT 15
US-09-014-969-14
; Sequence 14, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavalie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09,14,969
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 2447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-014-969-14

Query Match 4.8%; Score 137; DB 2; Length 2447;
Best Local Similarity 84.9%; Pred. No. 4.6e-22;
Matches 152; Conservative 1; Mismatches 26; Indels 0; Gaps 0;
QY 2668 TCTCTTGACACATTTTAATAAATAAGGTTGGCTTCTGAACTACAAAAA 2727
DB 2208 TTTGTACTTTAAATGTGACAAATAAACCTTTTGGGAGAAAAA 2267
QY 2728 AAAAAA 2787
DB 2268 AAAAAA 2327
QY 2788 AAAAAA 2846
DB 2328 AAAAAA 2386

Search completed: May 6, 2005, 17:21:02
Job time : 381 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2005, 13:19:57 ; Search time 1080 Seconds
(without alignments)
16113.018 Million cell updates/sec

Perfect score: 2846
Sequence: 1 cgcctggcaccagccgcgg.....aaaaaaaaaaaaaaaaaaaaa 2846

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5654200 seqs, 3057283753 residues

Total number of hits satisfying chosen parameters: 11308400

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published Applications NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
27	2846	100.0	2846	10	US-09-997-428-230
560	2846	100.0	2846	16	US-10-174-587-169
624	2846	100.0	2846	16	US-10-063-742-37
739	2846	100.0	2846	19	US-10-972-317-37
740	2714.4	95.4	2846	15	US-10-101-510-644
741	2292.4	80.5	2632	17	US-10-274-639-38
742	2292.4	80.5	2632	17	US-10-333-574-38
743	2197.6	77.2	2306	14	US-10-004-551-3
744	2197.6	77.2	2306	15	US-10-098-871-25
745	2142.2	75.3	2259	13	US-10-067-422-2
746	1988.4	69.9	2144	15	US-10-037-270-969
747	1988.4	69.9	2144	17	US-10-117-722-969

748	1984.8	69.7	2142	15	US-10-037-270-1006	Sequence 1006, Ap
749	1984.8	69.7	2142	17	US-10-117-722-1006	Sequence 1006, Ap
750	1722	60.5	1867	14	US-10-004-551-1	Sequence 1, Appl
c 751	538.8	18.9	548	15	US-10-101-510-29	Sequence 29, Appl
c 752	409.4	14.4	997	11	US-09-876-143-1083	Sequence 1083, Ap
c 753	337	11.8	337	9	US-09-954-531-7893	Sequence 789, App
c 754	337	11.8	337	9	US-09-954-531-1223	Sequence 1223, Ap
c 755	337	11.8	337	19	US-10-843-641A-1856	Sequence 1856, Ap
c 756	337	11.8	337	19	US-10-843-641A-2290	Sequence 2290, Ap
c 757	283	9.9	403	10	US-09-918-995-6744	Sequence 6744, Ap
758	279.4	9.8	297	17	US-10-242-535A-12276	Sequence 12276, A
759	279.4	9.8	297	17	US-10-085-783A-12276	Sequence 12276, A
760	253.8	8.9	432	11	US-09-876-143-696	Sequence 696, App
761	218.4	7.7	286	13	US-10-027-632-275184	Sequence 275184, A
c 762	218.4	7.7	554	17	US-10-027-632-275184	Sequence 275184, A
c 763	218.4	7.7	554	17	US-09-903-393-1	Sequence 1, Appl
764	213.6	7.5	369	10	US-10-021-323-13303	Sequence 13303, A
765	145.8	5.1	476	18	US-10-021-323-13303	Sequence 13303, A
766	145.8	5.1	1423	18	US-10-767-795-3350	Sequence 3350, Ap
767	145.6	5.1	2057	17	US-10-266-829-15	Sequence 15, Appl
768	145.2	5.1	2177	18	US-10-425-115-115991	Sequence 115991, A
769	144.8	5.1	603	18	US-10-425-115-62402	Sequence 62402, A
770	144.8	5.1	608	18	US-10-021-323-636	Sequence 636, App
771	144.6	5.1	683	18	US-10-425-115-92182	Sequence 92182, A
c 772	144.4	5.1	483	18	US-10-021-323-16622	Sequence 16622, A
773	144	5.1	381	18	US-10-357-930-58681	Sequence 58681, A
c 774	144	5.1	597	18	US-10-021-323-138	Sequence 138, App
c 775	143.8	5.1	375	18	US-10-357-930-49930	Sequence 49930, A
776	143.8	5.1	488	18	US-10-425-115-47693	Sequence 47693, A
c 777	143.8	5.1	517	18	US-10-021-323-11054	Sequence 11054, A
778	143.8	5.1	547	18	US-10-021-323-8671	Sequence 8671, Ap
779	143.8	5.1	1999	18	US-10-723-860-7767	Sequence 7767, Ap
780	143.6	5.0	411	18	US-10-425-115-92368	Sequence 92368, A
781	143.6	5.0	2070	17	US-10-424-599-49593	Sequence 49593, A
782	143.2	5.0	547	18	US-10-021-323-6195	Sequence 6195, Ap
783	143.2	5.0	1400	17	US-10-424-599-125443	Sequence 125443, A
784	143	5.0	433	18	US-10-425-115-12621	Sequence 12621, A
785	143	5.0	2226	17	US-10-374-780A-1714	Sequence 1714, Ap
786	143	5.0	2226	17	US-10-412-699B-1354	Sequence 1354, Ap
787	142.8	5.0	458	18	US-10-021-323-11004	Sequence 11004, A
c 788	142.8	5.0	528	18	US-10-021-323-1809	Sequence 1809, Ap
c 789	142.8	5.0	565	18	US-10-021-323-11125	Sequence 11125, A
c 790	142.6	5.0	1301	18	US-10-021-323-16890	Sequence 16890, A
791	142.6	5.0	547	18	US-10-425-115-179473	Sequence 179473, A
792	142.6	5.0	2922	18	US-10-357-930-23149	Sequence 23149, A
c 793	142.4	5.0	560	18	US-10-021-323-2253	Sequence 2253, Ap
794	142.2	5.0	315	18	US-10-425-115-134227	Sequence 134227, A
c 795	142.2	5.0	397	9	US-09-960-352-13784	Sequence 13784, A
c 796	142.2	5.0	409	9	US-09-822-849A-37	Sequence 37, Appl
797	142.2	5.0	519	17	US-10-424-599-47977	Sequence 47977, A
798	142.2	5.0	524	18	US-10-425-115-56601	Sequence 56601, A
799	142.2	5.0	544	18	US-10-357-930-56643	Sequence 56643, A
c 800	142.2	5.0	681	9	US-09-822-830A-26	Sequence 26, Appl
c 801	142	5.0	496	18	US-10-021-323-17062	Sequence 17062, A
c 802	142	5.0	542	18	US-10-425-115-7873	Sequence 7873, Ap
c 803	142	5.0	684	18	US-10-425-115-110165	Sequence 110165, A
c 804	142	5.0	1215	18	US-10-723-860-5254	Sequence 5254, Ap
c 805	141.8	5.0	257	9	US-09-960-352-8890	Sequence 8890, Ap
806	141.8	5.0	2289	18	US-10-425-115-48241	Sequence 48241, A
c 807	141.8	5.0	2575	18	US-10-723-860-7683	Sequence 7683, Ap
c 808	141.6	5.0	487	18	US-10-021-323-2841	Sequence 2841, Ap
c 809	141.6	5.0	774	19	US-10-487-901-4626	Sequence 4626, Ap
c 810	141.6	5.0	8392	15	US-10-311-455-1463	Sequence 1463, Ap
c 811	141.6	5.0	11416	15	US-10-311-455-91	Sequence 91, Appl
c 812	141.6	5.0	14616	17	US-10-221-613-19	Sequence 19, Appl
c 813	141.6	5.0	16033	15	US-10-311-455-1377	Sequence 1377, Ap
c 814	141.4	5.0	286	9	US-09-960-352-13342	Sequence 13342, A
815	141.4	5.0	560	18	US-10-425-115-21207	Sequence 21207, A
816	141.4	5.0	609	18	US-10-437-963-23843	Sequence 23843, A
817	141.4	5.0	1123	18	US-10-739-930-3770	Sequence 3770, Ap
818	141.2	5.0	547	18	US-10-437-963-20806	Sequence 20806, A
819	141.2	5.0	904	18	US-10-425-115-51691	Sequence 51691, A
820	141.2	5.0	1245	18	US-10-425-115-15266	Sequence 15266, A

821	141.2	5.0	1678	18	US-10-425-115-71345	Sequence 71345, A	894	140	4.9	3101	17	US-10-424-599-95067	Sequence 95067, A
C 822	141.2	5.0	6775	18	US-10-433-793-189	Sequence 189, App	895	140	4.9	3931	15	US-10-723-860-5012	Sequence 5012, App
C 823	141	5.0	403	18	US-10-425-115-155989	Sequence 155989, A	896	140	4.9	3973	18	US-10-311-455-144	Sequence 144, App
C 824	141	5.0	421	18	US-10-425-115-167936	Sequence 167936, A	897	140	4.9	40324	18	US-10-433-793-179	Sequence 179, App
C 825	141	5.0	737	17	US-10-424-599-95307	Sequence 95307, A	898	139.8	4.9	516	18	US-10-437-963-99239	Sequence 99239, A
C 826	141	5.0	936	17	US-10-424-599-69900	Sequence 69900, A	899	139.8	4.9	528	17	US-10-424-599-37260	Sequence 37260, A
C 827	141	5.0	2265	18	US-10-425-115-28893	Sequence 28893, A	900	139.8	4.9	545	17	US-10-021-323-6889	Sequence 6889, App
C 828	141	5.0	4824	18	US-10-723-860-5191	Sequence 5191, App	901	139.8	4.9	564	17	US-10-424-599-39558	Sequence 39558, A
C 829	140.8	4.9	165	9	US-09-764-846-344	Sequence 344, App	902	139.8	4.9	1047	17	US-10-021-323-8346	Sequence 8346, App
C 830	140.8	4.9	165	10	US-09-764-872-709	Sequence 709, App	903	139.8	4.9	1047	17	US-10-366-288-47	Sequence 47, Appl
C 831	140.8	4.9	165	10	US-09-764-891-7491	Sequence 7491, App	904	139.8	4.9	1416	17	US-10-295-027-688	Sequence 688, App
C 832	140.8	4.9	165	10	US-09-764-891-9815	Sequence 9815, App	905	139.8	4.9	2235	19	US-10-087-553A-987	Sequence 987, App
C 833	140.8	4.9	165	14	US-10-091-483-344	Sequence 344, App	906	139.8	4.9	7115	18	US-10-723-860-7372	Sequence 7372, App
C 834	140.8	4.9	165	15	US-10-205-428-956	Sequence 956, App	907	139.6	4.9	432	18	US-10-425-115-94211	Sequence 94211, A
C 835	140.8	4.9	341	18	US-10-021-323-451	Sequence 451, App	908	139.6	4.9	490	18	US-10-357-930-57078	Sequence 57078, A
C 836	140.8	4.9	355	18	US-10-021-323-8650	Sequence 8650, App	909	139.6	4.9	540	18	US-10-021-323-10245	Sequence 10245, A
C 837	140.8	4.9	478	18	US-10-021-323-6774	Sequence 6774, App	910	139.6	4.9	545	18	US-10-021-323-6099	Sequence 6099, App
C 838	140.8	4.9	489	18	US-10-021-323-9165	Sequence 9165, App	911	139.6	4.9	578	18	US-10-021-323-7450	Sequence 7450, App
C 839	140.8	4.9	502	18	US-10-357-930-57784	Sequence 57784, A	912	139.6	4.9	698	9	US-09-764-846-131	Sequence 131, App
C 840	140.8	4.9	516	18	US-10-021-323-16986	Sequence 16986, A	913	139.6	4.9	698	14	US-10-091-483-131	Sequence 131, App
C 841	140.8	4.9	571	18	US-10-021-323-10114	Sequence 10114, A	914	139.6	4.9	736	17	US-10-424-599-60906	Sequence 60906, A
C 842	140.8	4.9	1696	14	US-10-274-971-1	Sequence 1, Appli	915	139.6	4.9	935	18	US-10-425-115-112572	Sequence 112572, A
C 843	140.8	4.9	1899	18	US-10-425-115-72710	Sequence 72710, A	916	139.6	4.9	1093	18	US-10-425-115-44079	Sequence 44079, A
C 844	140.8	4.9	2191	18	US-10-425-115-140658	Sequence 140658, A	917	139.6	4.9	1642	17	US-10-424-599-42140	Sequence 42140, A
C 845	140.8	4.9	8079	17	US-10-240-589C-122	Sequence 122, App	918	139.6	4.9	1678	18	US-10-437-963-95688	Sequence 95688, A
C 846	140.8	4.9	469	18	US-10-021-323-16830	Sequence 16830, A	919	139.6	4.9	2549	18	US-10-723-860-5438	Sequence 5438, App
C 847	140.6	4.9	549	18	US-10-437-963-43799	Sequence 43799, A	920	139.6	4.9	15749	18	US-10-723-860-6482	Sequence 6482, App
C 848	140.6	4.9	1233	18	US-10-425-115-82555	Sequence 82555, A	921	139.4	4.9	437	17	US-10-424-599-87401	Sequence 87401, A
C 849	140.6	4.9	1504	18	US-10-425-115-63627	Sequence 63627, A	922	139.4	4.9	509	18	US-10-021-323-6707	Sequence 6707, App
C 850	140.6	4.9	1521	17	US-10-172-118-1450	Sequence 1450, App	923	139.4	4.9	515	18	US-10-425-115-169633	Sequence 169633, A
C 851	140.6	4.9	1521	17	US-10-342-887-1450	Sequence 1450, App	924	139.4	4.9	516	18	US-10-021-323-10534	Sequence 10534, A
C 852	140.6	4.9	1576	18	US-10-723-860-5808	Sequence 5808, App	925	139.4	4.9	552	18	US-10-021-323-17351	Sequence 17351, A
C 853	140.6	4.9	1803	17	US-10-374-780A-1279	Sequence 1279, App	926	139.4	4.9	1880	18	US-10-425-115-44753	Sequence 44753, A
C 854	140.6	4.9	1803	17	US-10-412-699B-1438	Sequence 1438, App	927	139.4	4.9	3673778	16	US-10-312-841-2	Sequence 2, Appli
C 855	140.6	4.9	1811	17	US-10-424-599-59218	Sequence 59218, A	928	139.2	4.9	431	18	US-10-021-323-15260	Sequence 15260, A
C 856	140.6	4.9	2525	17	US-10-424-599-101605	Sequence 101605, A	929	139.2	4.9	467	18	US-10-437-963-94117	Sequence 94117, A
C 857	140.6	4.9	2809	17	US-10-172-118-340	Sequence 340, App	930	139.2	4.9	571	18	US-10-021-323-7115	Sequence 7115, App
C 858	140.6	4.9	2809	17	US-10-342-887-340	Sequence 340, App	931	139.2	4.9	575	17	US-10-424-599-71318	Sequence 71318, A
C 859	140.6	4.9	3505	17	US-10-389-566-204	Sequence 204, App	932	139.2	4.9	647	18	US-10-425-115-18397	Sequence 18397, A
C 860	140.6	4.9	327	9	US-09-960-352-4630	Sequence 4630, App	933	139.2	4.9	937	17	US-10-424-599-69518	Sequence 69518, A
C 861	140.4	4.9	381	18	US-10-021-323-10489	Sequence 10489, A	934	139.2	4.9	1071	17	US-10-170-385-338	Sequence 338, App
C 862	140.4	4.9	495	18	US-10-021-323-2679	Sequence 2679, App	935	139.2	4.9	1235	18	US-10-425-115-165957	Sequence 165957, A
C 863	140.4	4.9	515	17	US-10-424-599-106126	Sequence 106126, A	936	139.2	4.9	1466	18	US-10-425-115-176985	Sequence 176985, A
C 864	140.4	4.9	576	17	US-10-424-599-126135	Sequence 126135, A	937	139.2	4.9	1975	18	US-10-425-115-176985	Sequence 176985, A
C 865	140.4	4.9	592	18	US-10-425-115-105613	Sequence 105613, A	938	139.2	4.9	2190	17	US-10-425-115-80851	Sequence 80851, A
C 866	140.4	4.9	899	18	US-10-437-963-27088	Sequence 27088, A	939	139.2	4.9	4237	9	US-10-424-599-9903	Sequence 9903, App
C 867	140.4	4.9	945	18	US-10-425-115-13415	Sequence 13415, A	940	139.2	4.9	21354	17	US-09-745-763-20	Sequence 20, Appl
C 868	140.4	4.9	1176	18	US-10-425-115-60769	Sequence 60769, A	941	139	4.9	422	18	US-10-221-744A-512	Sequence 512, App
C 869	140.4	4.9	1198	9	US-09-789-561-55	Sequence 55, Appl	942	139	4.9	439	18	US-10-425-115-108647	Sequence 108647, A
C 870	140.4	4.9	1198	19	US-10-883-936-55	Sequence 55, Appl	943	139	4.9	439	18	US-10-357-930-57531	Sequence 57531, A
C 871	140.4	4.9	1362	17	US-10-424-599-37296	Sequence 37296, A	944	139	4.9	537	18	US-10-021-323-7228	Sequence 7228, App
C 872	140.4	4.9	1958	17	US-10-424-599-60709	Sequence 60709, A	945	139	4.9	564	18	US-10-425-115-148098	Sequence 148098, A
C 873	140.4	4.9	2094	18	US-10-425-115-51614	Sequence 51614, A	946	139	4.9	582	18	US-10-425-115-177666	Sequence 177666, A
C 874	140.4	4.9	2094	18	US-10-425-115-51614	Sequence 51614, A	947	139	4.9	654	18	US-10-425-115-83069	Sequence 83069, A
C 875	140.4	4.9	11729	15	US-10-311-455-868	Sequence 868, App	948	139	4.9	654	17	US-10-424-599-116277	Sequence 116277, A
C 876	140.4	4.9	260	17	US-10-242-535A-40371	Sequence 40371, A	949	139	4.9	716	19	US-10-764-420-422	Sequence 422, App
C 877	140.2	4.9	260	17	US-10-085-783A-40371	Sequence 40371, A	950	139	4.9	2050	18	US-10-723-860-6437	Sequence 6437, App
C 878	140.2	4.9	638	17	US-10-424-599-125433	Sequence 125433, A	951	139	4.9	2520	17	US-10-389-566-205	Sequence 205, App
C 879	140.2	4.9	1495	17	US-10-424-599-35899	Sequence 35899, A	952	139	4.9	5845	15	US-10-311-455-1635	Sequence 1635, App
C 880	140	4.9	242	9	US-09-960-352-3873	Sequence 3873, App	953	139	4.9	7306	15	US-10-311-455-1610	Sequence 1610, App
C 881	140	4.9	359	18	US-10-425-115-99058	Sequence 99058, A	954	139	4.9	12007	15	US-10-311-455-690	Sequence 690, App
C 882	140	4.9	564	18	US-10-021-323-7972	Sequence 7972, App	955	139	4.9	3673778	16	US-10-312-841-1	Sequence 1, Appli
C 883	140	4.9	630	18	US-10-425-115-95100	Sequence 95100, A	956	138.8	4.9	359	18	US-10-437-963-76171	Sequence 76171, A
C 884	140	4.9	684	18	US-10-425-115-168572	Sequence 168572, A	957	138.8	4.9	466	17	US-10-424-599-71764	Sequence 71764, A
C 885	140	4.9	760	18	US-10-357-930-29499	Sequence 29499, A	958	138.8	4.9	486	18	US-10-021-323-8387	Sequence 8387, App
C 886	140	4.9	973	17	US-10-424-599-58879	Sequence 58879, A	959	138.8	4.9	496	18	US-10-021-323-4109	Sequence 4109, App
C 887	140	4.9	1068	18	US-10-437-963-86611	Sequence 86611, A	960	138.8	4.9	524	18	US-10-425-115-137716	Sequence 137716, A
C 888	140	4.9	1110	18	US-10-437-963-86659	Sequence 86659, A	961	138.8	4.9	546	18	US-10-425-115-162816	Sequence 162816, A
C 889	140	4.9	1463	17	US-10-424-599-88284	Sequence 88284, A	962	138.8	4.9	662	18	US-10-425-115-104281	Sequence 104281, A
C 890	140	4.9	1603	18	US-10-357-930-22091	Sequence 22091, A	963	138.8	4.9	718	18	US-10-425-115-154975	Sequence 154975, A
C 891	140	4.9	1603	18	US-10-357-930-23103	Sequence 23103, A	964	138.8	4.9	895	18	US-10-425-115-135838	Sequence 135838, A
C 892	140	4.9	1603	18	US-10-357-930-27953	Sequence 27953, A	965	138.8	4.9	924	18	US-10-425-115-173094	Sequence 173094, A
C 893	140	4.9	1603	18	US-10-357-930-28971	Sequence 28971, A	966	138.8	4.9	936	9	US-09-739-907-47	Sequence 47, Appl

967	138.8	4.9	936	11	US-09-938-671-47	Sequence 47, Appl	1040	138	4.8	2372	18	US-10-425-115-58985	Sequence 5985, A
968	138.8	4.9	936	19	US-10-935-098-47	Sequence 47, Appl	c1041	138	4.8	2585	18	US-10-425-115-54177	Sequence 54177, A
969	138.8	4.9	1070	18	US-10-425-115-61473	Sequence 61473, A	c1042	138	4.8	8946	15	US-10-311-455-884	Sequence 884, App
970	138.8	4.9	1186	18	US-10-425-115-129960	Sequence 129960, A	c1043	138	4.8	113515	15	US-10-311-455-2147	Sequence 2147, App
c 971	138.8	4.9	1302	18	US-10-425-115-83709	Sequence 83709, A	1044	137.8	4.8	375	17	US-10-424-599-58586	Sequence 58586, A
972	138.8	4.9	1929	8	US-10-425-115-161709	Sequence 161709, A	1045	137.8	4.8	388	17	US-10-424-599-131162	Sequence 131162, A
973	138.8	4.9	2753	9	US-09-789-561-15	Sequence 15, Appl	1046	137.8	4.8	522	18	US-10-021-323-869	Sequence 869, App
974	138.8	4.9	2753	19	US-10-883-936-15	Sequence 15, Appl	1047	137.8	4.8	524	18	US-10-425-115-109499	Sequence 109499, A
c 975	138.8	4.9	15832	14	US-10-239-676-106	Sequence 106, App	1048	137.8	4.8	526	18	US-10-425-115-130137	Sequence 130137, A
c 976	138.8	4.9	15832	15	US-10-311-455-1316	Sequence 1316, App	1049	137.8	4.8	587	18	US-10-425-115-172648	Sequence 172648, A
c 977	138.8	4.9	15832	15	US-10-240-453-118	Sequence 118, App	1050	137.8	4.8	619	18	US-10-425-115-102831	Sequence 102831, A
978	138.6	4.9	309	18	US-10-357-930-45013	Sequence 45013, A	1051	137.8	4.8	657	18	US-10-425-115-60368	Sequence 60368, A
c 979	138.6	4.9	313	18	US-10-021-323-13390	Sequence 13390, A	1052	137.8	4.8	684	18	US-10-425-115-62433	Sequence 62433, A
980	138.6	4.9	481	18	US-10-021-323-14917	Sequence 14917, A	1053	137.8	4.8	738	18	US-10-425-115-178509	Sequence 178509, A
981	138.6	4.9	514	18	US-10-425-115-74503	Sequence 74503, A	1054	137.8	4.8	1159	18	US-10-425-115-6815	Sequence 6815, App
982	138.6	4.9	538	18	US-10-021-323-870	Sequence 870, App	1055	137.8	4.8	2333	17	US-10-424-599-127867	Sequence 127867, A
983	138.6	4.9	545	17	US-10-424-599-4829	Sequence 4829, App	1056	137.8	4.8	2617	17	US-10-425-115-151022	Sequence 151022, A
984	138.6	4.9	578	17	US-10-424-599-133291	Sequence 133291, A	1057	137.8	4.8	5195	15	US-10-311-455-894	Sequence 894, App
985	138.6	4.9	583	18	US-10-767-795-134	Sequence 134, App	1058	137.8	4.8	6944	15	US-10-172-086-112	Sequence 112, App
986	138.6	4.9	595	18	US-10-425-115-175716	Sequence 175716, A	1059	137.8	4.8	6944	18	US-10-311-507-114	Sequence 114, App
987	138.6	4.9	640	18	US-10-021-323-8853	Sequence 8853, App	1060	137.8	4.8	6944	18	US-10-480-846-112	Sequence 112, App
c 988	138.6	4.9	893	14	US-10-198-846-7225	Sequence 7225, App	1061	137.6	4.8	325	17	US-10-424-599-59828	Sequence 59828, A
c 989	138.6	4.9	893	14	US-10-357-930-4784	Sequence 4784, App	1062	137.6	4.8	389	18	US-10-437-963-8873	Sequence 8873, App
c 990	138.6	4.9	2134	18	US-10-425-115-176649	Sequence 176649, A	1063	137.6	4.8	406	10	US-09-814-353-4900	Sequence 4900, App
991	138.6	4.9	2055	18	US-10-425-115-128140	Sequence 128140, A	1064	137.6	4.8	406	10	US-09-814-353-11195	Sequence 11195, A
c 992	138.6	4.9	14006	15	US-10-311-455-1931	Sequence 1931, App	1065	137.6	4.8	411	18	US-10-021-323-7694	Sequence 7694, App
c 993	138.6	4.9	396	9	US-09-825-284-53	Sequence 53, Appl	1066	137.6	4.8	419	9	US-09-960-352-11234	Sequence 11234, App
c 994	138.4	4.9	396	15	US-09-970-966-53	Sequence 53, Appl	1067	137.6	4.8	479	18	US-10-425-115-158896	Sequence 158896, A
c 995	138.4	4.9	396	15	US-10-212-677-53	Sequence 53, Appl	1068	137.6	4.8	485	18	US-10-021-323-8174	Sequence 8174, App
c 996	138.4	4.9	396	17	US-10-361-811-53	Sequence 53, Appl	1069	137.6	4.8	490	18	US-10-021-323-16197	Sequence 16197, A
c 997	138.4	4.9	396	17	US-10-369-186-53	Sequence 53, Appl	1070	137.6	4.8	512	18	US-10-425-115-1891	Sequence 1891, App
998	138.4	4.9	524	17	US-10-424-599-11691	Sequence 11691, A	1071	137.6	4.8	538	18	US-10-021-323-14752	Sequence 14752, A
c1000	138.4	4.9	567	18	US-10-021-323-8240	Sequence 8240, App	1072	137.6	4.8	556	18	US-10-357-930-40082	Sequence 40082, A
c1001	138.4	4.9	583	18	US-10-021-323-6081	Sequence 6081, App	1073	137.6	4.8	556	18	US-10-357-930-40082	Sequence 40182, A
c1002	138.4	4.9	602	18	US-10-425-115-61525	Sequence 61525, A	1074	137.6	4.8	556	18	US-10-357-930-42124	Sequence 42124, A
1003	138.4	4.9	687	17	US-10-424-599-115631	Sequence 115631, A	1075	137.6	4.8	556	18	US-10-357-930-43620	Sequence 43620, A
1004	138.4	4.9	704	18	US-10-425-115-21405	Sequence 21405, A	1076	137.6	4.8	563	18	US-10-021-323-13758	Sequence 13758, A
1005	138.4	4.9	767	17	US-10-424-599-45104	Sequence 45104, A	1077	137.6	4.8	600	18	US-10-425-115-76887	Sequence 76887, A
1006	138.4	4.9	1211	18	US-10-739-930-4124	Sequence 4124, App	1078	137.6	4.8	655	17	US-10-424-599-107600	Sequence 107600, A
1007	138.4	4.9	1316	9	US-10-425-115-109626	Sequence 109626, A	1079	137.6	4.8	697	18	US-10-425-115-20836	Sequence 20836, A
1008	138.4	4.9	2921	9	US-09-925-301-223	Sequence 223, App	1080	137.6	4.8	751	18	US-10-425-115-71448	Sequence 71448, A
c1009	138.4	4.9	3569	18	US-10-767-701-14981	Sequence 14981, A	1081	137.6	4.8	1278	18	US-10-425-115-58302	Sequence 58302, A
c1010	138.4	4.9	6486	18	US-10-433-726-80	Sequence 80, Appl	1082	137.6	4.8	1671	15	US-10-311-455-761	Sequence 761, App
c1011	138.4	4.9	7369	18	US-10-473-123-131	Sequence 131, App	1083	137.4	4.8	231	17	US-10-242-535A-30412	Sequence 30412, A
c1012	138.4	4.9	7369	19	US-10-486-319A-34	Sequence 34, Appl	1084	137.4	4.8	231	17	US-10-085-783A-30412	Sequence 30412, A
c1013	138.4	4.9	10369	15	US-10-311-455-365	Sequence 365, App	1085	137.4	4.8	464	15	US-10-106-698-307	Sequence 307, App
c1014	138.2	4.9	10369	17	US-10-221-714A-25	Sequence 25, Appl	1086	137.4	4.8	506	18	US-10-021-323-2311	Sequence 2311, App
1015	138.2	4.9	325	18	US-10-021-323-8658	Sequence 8658, App	1087	137.4	4.8	601	18	US-10-425-115-170372	Sequence 170372, A
c1016	138.2	4.9	334	17	US-10-424-599-120844	Sequence 120844, A	1088	137.4	4.8	605	17	US-10-424-599-39289	Sequence 39289, A
c1017	138.2	4.9	351	10	US-09-814-353-17579	Sequence 17579, A	1089	137.4	4.8	606	18	US-10-437-963-54715	Sequence 54715, A
c1018	138.2	4.9	452	18	US-10-021-323-4768	Sequence 4768, App	1090	137.4	4.8	627	17	US-10-424-599-50144	Sequence 50144, A
1019	138.2	4.9	485	18	US-10-021-323-6802	Sequence 6802, App	1091	137.4	4.8	640	17	US-10-424-599-122753	Sequence 122753, A
1020	138.2	4.9	552	18	US-10-425-115-42027	Sequence 42027, A	1092	137.4	4.8	641	17	US-10-424-599-117136	Sequence 117136, A
1021	138.2	4.9	626	18	US-10-425-115-52818	Sequence 52818, A	1093	137.4	4.8	1004	18	US-10-425-115-75154	Sequence 75154, A
1022	138.2	4.9	768	18	US-10-425-115-98337	Sequence 98337, A	1094	137.4	4.8	1016	17	US-10-424-599-133400	Sequence 133400, A
1023	138.2	4.9	1056	18	US-10-425-115-114365	Sequence 114365, A	1095	137.4	4.8	1103	17	US-10-425-115-68317	Sequence 68317, A
1024	138.2	4.9	1134	18	US-10-425-115-164438	Sequence 164438, A	1096	137.4	4.8	1367	18	US-10-425-115-85766	Sequence 85766, A
1025	138.2	4.9	1708	17	US-10-310-154-71	Sequence 71, Appl	1097	137.4	4.8	2971	18	US-10-425-115-103107	Sequence 103107, A
1026	138.2	4.9	2785	18	US-10-723-860-5447	Sequence 5447, App	1098	137.4	4.8	5241	17	US-10-221-613-414	Sequence 414, App
1027	138.2	4.9	3275	9	US-09-738-973-151	Sequence 151, App	1099	137.2	4.8	368	18	US-10-425-115-138566	Sequence 138566, A
1028	138.2	4.9	3275	15	US-10-854-133-151	Sequence 151, App	1100	137.2	4.8	393	9	US-09-960-352-4582	Sequence 4582, App
1029	138.2	4.9	3275	15	US-10-144-649A-151	Sequence 151, App	1101	137.2	4.8	394	18	US-10-425-115-118177	Sequence 118177, A
1030	138.2	4.9	3454	18	US-10-723-860-6412	Sequence 6412, App	1102	137.2	4.8	408	9	US-09-960-352-6263	Sequence 6263, App
c1031	138.2	4.9	6436	15	US-10-311-455-654	Sequence 654, App	1103	137.2	4.8	472	18	US-10-425-115-88743	Sequence 88743, A
c1032	138	4.8	499	18	US-10-021-323-1716	Sequence 1716, App	1104	137.2	4.8	502	18	US-10-021-323-11431	Sequence 11431, A
c1033	138	4.8	560	18	US-10-021-323-3016	Sequence 3016, App	1105	137.2	4.8	549	18	US-10-021-323-7101	Sequence 7101, App
c1034	138	4.8	574	18	US-10-021-323-7391	Sequence 7391, App	1106	137.2	4.8	568	17	US-10-424-599-117111	Sequence 117111, A
1035	138	4.8	577	18	US-10-425-115-89366	Sequence 89366, A	1107	137.2	4.8	568	18	US-10-425-115-22899	Sequence 22899, A
c1036	138	4.8	592	14	US-10-198-846-8340	Sequence 8340, App	1108	137.2	4.8	569	18	US-10-425-115-88900	Sequence 88900, A
1037	138	4.8	608	18	US-10-425-115-157602	Sequence 157602, A	1109	137.2	4.8	573	18	US-10-425-115-31452	Sequence 31452, A
1038	138	4.8	1137	18	US-10-739-930-635	Sequence 635, App	1110	137.2	4.8	590	17	US-10-424-599-118116	Sequence 118116, A
1039	138	4.8	2022	18	US-10-739-930-4367	Sequence 4367, App	1111	137.2	4.8	633	18	US-10-425-115-8940	Sequence 8940, App
							1112	137.2	4.8	647	18	US-10-425-115-170206	Sequence 170206, A

1113	137.2	4.8	671	18	US-10-021-323-9268	Sequence 9268, Ap	1186	136.6	4.8	1460	17	US-10-424-599-142655	Sequence 142655, A
c1114	137.2	4.8	711	17	US-10-424-599-42333	Sequence 42333, A	1187	136.6	4.8	1583	18	US-10-425-115-57459	Sequence 57459, A
1115	137.2	4.8	714	17	US-10-424-599-80204	Sequence 80204, A	1188	136.6	4.8	2094	18	US-10-424-599-133718	Sequence 133718, A
1116	137.2	4.8	1078	18	US-10-425-115-13215	Sequence 13215, A	1189	136.6	4.8	2207	18	US-10-425-115-145441	Sequence 145441, A
c1117	137.2	4.8	1285	17	US-10-424-599-115563	Sequence 115563, A	c1190	136.6	4.8	2235	17	US-10-424-599-70027	Sequence 70027, A
c1118	137.2	4.8	1302	18	US-10-425-115-56162	Sequence 56162, A	1191	136.6	4.8	2248	18	US-10-425-115-65796	Sequence 65796, A
c1119	137.2	4.8	1533	18	US-10-732-860-7968	Sequence 7968, Ap	c1192	136.6	4.8	11394	15	US-10-240-453-96	Sequence 96, Appl
1120	137.2	4.8	1617	18	US-10-425-115-164014	Sequence 164014, A	c1193	136.6	4.8	2140405	13	US-10-027-632-76212	Sequence 76212, A
1121	137.2	4.8	1743	17	US-10-424-599-56660	Sequence 56660, A	c1194	136.6	4.8	2140405	17	US-10-027-632-76212	Sequence 76212, A
1122	137.2	4.8	1808	9	US-09-989-920-46	Sequence 46, Appl	c1195	136.4	4.8	333	17	US-10-424-599-53217	Sequence 53217, A
1123	137.2	4.8	2009	18	US-10-425-115-1808	Sequence 1808, Ap	1196	136.4	4.8	424	18	US-10-437-963-34803	Sequence 34803, A
c1124	137.2	4.8	2096	18	US-10-425-115-27838	Sequence 27838, A	1197	136.4	4.8	424	18	US-10-425-115-52807	Sequence 52807, A
c1125	137.2	4.8	3177	15	US-10-311-455-624	Sequence 624, App	c1198	136.4	4.8	446	9	US-09-960-352-3400	Sequence 3400, Ap
1126	137	4.8	3187	18	US-10-021-323-6340	Sequence 6340, App	c1199	136.4	4.8	447	18	US-10-425-115-148961	Sequence 148961, A
1127	137	4.8	338	18	US-10-425-115-65485	Sequence 65485, A	c1200	136.4	4.8	469	18	US-10-021-323-6668	Sequence 6668, Ap
1128	137	4.8	339	18	US-10-425-115-98529	Sequence 98529, A	1201	136.4	4.8	516	18	US-10-357-930-55908	Sequence 55908, A
1129	137	4.8	372	18	US-10-425-115-24788	Sequence 24788, A	c1202	136.4	4.8	539	10	US-09-814-353-17862	Sequence 17862, A
1130	137	4.8	430	18	US-10-425-115-170993	Sequence 170993, A	1203	136.4	4.8	539	17	US-10-424-599-76890	Sequence 76890, A
1131	137	4.8	497	18	US-10-357-930-58292	Sequence 58292, A	c1204	136.4	4.8	553	18	US-10-021-323-7987	Sequence 7987, Ap
1132	137	4.8	554	18	US-10-425-115-23306	Sequence 23306, A	1205	136.4	4.8	601	17	US-10-424-599-59636	Sequence 59636, A
1133	137	4.8	561	18	US-10-425-115-169551	Sequence 169551, A	1206	136.4	4.8	617	17	US-10-424-599-71934	Sequence 71934, A
1134	137	4.8	626	18	US-10-425-115-62540	Sequence 62540, Ap	1207	136.4	4.8	822	17	US-10-424-599-111916	Sequence 11916, A
1135	137	4.8	1140	18	US-10-437-963-26438	Sequence 26438, A	1208	136.4	4.8	1519	18	US-10-425-115-17631	Sequence 17631, A
c1136	137	4.8	2142	17	US-10-424-599-118533	Sequence 118533, A	1209	136.4	4.8	1875	17	US-10-374-780A-1941	Sequence 1941, Ap
1137	137	4.8	2197	18	US-10-425-115-18496	Sequence 18496, A	c1210	136.4	4.8	5586	17	US-10-257-166-86	Sequence 86, Appl
c1138	137	4.8	2700	18	US-10-723-860-5126	Sequence 5126, Ap	c1211	136.4	4.8	24259	17	US-10-021-323-3385	Sequence 3385, Ap
c1139	137	4.8	6172	15	US-10-240-485-126	Sequence 126, App	1212	136.2	4.8	450	18	US-10-021-323-4616	Sequence 4616, Ap
c1140	136.8	4.8	241	9	US-09-960-352-5777	Sequence 5777, Ap	c1213	136.2	4.8	459	18	US-10-357-930-54303	Sequence 54303, A
1141	136.8	4.8	421	18	US-10-021-323-7658	Sequence 7658, Ap	1214	136.2	4.8	481	18	US-10-357-930-56267	Sequence 56267, A
1142	136.8	4.8	456	9	US-09-960-352-9659	Sequence 9659, Ap	1215	136.2	4.8	510	18	US-10-767-795-5097	Sequence 5097, Ap
1143	136.8	4.8	463	17	US-10-424-599-101158	Sequence 101158, A	c1216	136.2	4.8	518	18	US-10-021-323-4634	Sequence 4634, Ap
1144	136.8	4.8	520	18	US-10-425-115-132906	Sequence 132906, A	c1217	136.2	4.8	528	18	US-10-021-323-8131	Sequence 8131, Ap
1145	136.8	4.8	543	18	US-10-425-115-148211	Sequence 148211, A	c1218	136.2	4.8	541	18	US-10-437-963-8817	Sequence 8817, Ap
1146	136.8	4.8	570	18	US-10-357-930-59133	Sequence 59133, A	c1219	136.2	4.8	558	18	US-10-425-115-54818	Sequence 54818, A
1147	136.8	4.8	591	18	US-10-021-323-13007	Sequence 13007, A	1221	136.2	4.8	1093	17	US-10-424-599-95648	Sequence 95648, A
1148	136.8	4.8	612	17	US-10-424-599-50936	Sequence 50936, A	1222	136.2	4.8	1093	18	US-10-425-115-108606	Sequence 108606, A
1149	136.8	4.8	677	18	US-10-425-115-131288	Sequence 131288, A	1223	136.2	4.8	1138	18	US-10-425-115-54043	Sequence 54043, A
1150	136.8	4.8	762	17	US-10-424-599-34277	Sequence 34277, A	1224	136.2	4.8	1323	18	US-10-425-115-42749	Sequence 42749, A
1151	136.8	4.8	831	9	US-09-729-674-67	Sequence 67, Appl	1225	136.2	4.8	1405	18	US-10-424-599-96402	Sequence 96402, A
1152	136.8	4.8	831	18	US-10-913-553-67	Sequence 67, Appl	1226	136.2	4.8	1638	17	US-10-424-599-96402	Sequence 96402, A
1153	136.8	4.8	1091	18	US-10-723-860-6015	Sequence 6015, Ap	1227	136.2	4.8	2481	18	US-10-425-115-440	Sequence 440, App
1154	136.8	4.8	1131	18	US-10-425-115-59679	Sequence 59679, A	c1228	136.2	4.8	24259	17	US-10-221-714A-415	Sequence 415, App
1155	136.8	4.8	1170	18	US-10-425-115-136412	Sequence 136412, A	1229	136	4.8	138	17	US-10-242-535A-50216	Sequence 50216, A
1156	136.8	4.8	1492	18	US-10-425-115-103271	Sequence 103271, A	1230	136	4.8	138	17	US-10-085-783A-50216	Sequence 50216, A
1157	136.8	4.8	2091	18	US-10-425-115-93227	Sequence 93227, A	1231	136	4.8	362	18	US-10-425-115-36607	Sequence 36607, A
1158	136.8	4.8	2148	17	US-10-739-930-2257	Sequence 2257, Ap	1232	136	4.8	419	17	US-10-424-599-58948	Sequence 58948, A
c1159	136.8	4.8	2270	17	US-10-424-599-44604	Sequence 44604, A	1233	136	4.8	446	18	US-10-424-599-18435	Sequence 18435, A
1160	136.8	4.8	2322	17	US-10-424-599-1231	Sequence 1231, Ap	c1234	136	4.8	483	18	US-10-021-323-16008	Sequence 16008, A
1161	136.8	4.8	3758	18	US-10-437-963-81706	Sequence 81706, A	1235	136	4.8	489	18	US-10-425-115-144831	Sequence 144831, A
c1162	136.8	4.8	6161	15	US-10-311-455-384	Sequence 384, App	c1236	136	4.8	489	18	US-10-021-323-4517	Sequence 4517, Ap
c1163	136.8	4.8	6192	17	US-10-473-126-277	Sequence 277, App	c1237	136	4.8	508	18	US-10-021-323-3403	Sequence 3403, Ap
c1164	136.8	4.8	7369	18	US-10-473-126-277	Sequence 277, App	1238	136	4.8	526	18	US-10-021-323-14764	Sequence 14764, A
c1165	136.8	4.8	7369	19	US-10-486-319A-56	Sequence 56, Appl	c1239	136	4.8	527	18	US-10-021-323-16206	Sequence 16206, A
1166	136.6	4.8	212	17	US-10-242-535A-22243	Sequence 22243, A	c1239	136	4.8	586	18	US-10-437-963-45637	Sequence 45637, A
1167	136.6	4.8	212	17	US-10-085-783A-22243	Sequence 22243, A	c1241	136	4.8	615	18	US-10-425-115-172581	Sequence 172581, A
c1168	136.6	4.8	220	9	US-09-960-352-14522	Sequence 14522, A	1240	136	4.8	643	17	US-10-424-599-97217	Sequence 97217, A
1169	136.6	4.8	394	18	US-10-357-930-13555	Sequence 13555, A	1242	136	4.8	658	18	US-10-425-115-51887	Sequence 51887, A
1170	136.6	4.8	408	18	US-10-357-930-34697	Sequence 34697, A	1243	136	4.8	685	18	US-10-425-115-131293	Sequence 131293, A
1171	136.6	4.8	408	18	US-10-357-930-43554	Sequence 43554, A	1244	136	4.8	871	18	US-10-425-115-177814	Sequence 177814, A
1172	136.6	4.8	426	18	US-10-021-323-9484	Sequence 9484, Ap	1245	136	4.8	897	18	US-10-425-115-97521	Sequence 97521, A
1173	136.6	4.8	484	18	US-10-357-930-58027	Sequence 58027, A	c1246	136	4.8	947	18	US-10-425-115-25975	Sequence 25975, A
1174	136.6	4.8	531	17	US-10-424-599-54674	Sequence 54674, A	1247	136	4.8	1012	18	US-10-425-115-168545	Sequence 168545, A
1175	136.6	4.8	539	18	US-10-425-115-152949	Sequence 152949, A	c1248	136	4.8	1086	18	US-10-425-115-168545	Sequence 168545, A
1176	136.6	4.8	545	18	US-10-425-115-38204	Sequence 38204, A	1249	136	4.8	1233	17	US-10-424-599-44264	Sequence 44264, A
1177	136.6	4.8	554	18	US-10-425-115-882	Sequence 882, App	1250	136	4.8	1243	18	US-10-425-115-133710	Sequence 133710, A
1178	136.6	4.8	566	18	US-10-767-701-17472	Sequence 17472, A	1251	136	4.8	1712	18	US-10-425-115-13539	Sequence 13539, A
1179	136.6	4.8	584	18	US-10-425-115-33678	Sequence 33678, A	1252	136	4.8	1806	18	US-10-775-920-425	Sequence 225, App
1180	136.6	4.8	588	18	US-10-437-963-55397	Sequence 55397, A	1253	136	4.8	2323	18	US-10-425-115-19557	Sequence 19557, A
1181	136.6	4.8	596	17	US-10-424-599-18370	Sequence 18370, A	1254	136	4.8	3908	18	US-10-425-115-70814	Sequence 70814, A
c1182	136.6	4.8	599	14	US-10-198-846-8885	Sequence 8885, Ap	c1255	135.8	4.8	385	18	US-10-425-115-125187	Sequence 125187, A
1183	136.6	4.8	627	18	US-10-021-323-73	Sequence 73, Appl	1256	135.8	4.8	396	18	US-10-357-930-57615	Sequence 57615, A
1184	136.6	4.8	701	17	US-10-424-599-66331	Sequence 66331, A	1257	135.8	4.8	432	17	US-10-424-599-83231	Sequence 83231, A
1185	136.6	4.8	1398	18	US-10-425-115-169951	Sequence 169951, A	1258	135.8	4.8	443	18	US-10-021-323-6814	Sequence 6814, Ap

1259	135.8	4.8	500	18	US-10-425-115-170711	Sequence 170711, App	1332	135.4	4.8	3415	9	US-09-823-245A-438	Sequence 438, App
1260	135.8	4.8	528	18	US-10-425-115-7487	Sequence 7487, App	c1333	135.2	4.8	378	18	US-10-425-115-80509	Sequence 80509, A
1261	135.8	4.8	532	17	US-10-424-599-43810	Sequence 43810, A	c1334	135.2	4.8	385	18	US-10-357-930-54260	Sequence 54260, A
1262	135.8	4.8	549	18	US-10-357-930-56681	Sequence 56681, A	1335	135.2	4.8	389	17	US-10-425-115-11841	Sequence 11841, A
1263	135.8	4.8	567	17	US-10-424-599-68710	Sequence 68710, A	1336	135.2	4.8	416	17	US-10-424-599-71220	Sequence 71220, A
1264	135.8	4.8	574	18	US-10-021-323-11147	Sequence 11147, A	1337	135.2	4.8	446	18	US-10-425-115-136246	Sequence 136246, A
1265	135.8	4.8	582	18	US-10-425-115-115626	Sequence 115626, App	1338	135.2	4.8	522	18	US-10-357-930-49914	Sequence 49914, A
1266	135.8	4.8	593	18	US-10-021-323-7120	Sequence 7120, App	c1339	135.2	4.8	538	18	US-10-425-115-93124	Sequence 93124, A
1267	135.8	4.8	594	17	US-10-424-599-116262	Sequence 116262, A	1340	135.2	4.8	1129	18	US-10-425-115-81745	Sequence 81745, A
1268	135.8	4.8	1099	18	US-10-425-115-36774	Sequence 36774, A	1341	135.2	4.8	1129	18	US-10-425-115-88252	Sequence 88252, A
1269	135.8	4.8	1266	17	US-10-310-154-230	Sequence 43121, A	1342	135.2	4.8	1273	18	US-10-425-115-138631	Sequence 138631, A
1270	135.8	4.8	1383	17	US-10-424-599-88491	Sequence 230, App	1343	135.2	4.8	1475	17	US-10-424-599-65356	Sequence 65356, A
1271	135.8	4.8	2172	17	US-10-424-599-88491	Sequence 88491, A	1344	135.2	4.8	1868	18	US-10-425-115-165307	Sequence 165307, A
1272	135.8	4.8	2203	18	US-10-425-115-71810	Sequence 71810, A	1345	135.2	4.8	2060	17	US-10-424-599-89326	Sequence 89326, A
1273	135.8	4.8	2501	18	US-10-473-126-218	Sequence 218, App	1346	135.2	4.8	2394	9	US-09-800-729-33	Sequence 33, Appl
1274	135.8	4.8	2501	18	US-10-473-126-364	Sequence 364, App	1347	135	4.7	195	17	US-10-282-122A-13382	Sequence 13382, A
1275	135.8	4.8	4001	15	US-10-172-086-96	Sequence 96, Appl	1348	135	4.7	240	17	US-10-242-535A-8132	Sequence 8132, App
1276	135.8	4.8	4001	18	US-10-311-507-10	Sequence 10, Appl	1349	135	4.7	240	17	US-10-085-783A-8132	Sequence 8132, App
1277	135.8	4.8	4001	18	US-10-480-846-96	Sequence 96, Appl	c1350	135	4.7	341	18	US-10-425-115-7243	Sequence 7243, A
1278	135.8	4.8	5306	15	US-10-311-455-484	Sequence 484, App	1351	135	4.7	344	18	US-10-425-115-165946	Sequence 165946, A
1279	135.8	4.8	6134	18	US-10-433-793-170	Sequence 170, App	1352	135	4.7	368	18	US-10-021-323-5024	Sequence 5024, App
1280	135.8	4.8	7061	15	US-10-311-455-969	Sequence 969, App	1353	135	4.7	384	18	US-10-425-115-101577	Sequence 101577, A
1281	135.8	4.8	7061	17	US-10-221-613-147	Sequence 147, App	c1354	135	4.7	417	18	US-10-357-930-9115	Sequence 9115, App
1282	135.8	4.8	14798	15	US-10-311-455-1005	Sequence 1005, App	1355	135	4.7	422	18	US-10-425-115-54417	Sequence 54417, A
1283	135.8	4.8	17934	15	US-10-311-455-1692	Sequence 1692, App	c1356	135	4.7	444	18	US-10-425-115-66130	Sequence 66130, A
1284	135.8	4.8	35962	18	US-10-473-126-98	Sequence 98, Appl	1357	135	4.7	506	17	US-10-424-599-122103	Sequence 122103, A
1285	135.8	4.8	35962	18	US-10-473-126-244	Sequence 244, App	1358	135	4.7	527	18	US-10-425-115-133198	Sequence 133198, A
1286	135.6	4.8	376	18	US-10-425-115-80307	Sequence 80307, A	1359	135	4.7	529	18	US-10-425-115-102902	Sequence 102902, A
1287	135.6	4.8	389	18	US-10-425-115-182836	Sequence 182836, App	c1360	135	4.7	578	18	US-10-021-323-8035	Sequence 8035, App
1288	135.6	4.8	429	10	US-09-918-985-8461	Sequence 8461, App	1361	135	4.7	584	18	US-10-425-115-179304	Sequence 179304, A
1289	135.6	4.8	468	18	US-10-021-323-8271	Sequence 8271, App	1362	135	4.7	587	18	US-10-425-115-93990	Sequence 93990, A
1290	135.6	4.8	468	18	US-10-425-115-95424	Sequence 95424, A	1363	135	4.7	606	17	US-10-424-599-54586	Sequence 54586, A
c1291	135.6	4.8	557	18	US-10-021-323-2566	Sequence 2566, App	1364	135	4.7	679	18	US-10-425-115-54897	Sequence 54897, A
1292	135.6	4.8	631	18	US-10-425-115-140103	Sequence 140103, A	c1365	135	4.7	1128	18	US-10-437-963-65728	Sequence 65728, A
1293	135.6	4.8	660	17	US-10-424-599-24054	Sequence 24054, A	1366	135	4.7	1360	17	US-10-424-599-81801	Sequence 81801, A
1294	135.6	4.8	722	17	US-10-424-599-61867	Sequence 61867, A	1367	135	4.7	1395	18	US-10-425-115-143733	Sequence 143733, A
c1295	135.6	4.8	735	17	US-10-424-599-53073	Sequence 53073, A	1368	135	4.7	1904	17	US-10-424-599-35528	Sequence 35528, A
1296	135.6	4.8	761	18	US-10-425-115-17031	Sequence 17031, A	1369	134.8	4.7	411	9	US-09-960-352-14521	Sequence 14521, A
c1297	135.6	4.8	817	18	US-10-437-963-69665	Sequence 69665, A	1370	134.8	4.7	435	18	US-10-021-323-11676	Sequence 11676, A
1298	135.6	4.8	987	17	US-10-424-599-114407	Sequence 114407, A	c1371	134.8	4.7	513	17	US-10-424-599-08821	Sequence 8821, App
1299	135.6	4.8	1038	18	US-10-425-115-149229	Sequence 149229, App	1372	134.8	4.7	515	18	US-10-357-930-54538	Sequence 54538, A
1300	135.6	4.8	1178	18	US-10-437-963-56455	Sequence 56455, A	c1373	134.8	4.7	563	18	US-10-437-963-52353	Sequence 52353, A
1301	135.6	4.8	1187	18	US-10-425-115-91578	Sequence 91578, A	c1374	134.8	4.7	573	18	US-10-425-115-131298	Sequence 131298, A
1302	135.6	4.8	1459	18	US-10-818-809-3	Sequence 3, Appl	1375	134.8	4.7	608	17	US-10-424-599-90628	Sequence 90628, A
c1303	135.6	4.8	1468	18	US-10-425-115-155843	Sequence 155843, A	1376	134.8	4.7	1125	18	US-10-425-115-59739	Sequence 59739, A
1304	135.6	4.8	1567	18	US-10-425-115-105450	Sequence 105450, A	1377	134.8	4.7	1147	18	US-10-425-115-50255	Sequence 50255, A
1305	135.6	4.8	1881	17	US-10-424-599-12512	Sequence 12512, A	1378	134.8	4.7	1284	17	US-10-424-599-38912	Sequence 38912, A
1306	135.6	4.8	1965	18	US-10-425-115-141882	Sequence 141882, A	1379	134.8	4.7	1389	18	US-10-723-860-5322	Sequence 5322, App
1307	135.6	4.8	2099	18	US-10-425-115-87145	Sequence 87145, A	1380	134.8	4.7	1447	18	US-10-437-963-46106	Sequence 46106, A
c1308	135.6	4.8	3413	18	US-10-437-963-64459	Sequence 64459, A	1381	134.8	4.7	1635	18	US-10-425-115-85095	Sequence 85095, A
1309	135.6	4.8	9095	18	US-10-433-793-91	Sequence 91, Appl	1382	134.8	4.7	2288	17	US-10-424-599-67031	Sequence 67031, A
c1310	135.6	4.8	40862	15	US-10-311-455-2045	Sequence 2045, App	c1383	134.6	4.7	353	18	US-10-021-323-8039	Sequence 8039, App
1311	135.6	4.8	123197	13	US-10-027-632-179264	Sequence 179264, App	1384	134.6	4.7	357	18	US-10-425-115-139732	Sequence 139732, A
c1312	135.6	4.8	123197	17	US-10-027-632-179264	Sequence 179264, App	1385	134.6	4.7	360	18	US-10-357-930-59073	Sequence 59073, A
c1313	135.4	4.8	181	9	US-09-960-352-1301	Sequence 1301, App	c1386	134.6	4.7	391	18	US-10-357-930-8140	Sequence 81420, App
1314	135.4	4.8	401	17	US-10-424-599-139036	Sequence 139036, A	c1387	134.6	4.7	398	18	US-10-425-115-64127	Sequence 64127, A
1315	135.4	4.8	412	18	US-10-357-930-54301	Sequence 54301, A	c1388	134.6	4.7	398	18	US-10-425-115-64127	Sequence 64127, A
c1316	135.4	4.8	498	18	US-10-425-115-12386	Sequence 12386, A	1389	134.6	4.7	441	18	US-10-425-115-48377	Sequence 48377, A
1317	135.4	4.8	517	17	US-10-424-599-129396	Sequence 129396, A	1390	134.6	4.7	504	18	US-10-425-115-51618	Sequence 51618, A
1318	135.4	4.8	578	17	US-10-424-599-129426	Sequence 129426, A	1391	134.6	4.7	524	17	US-10-424-599-50104	Sequence 50104, A
1319	135.4	4.8	608	18	US-10-437-963-19184	Sequence 19184, A	1392	134.6	4.7	579	18	US-10-357-930-58709	Sequence 58709, A
1320	135.4	4.8	609	17	US-10-424-599-97699	Sequence 97699, A	1393	134.6	4.7	603	18	US-10-425-115-40308	Sequence 40308, A
1321	135.4	4.8	634	18	US-10-425-115-122963	Sequence 122963, A	1394	134.6	4.7	628	17	US-10-424-599-62262	Sequence 62262, A
1322	135.4	4.8	936	17	US-10-424-599-112681	Sequence 112681, A	1395	134.6	4.7	1145	18	US-10-437-963-36924	Sequence 36924, A
1323	135.4	4.8	1130	18	US-10-425-115-131870	Sequence 131870, A	1396	134.6	4.7	1494	13	US-10-062-254-259	Sequence 259, App
1324	135.4	4.8	1171	18	US-10-425-115-90042	Sequence 90042, A	1397	134.6	4.7	1885	17	US-10-424-599-41943	Sequence 41943, A
1325	135.4	4.8	1269	18	US-10-425-115-119668	Sequence 119668, A	1398	134.4	4.7	225	9	US-09-925-299-744	Sequence 744, App
1326	135.4	4.8	1512	18	US-10-425-115-131408	Sequence 131408, A	1399	134.4	4.7	225	10	US-10-021-323-7947	Sequence 7947, App
1327	135.4	4.8	1667	18	US-10-425-115-39856	Sequence 39856, A	1400	134.4	4.7	319	18	US-10-425-115-12313	Sequence 12313, A
1328	135.4	4.8	2138	18	US-10-437-963-66396	Sequence 66396, A	c1401	134.4	4.7	391	18	US-10-021-323-7863	Sequence 7863, App
1329	135.4	4.8	2146	13	US-10-003-392-3	Sequence 3, Appl	c1402	134.4	4.7	414	18	US-10-425-115-169784	Sequence 169784, A
1330	135.4	4.8	2146	19	US-10-916-247-3	Sequence 3, Appl	c1403	134.4	4.7	416	18	US-10-357-930-16119	Sequence 16119, A
1331	135.4	4.8	2366	18	US-10-425-115-86057	Sequence 86057, A	1404	134.4	4.7	423	10	US-09-918-995-7147	Sequence 7147, App

1405	134.4	4.7	436	18	US-10-425-115-172404	Sequence 172404, A	133.8	4.7	283	9	US-09-960-352-9095	Sequence 9095, Ap
1406	134.4	4.7	499	18	US-10-021-323-10189	Sequence 10189, A	133.8	4.7	371	18	US-10-425-115-3430	Sequence 3430, Ap
1407	134.4	4.7	501	18	US-10-425-115-155716	Sequence 155716, A	133.8	4.7	404	18	US-10-425-115-131668	Sequence 131668, A
1408	134.4	4.7	508	17	US-10-424-599-46262	Sequence 46262, A	133.8	4.7	415	9	US-09-960-352-2223	Sequence 2223, Ap
1409	134.4	4.7	520	18	US-10-021-323-7699	Sequence 7699, Ap	133.8	4.7	474	18	US-10-357-930-54257	Sequence 54257, A
1410	134.4	4.7	525	18	US-10-425-115-130292	Sequence 130292, A	133.8	4.7	501	17	US-10-424-599-137556	Sequence 137556, A
1411	134.4	4.7	530	17	US-10-424-599-137880	Sequence 137880, A	133.8	4.7	596	17	US-10-424-599-39793	Sequence 39793, A
1412	134.4	4.7	544	18	US-10-425-115-26104	Sequence 26104, A	133.8	4.7	597	18	US-10-425-115-157303	Sequence 157303, A
1413	134.4	4.7	548	18	US-10-021-323-16019	Sequence 16019, A	133.8	4.7	603	18	US-10-425-115-124798	Sequence 124798, A
1414	134.4	4.7	554	17	US-10-424-599-17501	Sequence 17501, A	133.8	4.7	681	18	US-10-198-846-7214	Sequence 7214, Ap
1415	134.4	4.7	561	18	US-10-425-115-106556	Sequence 106556, A	133.8	4.7	861	14	US-10-198-846-7214	Sequence 7214, A
1416	134.4	4.7	565	18	US-10-425-115-125186	Sequence 125186, A	133.8	4.7	874	10	US-09-814-353-21741	Sequence 50083, A
1417	134.4	4.7	584	18	US-10-425-115-74017	Sequence 74017, A	133.8	4.7	963	17	US-10-424-599-50083	Sequence 77593, A
1418	134.4	4.7	597	18	US-10-425-115-176855	Sequence 176855, A	133.8	4.7	2361	18	US-10-425-115-77593	Sequence 47, Appl
1419	134.4	4.7	606	17	US-10-424-599-93300	Sequence 93300, A	133.8	4.7	2566	18	US-10-734-564-47	Sequence 80144, A
1420	134.4	4.7	608	10	US-09-814-353-5190	Sequence 5190, Ap	133.8	4.7	3260	18	US-10-437-963-80144	Sequence 1774, Ap
1421	134.4	4.7	608	10	US-09-814-353-11478	Sequence 11478, A	133.8	4.7	6115	15	US-10-311-455-1774	Sequence 7233, Ap
1422	134.4	4.7	616	18	US-10-021-323-5390	Sequence 5390, Ap	133.6	4.7	259	9	US-09-960-352-7233	Sequence 146743, A
1423	134.4	4.7	641	17	US-10-424-599-106274	Sequence 106274, A	133.6	4.7	432	18	US-10-425-115-146743	Sequence 115781, A
1424	134.4	4.7	1015	17	US-10-424-599-96139	Sequence 96139, A	133.6	4.7	472	18	US-10-425-115-115781	Sequence 15842, A
1425	134.4	4.7	1220	17	US-10-424-599-56718	Sequence 56718, A	133.6	4.7	477	10	US-09-918-995-15842	Sequence 141320, A
1426	134.4	4.7	1255	18	US-10-437-963-87628	Sequence 87628, A	133.6	4.7	504	17	US-10-424-599-141320	Sequence 63146, A
1427	134.4	4.7	1589	18	US-10-425-115-101269	Sequence 101269, A	133.6	4.7	511	18	US-10-425-115-63146	
1428	134.4	4.7	2033	14	US-10-425-115-114209	Sequence 114209, A						
1429	134.4	4.7	6409	18	US-10-159-151-1	Sequence 1, Appli						
1430	134.4	4.7	6409	19	US-10-884-128-1	Sequence 1, Appli						
1431	134.2	4.7	196	18	US-10-668-749A-5	Sequence 5, Appli						
1432	134.2	4.7	217	9	US-09-960-352-6539	Sequence 6539, Ap						
1433	134.2	4.7	372	18	US-10-425-115-69147	Sequence 69147, A						
1434	134.2	4.7	403	18	US-10-021-323-8207	Sequence 8207, Ap						
1435	134.2	4.7	445	18	US-10-425-115-69016	Sequence 69016, A						
1436	134.2	4.7	457	18	US-10-425-115-95616	Sequence 95616, A						
1437	134.2	4.7	462	18	US-10-437-963-80671	Sequence 80671, A						
1438	134.2	4.7	491	10	US-09-918-995-11962	Sequence 11962, A						
1439	134.2	4.7	494	18	US-10-437-963-47523	Sequence 47523, A						
1440	134.2	4.7	501	18	US-10-357-930-59111	Sequence 59111, A						
1441	134.2	4.7	524	18	US-10-425-115-11283	Sequence 11283, A						
1442	134.2	4.7	529	18	US-10-021-323-10810	Sequence 10810, A						
1443	134.2	4.7	530	18	US-10-425-115-139313	Sequence 139313, A						
1444	134.2	4.7	542	18	US-10-021-323-6883	Sequence 6883, Ap						
1445	134.2	4.7	553	17	US-10-424-599-6106	Sequence 6106, Ap						
1446	134.2	4.7	570	18	US-10-021-323-143	Sequence 143, App						
1447	134.2	4.7	611	18	US-10-425-115-178893	Sequence 178893, A						
1448	134.2	4.7	649	18	US-10-425-115-72863	Sequence 72863, A						
1449	134.2	4.7	1300	18	US-10-668-749A-1	Sequence 1, Appli						
1450	134.2	4.7	1484	18	US-10-425-115-24588	Sequence 24588, A						
1451	134.2	4.7	2444	18	US-10-425-115-122151	Sequence 122151, A						
1452	134.2	4.7	2721	18	US-10-425-115-26594	Sequence 26594, A						
1453	134.2	4.7	7657	14	US-10-239-676-185	Sequence 185, App						
1454	134.2	4.7	7657	15	US-10-311-455-1995	Sequence 1995, Ap						
1455	134.2	4.7	37973	15	US-10-311-455-2169	Sequence 2169, Ap						
1456	134	4.7	242	9	US-09-960-352-3217	Sequence 3217, Ap						
1457	134	4.7	305	17	US-10-231-956A-85	Sequence 85, Appl						
1458	134	4.7	342	18	US-10-021-323-9783	Sequence 9783, Ap						
1459	134	4.7	472	18	US-10-357-930-57039	Sequence 57039, A						
1460	134	4.7	508	17	US-10-424-599-142552	Sequence 142552, A						
1461	134	4.7	510	18	US-10-437-963-1928	Sequence 1928, Ap						
1462	134	4.7	581	18	US-10-425-115-36960	Sequence 36960, A						
1463	134	4.7	593	18	US-10-021-323-4285	Sequence 4285, Ap						
1464	134	4.7	598	18	US-10-021-323-11423	Sequence 11423, A						
1465	134	4.7	612	18	US-10-425-115-56968	Sequence 56968, A						
1466	134	4.7	703	18	US-10-425-115-6829	Sequence 6829, Ap						
1467	134	4.7	756	10	US-09-814-353-6226	Sequence 6226, Ap						
1468	134	4.7	756	10	US-09-814-353-12504	Sequence 12504, A						
1469	134	4.7	789	18	US-10-425-115-39743	Sequence 39743, A						
1470	134	4.7	810	18	US-10-425-115-45770	Sequence 45770, A						
1471	134	4.7	980	18	US-10-723-860-4894	Sequence 4894, Ap						
1472	134	4.7	1255	17	US-10-424-599-95539	Sequence 95539, A						
1473	134	4.7	1311	17	US-10-411-120-36	Sequence 36, Appl						
1474	134	4.7	1385	17	US-10-424-599-67834	Sequence 67834, A						
1475	134	4.7	3343	18	US-10-425-115-4626	Sequence 4626, Ap						
1476	134	4.7	8899	15	US-10-311-455-810	Sequence 810, App						
1477	134	4.7	8899	17	US-10-257-166-156	Sequence 156, App						

Search completed: May 6, 2005, 17:55:40
Job time : 1113 secs

```

Run on: May 8, 2005, 11:21:33 ; Search time 994 Seconds
          (without alignments)
          16949.280 Million cell updates/sec

Title: US-10-063-692-37
Perfect score: 2846
Sequence: 1 cgtctgggaccgcccgcgg.....aaaaaaaaaaaaaaaaaaaaa 2846
Scoring table: OLIGO NUC
               Gapop 60.0 , Gapext 60.0
               4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Database : N Geneseq16Dec04:*
          1: Geneseqn1980s:*
          2: Geneseqn1990s:*
          3: Geneseqn2000s:*
          4: Geneseqn2001as:*
          5: Geneseqn2001bs:*
          6: Geneseqn2002as:*
          7: Geneseqn2002bs:*
          8: Geneseqn2003as:*
          9: Geneseqn2003bs:*
          10: Geneseqn2003cs:*
          11: Geneseqn2003ds:*
          12: Geneseqn2004as:*
          13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description
RESULT 1
ID AA265034 standard; cDNA; 2846 BP.
DE Membrane-bound protein PRO1344 encoding cDNA.
PN WO963088-A2.
PD 09-DEC-1999.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2846; DB 3; Length 2846;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 2
ID AAS46009 standard; cDNA; 2846 BP.
DE Human DNA encoding PRO polypeptide sequence #85.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2846; DB 4; Length 2846;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 3
ID AAF92076 standard; cDNA; 2846 BP.
DE Human PRO1344 cDNA.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2846; DB 4; Length 2846;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 4
ID AAF41180 standard; cDNA; 2846 BP.
DE Human PRO1344 (UNQ659) nucleotide sequence SEQ ID NO:230.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2846; DB 5; Length 2846;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 5
ID ABS74396 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2846; DB 6; Length 2846;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 6
ID ACD21867 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003027267-A1.
PD 06-FEB-2003.

```

```

ID ACA89459 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003036141-A1.
PD 20-FEB-2003.
  Query Match 100.0%; Score 2846; DB 8; Length 2846;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 7
ID ACA73469 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2846; DB 8; Length 2846;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 8
ID ACA5784 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2846; DB 8; Length 2846;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 9
ID ACA66618 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO protein #85.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2846; DB 8; Length 2846;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 10
ID ACA64316 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US200303531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2846; DB 8; Length 2846;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 11
ID ACA91182 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2846; DB 8; Length 2846;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 12
ID ACD81559 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2846; DB 8; Length 2846;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 13
ID ACF20193 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040063-A1.
PD 27-FEB-2003.
  Query Match 100.0%; Score 2846; DB 8; Length 2846;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 14
ID ACF19579 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040064-A1.
PD 27-FEB-2003.
  Query Match 100.0%; Score 2846; DB 8; Length 2846;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 15
ID ACD21867 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003027267-A1.
PD 06-FEB-2003.

```

Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 16
ID ACD13032 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003036160-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 17
ID ACD25135 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 18
ID ACF00184 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 19
ID ACA60381 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 20
ID ACA72241 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 21
ID ACD04765 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 22
ID ACD18226 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 23
ID ACD08233 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 24
ID ACA88667 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 25
ID ACA70109 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003036134-A1.
PD 20-FEB-2003.
Query Match
100.0%; Score 2846; DB 8; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 26
ID ACD12331 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 27
ID ACC74246 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 28
ID ACD15874 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #95.
FN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 29
ID ACD25442 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 30
ID ACD17919 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 31
ID ACC88206 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 32
ID ACD1560 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 33
ID ACD18627 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 34
ID ACA58828 standard; cDNA; 2846 BP.
DE cDNA encoding human secreted polypeptide PRO1344.
FN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 35
ID ABX98237 standard; cDNA; 2846 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 169.
FN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;

RESULT 36
ID ACD13988 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 37
ID ACD09768 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 38
ID ACC88513 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 39
ID ACD21253 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 40
ID ABX75625 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1344.
FN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 41
ID ACA64004 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #19.
FN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 42
ID ABX97828 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
FN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 43
ID ACA97304 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 44
ID ACA57767 standard; cDNA; 2846 BP.
DE Human PRO1344 cDNA.
FN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 45
ID ACD14295 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
FN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 46
ID ACC91078 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 47
ID ACC8820 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 48
ID ACD07017 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
FN US20030308353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 49
ID ACA67468 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
FN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 50
ID ACC81523 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 51
ID ACA91268 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #19.
FN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 52
ID ACC89127 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 53
ID ACC86483 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 54
ID ACC89741 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 55
ID ACC92920 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 56
ID ABX80775 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein cDNA, #94.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 57
ID ACA72548 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 58
ID ACA89066 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 59
ID ACA69802 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 60
ID ACA96945 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 61
ID ACA90941 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 62
ID ACA70723 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 63
ID ACA95233 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 64
ID ACD4284 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 65
ID ACC86176 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 66
ID ACD45167 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane polypeptide PRO1344 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 67
ID ACC90048 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 68
ID ACD12656 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 69
ID ACF19886 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 70
ID ABX76830 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 71
ID ACA73162 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 72
ID ACA68705 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 73
ID ACA74549 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 74
ID ACA70416 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 75
ID ACD14602 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
Pred. No. 0;
RESULT 76
ID ACA93715 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.

PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 77
ID ACA68274 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 78
ID ABX98739 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 79
ID ACC81216 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 80
ID ACA95540 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 81
ID ACD04458 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 82
ID ACC87899 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 83
ID ACF12561 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 84
ID ACH66262 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 85
ID ABX79455 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein cDNA, #94.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 86
ID ACA96276 standard; cDNA; 2846 BP.

DE Human PRO polynucleotide #85.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 87
ID ACA65050 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 88
ID ACA73776 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 89
ID ACA74188 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 90
ID ACA96583 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 91
ID ACD10689 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 92
ID ACC91385 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 93
ID ACA93476 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 94
ID ACD02720 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 95
ID ACC87285 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 96
ID ACC85869 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027262-A1.

```
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 97
ID ACA74856 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 98
ID ACA65357 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 99
ID ACA94174 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 100
ID ACA97918 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 101
ID ACA91420 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 102
ID ACA90634 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 103
ID ACD16181 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 104
ID ACD17342 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 105
ID ACC91999 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 106
ID ACD02316 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 107
ID ACA74856 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 108
ID ACA91727 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 109
ID ACA71371 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 110
ID AC090771 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 111
ID ACA65781 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO protein #85.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 112
ID ACA68944 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 113
ID ACA92974 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 114
ID ACA94926 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 115
ID ACD16488 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 116
ID ACD15567 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;
RESULT 117
```

ID ACA98466 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
FN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 118
ID ABX17058 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #55.
FN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 119
ID ABX16670 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein #85.
FN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 8; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 120
ID ACA67913 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 121
ID ACA63391 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #19.
FN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 122
ID ACA97611 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
FN US2003032115-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 123
ID ACA99060 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003032140-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 124
ID ACC91692 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 125
ID ACP11103 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 126
ID ACD14953 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003044922-A1.

PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 127
ID ACA88362 standard; cDNA; 2846 BP.
DE Human secreted and transmembrane polypeptide PRO1344 cDNA.
FN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 128
ID ACD81869 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
FN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 129
ID ACD11717 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 130
ID ACC95846 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 131
ID ACF16409 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 132
ID ACF02527 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 133
ID ACF02834 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 134
ID ACF21421 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 135
ID ACF10105 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 136

ID ACF77998 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 137
ID ACD46703 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 138
ID ACD49466 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 139
ID ACF28233 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 140
ID ACD88923 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 141
ID ACD84318 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 142
ID ACD99092 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 143
ID ADA77921 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 144
ID ACF48834 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 145
ID ACD09154 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.

PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 146
ID ACF11947 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 147
ID ACF41181 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 148
ID ACF15795 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 149
ID ACF16102 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 150
ID ADB17094 standard; cDNA; 2846 BP.
DE Human cDNA clone (SeqID 37) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 151
ID ACD31929 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 152
ID ACF18737 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 153
ID ACF09184 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 154
ID ACF78305 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 155
ID ACF51904 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 156
ID ACF26391 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 157
ID ACF224184 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 158
ID ACF63495 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 159
ID ACF50369 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 160
ID ACH07840 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 161
ID ACF13646 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 162
ID ACD41572 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 163
ID ADA37741 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 164

ID ACF31985 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 165
ID ACF23263 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 166
ID ACF39953 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 167
ID ACD45475 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 168
ID ACF53132 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 169
ID ACF27312 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 170
ID ACF45150 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 171
ID ACF29768 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 172
ID ACD89844 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 173
ID ACD84625 standard; cDNA; 2846 BP.

DE Human PRO polynucleotide #85.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 174
ID ACD98785 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 175
ID ACF77077 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 176
ID ACF76770 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 177
ID ACF49755 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 178
ID ACF50062 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 179
ID ADA21427 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1344.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 180
ID ACD09461 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 181
ID ACD08540 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 182
ID ACH03594 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 183

DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 184
ID ACC94762 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 185
ID ACD22481 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 186
ID ACF15181 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 187
ID ACC97276 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 188
ID ACC92306 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 189
ID ACF13953 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 190
ID ACF14260 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 191
ID ADA10214 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1344.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 192
ID ACF09491 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 193
ID ACD45782 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 194
ID ACD47931 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 195
ID ACD67662 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 196
ID ACF25470 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 197
ID ACF29154 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 198
ID ACD84932 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 199
ID ACD84011 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 200
ID ACD88002 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 201
ID ACF30689 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 202
ID ACF32292 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 203
ID ACH1952 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 204
ID ACH12259 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 205
ID ADA19899 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 206
ID ACD40651 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 207
ID ADB17282 standard; cDNA; 2846 BP.
DE Human cDNA clone (SeqID 37) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 208
ID ADA17758 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 209
ID ACF18123 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 210
ID ACF08570 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 211
ID ACF31371 standard; cDNA; 2846 BP.

DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 212
ID ACF52211 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 213
ID ACD50080 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 214
ID ACF38783 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 215
ID ACF26698 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 216
ID ACF24798 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 217
ID ACF46378 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 218
ID ACF27926 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 219
ID ACD89230 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 220
ID ACF63802 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 221
ID ACF60442 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 222
ID ACH12566 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 223
ID ACH09989 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 224
ID ACD03844 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 225
ID ACD10382 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 226
ID ACD12024 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 227
ID ACF42409 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 228
ID ADA27866 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 229
ID ACF18430 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 230
ID ACF63802 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

ID ACF02220 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 231
ID ACF21728 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 232
ID ACF10412 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 233
ID ACF33864 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 234
ID ACF44826 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 235
ID ACD90458 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 236
ID ACD91071 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 237
ID ACF30382 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 238
ID ACD87081 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 239
ID ACF60135 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

FN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 240
ID ACF46685 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 241
ID ACF75542 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 242
ID ADA79713 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 243
ID ACF17202 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 244
ID ACF22956 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 245
ID ACF07956 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 246
ID ACF08263 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 247
ID ACF40567 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 248
ID ACF53746 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 249
ID ACD47010 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 250
ID ACF47913 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 251
ID ACF47299 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 252
ID ACF46071 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 253
ID ACD86160 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 254
ID ACF52518 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 255
ID ACF52825 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 256
ID ACF64818 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 257
ID ACF76463 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 258
ID ACF61363 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 259
ID ACF61670 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 260
ID ACD30701 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 261
ID ACD31622 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 262
ID ACD32543 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 263
ID ADA20071 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 264
ID ACD82108 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 265
ID ACF17509 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 266
ID ADA94446 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 267
ID ACF07342 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 268
ID ACF20500 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 269
ID ACF20807 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 270
ID ACF21114 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 271
ID ACF47624 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 272
ID ACF47606 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 273
ID ACF53439 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 274
ID ACD86774 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 275
ID ACH05022 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
FN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 276
ID ACF44519 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 277
ID ADA81440 standard; cDNA; 2846 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 278
ID ACD22174 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 279
ID ACD24521 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 280
ID ACD39724 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
FN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 281
ID ACD40031 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
FN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 282
ID ACF13339 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 283
ID ACF03141 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 284
ID ACF78612 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 285
ID ACF13333 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 286
ID ACF50676 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;

RESULT 287
ID ACF34171 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 288
ID ACD46396 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 289
ID ACD48238 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 290
ID ACF27619 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 291
ID ACF24491 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 292
ID ACD85546 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 293
ID ACD90151 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 294
ID ACD83704 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 295
ID ACF49141 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
ID ACH07226 standard; cDNA; 2846 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 297
ID ACH07533 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 298
ID ACH08147 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 299
ID ACH11338 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 300
ID ACH11645 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 301
ID ACH10296 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 302
ID ACF01299 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 303
ID ACF40874 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 304
ID ACD24214 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044518-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 305
ID ACD31315 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032132-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 306
ID ACF17816 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 307
ID ADA38671 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 308
ID ACF32599 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 309
ID ACF40260 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 310
ID ACF48220 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 311
ID ACF38169 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 312
ID ACF25105 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 313
ID ACF27005 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 314
ID ACF29461 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 315
ID ACD87695 standard; cDNA; 2846 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 316
ID ACF76156 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 317
ID ACF49448 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 318
ID ACF43905 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 319
ID ACH06250 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 320
ID ACH06557 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 321
ID ADA83238 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 322
ID ACC92613 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 323
ID ACC93227 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 324
ID ACF19272 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 325
ID ACD12963 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 326
ID ACF06421 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 327
ID ACC94455 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054467-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 328
ID ACC97883 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 329
ID ACC94148 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 330
ID ACF42102 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054469-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 331
ID ACD31008 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 332
ID ACD43037 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003054463-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 333
ID ACD43344 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003054466-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 334
ID ACF14874 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059879-A1.
PD 27-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 335
ID ADA92792 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 336
ID ACF01606 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 337
ID ACF31678 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064469-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 338
ID ACD67355 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003064453-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 339
ID ACD48545 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064466-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 340
ID ACD48852 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064468-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 341
ID ACF51290 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068760-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 342
ID ACF54053 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068769-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 343
ID ACF5777 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003045700-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
RESULT 344
ID ACF14874 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059879-A1.
PD 27-MAR-2003.

RESULT 344
ID ACF39090 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 345
ID ACF28847 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 346
ID ACD90764 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 347
ID ACD86467 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 348
ID ACH05329 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
FN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 349
ID ACF65125 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 350
ID ADB20281 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 351
ID ACF43598 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 352
ID ACH09068 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 353
ID ACH09375 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003044524-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 354
ID ADA78533 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 355
ID ACF09798 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 356
ID ACF50983 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 357
ID ACF23877 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 358
ID ACD88309 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 359
ID ACH09682 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 360
ID ACH10603 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 361
ID ACD11410 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 362
ID ACC96460 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003044524-A1.

PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 363
ID ACC98490 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 364
ID ACF1795 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 365
ID ACF16716 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 366
ID ACD32236 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 367
ID ACD30394 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 368
ID ACD41265 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 369
ID ACF07649 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 370
ID ACF31064 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 371
ID ACF77384 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 372
ID ACF11026 standard; cDNA; 2846 BP.

DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 373
ID ACF32906 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 374
ID ACF26084 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 375
ID ACD83397 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
FN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 376
ID ACF23570 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 377
ID ACF42984 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 378
ID ACF43291 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 379
ID ACH05943 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
FN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 380
ID ACH08761 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 381
ID ACC90355 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003027273-A1.

PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 382
ID ACF10719 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 20-FEB-2003.
RESULT 383
ID ACC93534 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 20-FEB-2003.
RESULT 384
ID ACC96153 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 385
ID ACD24828 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 13-MAR-2003.
RESULT 386
ID ACF01913 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003045739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 387
ID ACF22035 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 388
ID ACF22649 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 389
ID ACF08877 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 390
ID ACF33213 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 391

ID ACF54667 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 392
ID ACF48527 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 393
ID ACD47317 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 394
ID ACD49159 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 395
ID ACF37862 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 396
ID ACF30075 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 397
ID ACD87388 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 398
ID ACF61977 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;
PD 05-JUN-2003.
RESULT 399
ID ACH10910 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 400
ID ACD10075 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.

PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 401
ID ACD16800 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 402
ID ACF65430 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 403
ID ACC9097 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 404
ID ACF00491 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 405
ID ACD40958 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 406
ID ACF14567 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 407
ID ACF22342 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 408
ID ACF78919 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 409
ID ACF11640 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 410
ID ACF44212 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104556-A1.
PD 05-JUN-2003.

ID ADA22353 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1344.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 411
ID ACF51597 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 412
ID ACF33520 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 413
ID ACD49773 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 414
ID ACF37555 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 415
ID ACF28540 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 416
ID ACD88616 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 417
ID ACF75235 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 418
ID ACF61056 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 419
ID ACF44212 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104556-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 420
ID ACH08454 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 421
ID ACD39420 standard; DNA; 2846 BP.
DE Human PRO 1344 PCR primer #1.
FN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 422
ID ACC93841 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003036122-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 423
ID ACD20946 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 424
ID ACF06728 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003040065-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 425
ID ACD20639 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003044919-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 426
ID ACD22788 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003040077-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 427
ID ACF41488 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003044928-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 428
ID ADA06519 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #65.
FN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 429
ID ADA39212 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
FN US2003059782-A1.
PD 27-MAR-2003.

Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 430
ID ACF07035 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 431
ID ACF77691 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 432
ID ACD46089 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 433
ID ACF46992 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 434
ID ACF54360 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 435
ID ACF45764 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 436
ID ACF45457 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 437
ID ACF38476 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 438
ID ACD89537 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 439
ID ACD85239 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 440
ID ACD85853 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 441
ID ACF75949 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 442
ID ACF60749 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 443
ID ACH05636 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 444
ID ADA82604 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 445
ID ADB85610 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 446
ID ADB96238 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 447
ID ACF55895 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 448
ID ACF55281 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 449
ID ADB85912 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 450
ID ACF56202 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 451
ID ACF56509 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 452
ID ADB68289 standard; cDNA; 2846 BP.
DE Human PRO1344 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 453
ID ADB68096 standard; cDNA; 2846 BP.
DE Human PRO1344 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 454
ID ACF55588 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 455
ID ACF54974 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 456
ID ADB90913 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 457
ID ADC57710 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.

PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 458
ID ADC55074 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 459
ID ADC11941 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 460
ID ADC06993 standard; cDNA; 2846 BP.
DE Human PRO1344 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 461
ID ADC56363 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 462
ID ADC17172 standard; cDNA; 2846 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 37).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 463
ID ADC07418 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 464
ID ADC11408 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 465
ID ADC14870 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 466
ID ADC52365 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 467
ID ADC14530 standard; cDNA; 2846 BP.

DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 468
ID ADD08062 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 469
ID ADC81887 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 470
ID ADD07529 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 471
ID ADC82420 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 472
ID ADD05642 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 473
ID ADD08600 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 474
ID ADD06849 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 475
ID ADC83096 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 476
ID ADD55203 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 477
ID ADD36041 standard; cDNA; 2846 BP.

DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 478
ID ADD56161 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 479
ID ADD54599 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 480
ID ADE26753 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 481
ID ADE26220 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 482
ID ADF67157 standard; cDNA; 2846 BP.
DE Human PRO1344 nucleotide sequence SEQ ID NO:230.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 483
ID ADG01042 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 484
ID ADG08595 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 485
ID ADG02637 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 486
ID ADG01344 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 487
ID ADF95519 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 488
ID ADF95216 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 489
ID ADG12334 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 490
ID ADH24069 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 491
ID ADH34095 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 492
ID ADH29928 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 493
ID ADH23899 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 494
ID ADH08994 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 495
ID ADG85303 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 496
ID ADG01344 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

RESULT 496
ID ADH24579 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 497
ID ADH37435 standard; cDNA; 2846 BP.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 498
ID ADH02024 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 499
ID ADH37605 standard; cDNA; 2846 BP.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 500
ID ADG85643 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 501
ID ADH24239 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 502
ID ADH38533 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 503
ID ADG83654 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 504
ID ADH29462 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 505

ID ADH27578 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 506
ID ADH37775 standard; cDNA; 2846 BP.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 507
ID ADH37952 standard; cDNA; 2846 BP.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 508
ID ADH57372 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 509
ID ADH53514 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 510
ID ADH53684 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 511
ID ADH52020 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 512
ID ADH49875 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 513
ID ADI25385 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 514
ID ADH90178 standard; cDNA; 2846 BP.

DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 515
ID ADI25555 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 516
ID ADH97729 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 517
ID ADI35411 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
FN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 518
ID ADI03577 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 519
ID ADI11934 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
FN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 520
ID ADH90008 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 521
ID ADH99903 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 522
ID ADH98409 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 523
ID ADI11084 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
FN US2003181682-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 524
ID ADI11594 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
FN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 525
ID ADH98239 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 526
ID ADH98579 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 527
ID ADH98069 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 528
ID ABX78612 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
FN US2003027272-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 529
ID ACA75584 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003032127-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 530
ID ACA71064 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003032112-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 531
ID ACC87592 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003027278-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 532
ID ACC86978 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003036159-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 533
ID ACD04151 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.

PN US2003040070-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 534
ID ABX77859 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein #65.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 535
ID ABX80271 standard; DNA; 2846 BP.
DE Human secreted or transmembrane protein related PCR primer #50.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 536
ID ACA69177 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 537
ID ACA69482 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 538
ID ACA90327 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 539
ID ACC89434 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 540
ID ABX90248 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein cDNA, #94.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 541
ID ACA98225 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 542
ID ACA93867 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 543
ID ACD15260 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044923-A1.

PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 544
ID ACD08847 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 545
ID ACC96767 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 546
ID ACF15488 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 547
ID ABX64094 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 548
ID ACA72855 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 549
ID ACD03027 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 550
ID ACD01842 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 551
ID ACA92034 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 552
ID ADI05057 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 553
ID ADI03407 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181654-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 554
ID ADI04802 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 555
ID ADH78256 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 556
ID ADI19600 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 557
ID ADH90348 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 558
ID ADI03067 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 559
ID ADH77916 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 560
ID ADH97899 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 561
ID ADI01284 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 562
ID ADI01979 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 563
ID ADI03237 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 564
ID ADI11424 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 565
ID ADI02326 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 566
ID ADI11764 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 567
ID ADI05401 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 568
ID ADH79473 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 569
ID ADI19430 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 570
ID ADI05231 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 571
ID ADH79643 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 572
ID ADI01469 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181678-A1.
PN US2003-2003.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 573
ID ADI01639 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181679-A1.
PN US2003-2003.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 574
ID ADI01809 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181680-A1.
PN US2003-2003.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 575
ID ADH79813 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003191289-A1.
PN US2003-2003.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 576
ID ADI04631 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003171550-A1.
PN US2003-2003.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 577
ID ADI02767 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181651-A1.
PN US2003-2003.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 578
ID ADH78086 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
FN US2003181667-A1.
PN US2003-2003.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 579
ID ADI25725 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181670-A1.
PN US2003-2003.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 580
ID ADI25895 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181671-A1.
PN US2003-2003.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 581
ID ADI25895 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181671-A1.
PN US2003-2003.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 581
ID ADH98749 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 582
ID ADH79990 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 583
ID ADL32775 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 11; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 584
ID ADM30309 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 11; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 585
ID ADL93721 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 11; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 586
ID ADC52175 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 587
ID ADE74306 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 588
ID ADE74918 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003211574-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 589
ID ADF35356 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 590
ID ADG11606 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.

```
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 591
ID ADF96131 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 592
ID ADG04402 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003215912-A1.
PD 20-NOV-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 593
ID ADG00562 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003215911-A1.
PD 20-NOV-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 594
ID ADH06607 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 595
ID ADH06437 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 596
ID ADG68858 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180855-A1.
PD 25-SEP-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 597
ID ADH27748 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 598
ID ADH25089 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 599
ID ADH33721 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 600
ID ADG82818 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003215910-A1.
PD 20-NOV-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 601
ID ADH02364 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180839-A1.
PD 25-SEP-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 602
ID ADH07971 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 603
ID ADG69368 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 604
ID ADH39189 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180917-A1.
PD 25-SEP-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 605
ID ADH26099 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003068770-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 606
ID ADG83929 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180842-A1.
PD 25-SEP-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 607
ID ADH19476 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003228656-A1.
PD 11-DEC-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 608
ID ADG85473 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
```

Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 609
ID ADH06267 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 610
ID ADH30097 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 611
ID ADH24409 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 612
ID ADH33068 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 613
ID ADG69538 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 614
ID ADH07801 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 615
ID ADG85813 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 616
ID ADH39359 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 617
ID ADH33551 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 618
ID ADH33891 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 619
ID ADH01101 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 620
ID ADG69708 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 621
ID ADH20969 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 622
ID ADH02194 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 623
ID ADG69198 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 624
ID ADG85983 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 625
ID ADH24919 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 626
ID ADH39536 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 627

ID ADH20009 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
FN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 628
ID ADH02534 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
FN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 629
ID ADG69028 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 630
ID ADH07631 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 631
ID ADG86153 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 632
ID ADH24749 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 633
ID ADH25797 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 634
ID ADH38363 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 635
ID ADH57202 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 636
ID ADH52190 standard; cDNA; 2846 BP.

DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 637
ID ADH49556 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 638
ID ADH90518 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 639
ID ADI11254 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
FN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 640
ID ADH98919 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 641
ID ADI02149 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 642
ID ADH90688 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 643
ID ADJ54807 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
FN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 644
ID ADJ98563 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
FN US2003181797-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 12; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 645
ID ADJ98733 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.

PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 646
ID ADH78892 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 647
ID ADJ99126 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 648
ID ADJ99296 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 649
ID ADJ98914 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 650
ID ADH79062 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 651
ID ADK00922 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 652
ID ADK14443 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 653
ID ADJ64578 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 654
ID ADM31474 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2004048334-A1.

PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 655
ID ADM36521 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 656
ID ADM40326 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 657
ID ADM80892 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 658
ID ADM37934 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;
RESULT 659
ID ADK65407 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.2%; Score 2795; DB 10; Length 2846;
RESULT 660
ID ADA00368 standard; cDNA; 2843 BP.
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2723; DB 9; Length 2843;
RESULT 661
ID ACA67289 standard; cDNA; 2848 BP.
DE cDNA encoding human secreted polypeptide PRO1344.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 91.6%; Score 2606; DB 8; Length 2848;
RESULT 662
ID ACA89307 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 91.0%; Score 2591; DB 8; Length 2846;
RESULT 663
ID AB235533 standard; cDNA; 2845 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 644.
PN WO200274979-A2.
PD 26-SEP-2002.

PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match 89.8%; Score 2556; DB 6; Length 2845;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 664
ID ADL06663 standard; DNA; 2650 BP.
DE Human 3T3 cell conversion promoter FP938 DNA.
PN CN1403477-A.
PD 19-MAR-2003.
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
Query Match 84.1%; Score 2394; DB 10; Length 2650;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 665
ID ADL06661 standard; cDNA; 2650 BP.
DE Human 3T3 cell conversion promoter FP938 cDNA.
PN CN1403477-A.
PD 19-MAR-2003.
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
Query Match 84.1%; Score 2394; DB 10; Length 2650;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 666
ID ARA39951 standard; cDNA; 2747 BP.
DE Human TANGO 215 cDNA.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 83.4%; Score 2373; DB 3; Length 2747;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 667
ID AAF74433 standard; cDNA; 2306 BP.
DE Human PRO2 nucleotide sequence SEQ ID NO:3.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 71.8%; Score 2043; DB 4; Length 2306;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 668
ID AAS01222 standard; cDNA; 2306 BP.
DE DNA encoding human secreted protein, POLY13.
PN WO200119856-A2.
PD 22-MAR-2001.
PA (CURA-) CURAGEN CORP.
Query Match 71.8%; Score 2043; DB 5; Length 2306;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 669
ID ADP41309 standard; cDNA; 2311 BP.
DE Human CD-like molecule HSXDF41 cDNA, SEQ ID NO:108.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 71.2%; Score 2027; DB 7; Length 2311;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 670
ID ADH89027 standard; cDNA; 2305 BP.
DE Human POLYX polynucleotide #13.
PN US2003198958-A1.
PD 23-OCT-2003.
PA (SHIM/) SHIMKETS R A.
PA (FERN/) FERNANDES E.
PA (HERR/) HERRMANN J L.
PA (LIUX/) LIU X.
PA (YANG/) YANG M.
PA (BOLD/) BOLDOS F L.
PA (SMIT/) SMITHSON G.
PA (RAST/) RASTELLI L.
Query Match 67.5%; Score 1922; DB 12; Length 2305;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 671
ID AAA39952 standard; cDNA; 2163 BP.
DE Human TANGO 215 coding sequence cDNA.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 67.0%; Score 1908; DB 3; Length 2163;

Best Local Similarity 99.8%; Pred. No. 0;
RESULT 672
ID AAI60862 standard; cDNA; 2040 BP.
DE Human polynucleotide SEQ ID NO 4851.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 66.1%; Score 1882; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 673
ID AAI59076 standard; cDNA; 2144 BP.
DE Human polynucleotide SEQ ID NO 1279.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 66.1%; Score 1880; DB 4; Length 2144;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 674
ID ADQ9299 standard; cDNA; 2144 BP.
DE DNA encoding human GPCR-like protein seqid 969.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 66.1%; Score 1880; DB 5; Length 2144;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 675
ID ADB49059 standard; cDNA; 2144 BP.
DE Novel human cDNA SEQ ID NO 969.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
Query Match 66.1%; Score 1880; DB 9; Length 2144;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 676
ID AAI59113 standard; cDNA; 2142 BP.
DE Human polynucleotide SEQ ID NO 1316.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 64.2%; Score 1827; DB 4; Length 2142;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 677
ID ADQ99336 standard; cDNA; 2142 BP.
DE DNA encoding human GPCR-like protein seqid 1006.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 64.2%; Score 1827; DB 5; Length 2142;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 678
ID ADB49096 standard; cDNA; 2142 BP.
DE Novel human cDNA SEQ ID NO 1006.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
Query Match 64.2%; Score 1827; DB 9; Length 2142;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 679
ID AAD33261 standard; cDNA; 2022 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:35.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HOMA-) HUMAN GENOME SCI INC.
Query Match 63.1%; Score 1795; DB 6; Length 2022;
Best Local Similarity 99.8%; Pred. No. 0;

RESULT 680
ID AAC90025 standard; cDNA; 2259 BP.
DE Clone HFPEY75 coding sequence.
PN WO200061774-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 62.8%; Score 1787; DB 3; Length 2259;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 681
ID AAH47256 standard; cDNA; 2784 BP.
DE Human serine protease-like protein encoding cDNA (hc-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 61.4%; Score 1747; DB 4; Length 2784;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 682
ID AAH15142 standard; cDNA; 2784 BP.
DE Human cDNA sequence SEQ ID NO:13201.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 61.4%; Score 1747; DB 4; Length 2784;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 683
ID ADN04639 standard; cDNA; 2784 BP.
DE Antiproliferative cDNA sequence #529.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 61.4%; Score 1747; DB 12; Length 2784;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 684
ID ADS85021 standard; DNA; 2784 BP.
DE Human atopic dermatitis-related gene sequence SeqID23.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Query Match 61.4%; Score 1747; DB 13; Length 2784;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 685
ID ADS85033 standard; DNA; 2784 BP.
DE Human atopic dermatitis-related gene sequence SeqID35.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Query Match 61.4%; Score 1747; DB 13; Length 2784;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 686
ID AAD30584 standard; cDNA; 2632 BP.
DE Human protease, PRTS-17 cDNA.
PN WO200208396-A2.
PD 31-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 58.7%; Score 1672; DB 6; Length 2632;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 687
ID AAF74432 standard; cDNA; 1867 BP.
DE Human PRO1 nucleotide sequence SEQ ID NO:1.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 57.4%; Score 1633; DB 4; Length 1867;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 688
ID AAH47258 standard; cDNA; 2289 BP.
DE Human serine protease-like protein coding sequence.
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 47.1%; Score 1340; DB 4; Length 2289;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 689
ID AAD33241 standard; cDNA; 1101 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:15.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 27.9%; Score 795; DB 6; Length 1101;
Best Local Similarity 99.9%; Pred. No. 3.2e-250;
RESULT 690
ID AAH99144 standard; cDNA; 1058 BP.
DE Human EST-derived coding sequence SEQ ID NO: 1001.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 18.8%; Score 534; DB 4; Length 1058;
Best Local Similarity 100.0%; Pred. No. 5.3e-165;
RESULT 691
ID AAS68826 standard; cDNA; 1058 BP.
DE DNA encoding novel human diagnostic protein #22630.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 18.8%; Score 534; DB 5; Length 1058;
Best Local Similarity 100.0%; Pred. No. 5.3e-165;
RESULT 692
ID AAH08069 standard; cDNA; 705 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:4904.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 18.3%; Score 522; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 4.8e-161;
RESULT 693
ID AAI60899 standard; cDNA; 438 BP.
DE Human polynucleotide SEQ ID NO 4888.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.8%; Score 393; DB 4; Length 438;
Best Local Similarity 100.0%; Pred. No. 7.1e-119;
RESULT 694
ID ABK30409 standard; cDNA; 505 BP.
DE Human G-protein-coupled protease #179.
PN US6331427-B1.
PD 18-DEC-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 13.0%; Score 370; DB 6; Length 505;
Best Local Similarity 99.8%; Pred. No. 2.2e-111;
RESULT 695
ID ABL63519 standard; DNA; 337 BP.
DE Breast cancer related gene sequence SEQ ID NO:1856.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 11.8%; Score 337; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.5e-100;
RESULT 696
ID ABL63953 standard; DNA; 337 BP.
DE Breast cancer related gene sequence SEQ ID NO:2290.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 11.8%; Score 337; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.5e-100;
RESULT 697
ID ABK30334 standard; cDNA; 2886 BP.
DE Human G-protein-coupled protease #104.
PN US6331427-B1.
PD 18-DEC-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.6%; Score 329; DB 6; Length 2886;
Best Local Similarity 99.8%; Pred. No. 3.5e-98;

RESULT 698
ID AB234917 standard; cDNA; 548 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 29.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match
Best Local Similarity 11.0%; Score 314; DB 6; Length 548;
Pred. No. 4.2e-93;
RESULT 699
ID AAD33260 standard; cDNA; 477 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:34.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 8.7%; Score 247; DB 6; Length 477;
Pred. No. 3.2e-71;
RESULT 700
ID ACH19532 standard; cDNA; 403 BP.
DE Human adult lung cDNA #535.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 8.2%; Score 232; DB 9; Length 403;
Pred. No. 2.7e-66;
RESULT 701
ID ADQ21818 standard; cDNA; 286 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4638.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 7.1%; Score 202; DB 12; Length 286;
Pred. No. 1.8e-56;
RESULT 702
ID AAX40465 standard; cDNA; 340 BP.
DE Human secreted protein 5' EST SEQ ID NO: 65.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match
Best Local Similarity 6.4%; Score 181; DB 2; Length 340;
Pred. No. 1.2e-49;
RESULT 703
ID AD143251 standard; cDNA; 2226 BP.
DE Plant transcription factor polynucleotide #1150.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match
Best Local Similarity 4.8%; Score 136; DB 12; Length 2226;
Pred. No. 3.8e-35;
RESULT 704
ID AD002941 standard; cDNA; 2226 BP.
DE Soybean orthologue of Thalecress transcription factor, cDNA #174.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.

PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAWARA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match
Best Local Similarity 4.8%; Score 136; DB 12; Length 2226;
Pred. No. 3.8e-35;
RESULT 705
ID ABK28222 standard; DNA; 11394 BP.
DE DNA transcription associated complementary genomic DNA #48.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.8%; Score 136; DB 6; Length 11394;
Pred. No. 2.5e-35;
RESULT 706
ID AAK89974 standard; DNA; 165 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3550.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 135; DB 4; Length 165;
Pred. No. 1.5e-34;
RESULT 707
ID AAK90168 standard; DNA; 165 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3744.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 135; DB 4; Length 165;
Pred. No. 1.5e-34;
RESULT 708
ID AAK89381 standard; DNA; 165 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2957.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 135; DB 4; Length 165;
Pred. No. 1.5e-34;
RESULT 709
ID AAK73944 standard; DNA; 165 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28756.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 135; DB 4; Length 165;
Pred. No. 1.5e-34;
RESULT 710
ID AAK78761 standard; DNA; 165 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33573.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 135; DB 4; Length 165;
Pred. No. 1.5e-34;
RESULT 711
ID AAK81312 standard; DNA; 165 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36124.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 135; DB 4; Length 165;
Pred. No. 1.5e-34;

Best Local Similarity 100.0%; Pred. No. 1.5e-34;
RESULT 712
ID AAK79574 standard; DNA; 165 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34386.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 135; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-34;
RESULT 713
ID AAL07127 standard; DNA; 165 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9815.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 135; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-34;
RESULT 714
ID AAL04803 standard; DNA; 165 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7491.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 135; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-34;
RESULT 715
ID ABA08161 standard; DNA; 165 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 956.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 135; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-34;
RESULT 716
ID ABL97697 standard; DNA; 165 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2349.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 135; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-34;
RESULT 717
ID AAS29235 standard; DNA; 165 BP.
DE Genomic sequence #78 encoding novel human DNA-binding protein.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 135; DB 5; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-34;
RESULT 718
ID ABA17044 standard; DNA; 165 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9375.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 135; DB 5; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-34;
RESULT 719
ID AAL16672 standard; DNA; 165 BP.
DE Human pancreatic related protein-encoding exon, SEQ ID NO:36.
PN WO200155327-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 135; DB 5; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-34;
RESULT 720
ID AAS39812 standard; DNA; 165 BP.
DE Genomic sequence #231 encoding human colon associated polypeptide.
PN WO200155302-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 135; DB 5; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-34;

RESULT 721
ID ABS68375 standard; DNA; 165 BP.
DE Human DNA-binding protein genomic DNA sequence #78.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.7%; Score 135; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-34;
RESULT 722
ID ADB32772 standard; DNA; 165 BP.
DE Human novel colon related polypeptide DNA SEQ ID NO 709.
PN US2003050231-A1.
PD 13-MAR-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.7%; Score 135; DB 9; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-34;
RESULT 723
ID ADC25497 standard; CDNA; 165 BP.
DE Human CDNA from extracellular matrix gene 80 #9.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 135; DB 10; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-34;
RESULT 724
ID AAI87804 standard; CDNA; 398 BP.
DE Human polynucleotide SEQ ID NO 7864.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 135; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 1.2e-34;
RESULT 725
ID ACN49835 standard; CDNA; 450 BP.
DE Cotton primed seed EST Clone ID: LIB3825-031-Q6-N6-E4, SEQ:4616.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 135; DB 13; Length 450;
Best Local Similarity 100.0%; Pred. No. 1.2e-34;
RESULT 726
ID ACN53191 standard; CDNA; 564 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-003-Q1-N6-B10, SEQ:7972.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 135; DB 13; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.1e-34;
RESULT 727
ID AAF91862 standard; CDNA; 2753 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HDP1E85, SEQ ID NO:15.
PN WO200118022-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 135; DB 4; Length 2753;
Best Local Similarity 100.0%; Pred. No. 7.7e-35;
RESULT 728
ID ABA93725 standard; CDNA; 3028 BP.
DE Human differentiation/development cDNA clone amy2_2b19.
PN WO200198454-A2.
PD 27-DEC-2001.
PA (GERU-) GERMAN HUMAN GENOME PROJECT.
Query Match 4.7%; Score 135; DB 6; Length 3028;

Best Local Similarity 100.0%; Pred. No. 7.5e-35;
RESULT 729
ID ACF34512 standard; DNA; 3028 BP.
DE Gene encoding angiogenesis protein BNO146.
FN WO2003027285-A1.
PD 03-APR-2003.
PA (BTON-) BIONOMICS LTD.
Query Match 4.7%; Score 135; DB 8; Length 3028;
Best Local Similarity 100.0%; Pred. No. 7.5e-35;
RESULT 730
ID ABK34669 standard; cDNA; 3415 BP.
DE Human cDNA for novel secreted protein, SEQ ID 438.
FN WO200177290-A2.
PD 18-OCT-2001.
PA (GBMY) GENETICS INST INC.
Query Match 4.7%; Score 135; DB 6; Length 3415;
Best Local Similarity 100.0%; Pred. No. 7.3e-35;
RESULT 731
ID ADQ22192 standard; DNA; 3931 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5012.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.7%; Score 135; DB 12; Length 3931;
Best Local Similarity 100.0%; Pred. No. 7e-35;
RESULT 732
ID ADS54096 standard; DNA; 4316 BP.
DE Pretreated genomic DNA region 20.
FN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 135; DB 10; Length 4316;
Best Local Similarity 100.0%; Pred. No. 6.9e-35;
RESULT 733
ID ADS54224 standard; DNA; 4316 BP.
DE Pretreated genomic DNA region 148.
FN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 135; DB 10; Length 4316;
Best Local Similarity 100.0%; Pred. No. 6.9e-35;
RESULT 734
ID ADS89522 standard; DNA; 4316 BP.
DE Oligonucleotide of the invention SEQ ID NO:538.
FN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 135; DB 13; Length 4316;
Best Local Similarity 100.0%; Pred. No. 6.9e-35;
RESULT 735
ID ADS89248 standard; DNA; 4316 BP.
DE Oligonucleotide of the invention SEQ ID NO:264.
FN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 135; DB 13; Length 4316;
Best Local Similarity 100.0%; Pred. No. 6.9e-35;
RESULT 736
ID ABU32921 standard; DNA; 5195 BP.
DE Human immune system associated gene SEQ ID NO: 894.
FN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 135; DB 6; Length 5195;
Best Local Similarity 100.0%; Pred. No. 6.6e-35;
RESULT 737
ID ABL32511 standard; DNA; 5306 BP.
DE Human immune system associated gene SEQ ID NO: 484.
FN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 135; DB 6; Length 5306;
Best Local Similarity 100.0%; Pred. No. 6.5e-35;

RESULT 738
ID ABN80041 standard; DNA; 5387 BP.
DE Human chemically modified disease associated gene SEQ ID NO 58.
FN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 135; DB 6; Length 5387;
Best Local Similarity 100.0%; Pred. No. 6.5e-35;
RESULT 739
ID ABK34027 standard; DNA; 6944 BP.
DE Human DNA for staging of Astrocytomas, complement, #57.
FN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 135; DB 6; Length 6944;
Best Local Similarity 100.0%; Pred. No. 6.1e-35;
RESULT 740
ID ADA20447 standard; DNA; 6944 BP.
DE Prostate tumour related genomic DNA complement sample #56.
FN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 135; DB 8; Length 6944;
Best Local Similarity 100.0%; Pred. No. 6.1e-35;
RESULT 741
ID ADA84254 standard; DNA; 6944 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:112.
FN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 135; DB 8; Length 6944;
Best Local Similarity 100.0%; Pred. No. 6.1e-35;
RESULT 742
ID ABN80146 standard; DNA; 14920 BP.
DE Human chemically modified disease associated gene SEQ ID NO 163.
FN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 135; DB 6; Length 14920;
Best Local Similarity 100.0%; Pred. No. 5e-35;
RESULT 743
ID ABL34174 standard; DNA; 113515 BP.
DE Human immune system associated gene SEQ ID NO: 2147.
FN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 135; DB 6; Length 113515;
Best Local Similarity 100.0%; Pred. No. 3.1e-35;
RESULT 744
ID ABX36136 standard; cDNA; 181 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1301.
FN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.7%; Score 134; DB 8; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.2e-34;
RESULT 745
ID ACN53869 standard; cDNA; 355 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-B10, SEQ:8650.
FN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 355;
Best Local Similarity 100.0%; Pred. No. 2.7e-34;
RESULT 746
ID ABV58662 standard; cDNA; 381 BP.
DE Human prostate expression marker cDNA 58653.

PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 134; DB 5; Length 381;
Best Local Similarity 100.0%; Pred. No. 2.7e-34;
RESULT 747
ID ACN55708 standard; cDNA; 381 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-027-Q6-N6-E10, SEQ:10489.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 381;
Best Local Similarity 100.0%; Pred. No. 2.7e-34;
RESULT 748
ID AAI88514 standard; cDNA; 389 BP.
DE Human polynucleotide SEQ ID NO 8574.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 134; DB 4; Length 389;
Best Local Similarity 100.0%; Pred. No. 2.6e-34;
RESULT 749
ID ABV57596 standard; cDNA; 396 BP.
DE Human prostate expression marker cDNA 57587.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 134; DB 5; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.6e-34;
RESULT 750
ID ABK34899 standard; cDNA; 409 BP.
DE Human cDNA encoding secreted protein #37.
PN WO200172288-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 4.7%; Score 134; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 2.6e-34;
RESULT 751
ID ACN54703 standard; cDNA; 426 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-K6-D2, SEQ:9484.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 426;
Best Local Similarity 100.0%; Pred. No. 2.6e-34;
RESULT 752
ID ACN60479 standard; cDNA; 431 BP.
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-023-Q6-K6-D10, SEQ:15260.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.6e-34;
RESULT 753
ID ACN56223 standard; cDNA; 458 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-N6-A12, SEQ:11004.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 458;
Best Local Similarity 100.0%; Pred. No. 2.5e-34;

RESULT 754
ID ACN60136 standard; cDNA; 481 BP.
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-018-Q6-K6-C5, SEQ:14917.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 481;
Best Local Similarity 100.0%; Pred. No. 2.5e-34;
RESULT 755
ID ACN61841 standard; cDNA; 483 BP.
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-021-Q6-N6-F8, SEQ:16622.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.5e-34;
RESULT 756
ID ABV57059 standard; cDNA; 490 BP.
DE Human prostate expression marker cDNA 57050.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 134; DB 5; Length 490;
Best Local Similarity 100.0%; Pred. No. 2.5e-34;
RESULT 757
ID ACN49328 standard; cDNA; 496 BP.
DE Cotton primed seed EST Clone ID: LIB3825-031-Q6-K6-E6, SEQ:4109.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.5e-34;
RESULT 758
ID ACN50622 standard; cDNA; 508 BP.
DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-N6-E9, SEQ:5403.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 508;
Best Local Similarity 100.0%; Pred. No. 2.5e-34;
RESULT 759
ID ACN51926 standard; cDNA; 509 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-N6-G11, SEQ:6707.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 509;
Best Local Similarity 100.0%; Pred. No. 2.5e-34;
RESULT 760
ID ACN49853 standard; cDNA; 518 BP.
DE Cotton primed seed EST Clone ID: LIB3825-031-Q6-N6-G11, SEQ:4634.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.5e-34;

Best Local Similarity 100.0%; Pred. No. 2.5e-34;
RESULT 761
ID ACN59971 standard; cDNA; 538 BP.
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-036-Q1-K6-H1, SEQ:14752.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 762
ID ACN55464 standard; cDNA; 540 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-024-Q6-N6-A3, SEQ:10245.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 540;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 763
ID ACN51318 standard; cDNA; 545 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-F6, SEQ:6099.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 545;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 764
ID ACN53206 standard; cDNA; 553 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-003-Q1-N6-D8, SEQ:7987.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 765
ID ACN48235 standard; cDNA; 560 BP.
DE Cotton primed seed EST Clone ID: LIB3825-021-Q1-N6-B5, SEQ:3016.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 766
ID ACN45362 standard; cDNA; 570 BP.
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-A5, SEQ:143.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 570;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 767
ID ACN52669 standard; cDNA; 578 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-017-Q1-N6-A11, SEQ:7450.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 578;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 768
ID ADR59353 standard; cDNA; 583 BP.
DE Cotton cDNA sequence, SEQ ID 134.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match 4.7%; Score 134; DB 13; Length 583;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 769
ID ACN45357 standard; cDNA; 597 BP.
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-A11, SEQ:138.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 597;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 770
ID ACN56642 standard; cDNA; 598 BP.
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-001-Q1-N6-H1, SEQ:11423.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 771
ID ACN45855 standard; cDNA; 608 BP.
DE Cotton primed seed EST Clone ID: LIB3825-009-Q1-K6-G7, SEQ:636.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 608;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 772
ID ACN50609 standard; cDNA; 616 BP.
DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-N6-D5, SEQ:5390.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 134; DB 13; Length 616;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 773
ID AAC68125 standard; cDNA; 809 BP.
DE Human secreted protein cDNA sequence #45.
PN WO200058335-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 4.7%; Score 134; DB 3; Length 809;
Best Local Similarity 100.0%; Pred. No. 2.2e-34;
RESULT 774
ID AAX89609 standard; cDNA; 831 BP.
DE Human secreted protein clone bg570_1 encoding cDNA.
PN WO9935253-A1.
PD 15-JUL-1999.

PA (GEMY) GENETICS INST INC.
 Query Match 4.7%; Score 134; DB 2; Length 831;
 Best Local Similarity 100.0%; Pred. No. 2.2e-34;
 RESULT 775
 ID AAS59240 standard; cDNA; 831 BP.
 DE Human cDNA encoding a secreted protein bg570_1.
 PN W0200175068-A2.
 PD 11-OCT-2001.
 PA (GEMY) GENETICS INST INC.
 Query Match 4.7%; Score 134; DB 4; Length 831;
 Best Local Similarity 100.0%; Pred. No. 2.2e-34;
 RESULT 776
 ID ABA90909 standard; cDNA; 831 BP.
 DE Human polynucleotide SEQ ID NO 67.
 PN US2001039335-A1.
 PD 08-NOV-2001.
 PA (JACO/) JACOBS K.
 PA (MCCO/) MCCOY J M.
 PA (LAVA/) LAVALLIE E R.
 PA (COLL/) COLLINS-RACIE L A.
 PA (EVAN/) EVANS C.
 PA (MERB/) MERBERG D.
 PA (TREA/) TREACY M.
 PA (AGOS/) AGOSTINO M J.
 PA (STEI/) STEININGER R J.
 PA (SPAU/) SPAULDING V.
 PA (WONG/) WONG G G.
 PA (CLAR/) CLARK H.
 PA (PECH/) FECHTEL K.
 Query Match 4.7%; Score 134; DB 6; Length 831;
 Best Local Similarity 100.0%; Pred. No. 2.2e-34;
 RESULT 777
 ID ADQ22074 standard; DNA; 980 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4894.
 PN W02004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 4.7%; Score 134; DB 12; Length 980;
 Best Local Similarity 100.0%; Pred. No. 2.1e-34;
 RESULT 778
 ID ADM32854 standard; DNA; 1084 BP.
 DE DNA sequence of a human adenosine monophosphate deaminase (AMPD).
 PN W02004024880-A2.
 PD 25-MAR-2004.
 PA (EXEL-) EXELIXIS INC.
 Query Match 4.7%; Score 134; DB 12; Length 1084;
 Best Local Similarity 100.0%; Pred. No. 2.1e-34;
 RESULT 779
 ID ADQ23195 standard; DNA; 1091 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6015.
 PN W02004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 4.7%; Score 134; DB 12; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 2e-34;
 RESULT 780
 ID AAD02119 standard; cDNA; 1459 BP.
 DE Maize RAD51 orthologue #2 cDNA.
 PN W0200068370-A2.
 PD 16-NOV-2000.
 PA (PION-) PIONEER HI-BRED INT INC.
 Query Match 4.7%; Score 134; DB 4; Length 1459;
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;
 RESULT 781
 ID ADR25589 standard; DNA; 1521 BP.
 DE Breast cancer prognosis marker #1450.
 PN W02004065545-A2.
 PD 05-AUG-2004.
 PA (ROSE-) ROSETTA INPHARMATICS LLC.
 PA (NECA-) NETHERLANDS CANCER INST.
 Query Match 4.7%; Score 134; DB 13; Length 1521;
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;
 RESULT 782

ID ADP50501 standard; cDNA; 1521 BP.
 DE Human PRO cDNA sequence SEQ ID NO:1027.
 PN W02004039956-A2.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 4.7%; Score 134; DB 13; Length 1521;
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;
 RESULT 783
 ID ADQ22988 standard; DNA; 1576 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5808.
 PN W02004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 4.7%; Score 134; DB 12; Length 1576;
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;
 RESULT 784
 ID ABV28953 standard; cDNA; 1603 BP.
 DE Human prostate expression marker cDNA 28944.
 PN W0200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 134; DB 5; Length 1603;
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;
 RESULT 785
 ID ABV22100 standard; cDNA; 1603 BP.
 DE Human prostate expression marker cDNA 22091.
 PN W0200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 134; DB 5; Length 1603;
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;
 RESULT 786
 ID ABV23114 standard; cDNA; 1603 BP.
 DE Human prostate expression marker cDNA 23105.
 PN W0200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 134; DB 5; Length 1603;
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;
 RESULT 787
 ID ABV27940 standard; cDNA; 1603 BP.
 DE Human prostate expression marker cDNA 27931.
 PN W0200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.7%; Score 134; DB 5; Length 1603;
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;
 RESULT 788
 ID ADM47653 standard; DNA; 1708 BP.
 DE Polynucleotide sequence #71 useful in producing transgenic plants.
 PN US2003233670-A1.
 PD 18-DEC-2003.
 PA (EDGE/) EDGERTON M D.
 PA (CHOM/) CHOMET P S.
 PA (LACC/) LACCETTI L B.
 Query Match 4.7%; Score 134; DB 12; Length 1708;
 Best Local Similarity 100.0%; Pred. No. 1.8e-34;
 RESULT 789
 ID ADI42816 standard; DNA; 1803 BP.
 DE Plant transcription factor polynucleotide #820.
 PN US2004019927-A1.
 PD 29-JAN-2004.
 PA (SHER/) SHERMAN B K.
 PA (RIEC/) RIECHMANN J L.
 PA (JIAN/) JIANG C.
 PA (HEAR/) HEARD J E.
 PA (HAAK/) HAAKE V.
 PA (CREE/) CREELMAN R A.
 PA (RATC/) RATCLIFFE O.
 PA (ADAM/) ADAM L J.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J.
 PA (BROU/) BROUN P E.

PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 4.7%; Score 134; DB 12; Length 1803;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
RESULT 790
ID AD003025 standard; cDNA; 1803 BP.
DE Corn orthologue of Thalecress transcription factor, cDNA #126.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAWAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 4.7%; Score 134; DB 12; Length 1803;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
RESULT 791
ID ADN95834 standard; DNA; 1999 BP.
DE Human BEC/LEC-related gene sequence SeqID758.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 4.7%; Score 134; DB 11; Length 1999;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
RESULT 792
ID ADQ24947 standard; DNA; 1999 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7767.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.7%; Score 134; DB 12; Length 1999;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
RESULT 793
ID ADP23790 standard; cDNA; 1999 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:968.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 134; DB 13; Length 1999;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
RESULT 794
ID ACN39804 standard; cDNA; 2074 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325989, SEQ ID NO:4174.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 134; DB 13; Length 2074;
Best Local Similarity 100.0%; Pred. No. 1.7e-34;
RESULT 795
ID ADP56341 standard; cDNA; 2401 BP.
DE Human PRO cDNA sequence SEQ ID NO:2317.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 134; DB 13; Length 2401;
Best Local Similarity 100.0%; Pred. No. 1.7e-34;
RESULT 796

ID ADQ22618 standard; DNA; 2499 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5438.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.7%; Score 134; DB 12; Length 2499;
Best Local Similarity 100.0%; Pred. No. 1.7e-34;
RESULT 797
ID ADJ48201 standard; DNA; 2520 BP.
DE Maize oil-associated gene #19.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 4.7%; Score 134; DB 12; Length 2520;
Best Local Similarity 100.0%; Pred. No. 1.7e-34;
RESULT 798
ID ADP04916 standard; cDNA; 2789 BP.
DE Sea squirt cDNA with tissue specific expression in development Seq 511.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 4.7%; Score 134; DB 12; Length 2789;
Best Local Similarity 100.0%; Pred. No. 1.6e-34;
RESULT 799
ID ADR24479 standard; DNA; 2809 BP.
DE Breast cancer prognosis marker #340.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 4.7%; Score 134; DB 13; Length 2809;
Best Local Similarity 100.0%; Pred. No. 1.6e-34;
RESULT 800
ID AAZ07192 standard; cDNA; 3275 BP.
DE Human lung tumour protein SAL-25 5' cDNA sequence.
PN WO9938973-A2.
PD 05-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 4.7%; Score 134; DB 2; Length 3275;
Best Local Similarity 100.0%; Pred. No. 1.6e-34;
RESULT 801
ID AAC79145 standard; cDNA; 3275 BP.
DE Human lung tumour-specific cDNA #98.
PN WO200060077-A2.
PD 12-OCT-2000.
PA (CORI-) CORIXA CORP.
Query Match 4.7%; Score 134; DB 3; Length 3275;
Best Local Similarity 100.0%; Pred. No. 1.6e-34;
RESULT 802
ID AAD32320 standard; cDNA; 3275 BP.
DE Human lung tumour-specific protein SAL-25 cDNA.
PN WO200172295-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.7%; Score 134; DB 4; Length 3275;
Best Local Similarity 100.0%; Pred. No. 1.6e-34;
RESULT 803
ID ADP66459 standard; cDNA; 3275 BP.
DE Human lung tumour-specific related cDNA, SEQ ID No 151.
PN WO200292001-A2.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.7%; Score 134; DB 10; Length 3275;
Best Local Similarity 100.0%; Pred. No. 1.6e-34;
RESULT 804
ID ADE87713 standard; cDNA; 3275 BP.
DE Human lung tumour antigen cDNA #98.
PN US2003118599-A1.
PD 26-JUN-2003.

PA (CORI-) CORIXA CORP.
Query Match 4.7%; Score 134; DB 10; Length 3275;
Best Local Similarity 100.0%; Pred. No. 1.1e-34;
RESULT 805
ID AD022371 standard; DNA; 4824 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5191.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.7%; Score 134; DB 12; Length 4824;
Best Local Similarity 100.0%; Pred. No. 1.4e-34;
RESULT 806
ID ABL32788 standard; DNA; 6171 BP.
DE Human immune system associated gene SEQ ID NO: 761.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 134; DB 6; Length 6171;
Best Local Similarity 100.0%; Pred. No. 1.3e-34;
RESULT 807
ID AB067050 standard; DNA; 6486 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 80.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 134; DB 6; Length 6486;
Best Local Similarity 100.0%; Pred. No. 1.3e-34;
RESULT 808
ID AAX33181 standard; DNA; 6644 BP.
DE Base sequence of the plasmid pRx-ires-bar.
PN WO9913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 4.7%; Score 134; DB 2; Length 6644;
Best Local Similarity 100.0%; Pred. No. 1.3e-34;
RESULT 809
ID AD024552 standard; DNA; 7115 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7372.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.7%; Score 134; DB 12; Length 7115;
Best Local Similarity 100.0%; Pred. No. 1.3e-34;
RESULT 810
ID ACF62807 standard; DNA; 7369 BP.
DE Colon cancer analysis related genomic DNA SEQ ID NO:56.
PN WO2003014388-A2.
PD 20-FEB-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 134; DB 8; Length 7369;
Best Local Similarity 100.0%; Pred. No. 1.3e-34;
RESULT 811
ID AB210137 standard; DNA; 7369 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #277.
PN WO20027272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 134; DB 8; Length 7369;
Best Local Similarity 100.0%; Pred. No. 1.3e-34;
RESULT 812
ID AAX33182 standard; DNA; 7372 BP.
DE Base sequence of the plasmid pRx-Bcl-xl-bsr.
PN WO9913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 4.7%; Score 134; DB 2; Length 7372;
Best Local Similarity 100.0%; Pred. No. 1.3e-34;
RESULT 813
ID AAX33180 standard; DNA; 7797 BP.
DE Cowpox virus bsr full length gene sequence.
PN WO9913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.

Query Match 4.7%; Score 134; DB 2; Length 7797;
Best Local Similarity 100.0%; Pred. No. 1.3e-34;
RESULT 814
ID AAX33184 standard; DNA; 7996 BP.
DE Base sequence of the plasmid pRx-Bcl 2-i-hcd 25.
PN WO9913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 4.7%; Score 134; DB 2; Length 7996;
Best Local Similarity 100.0%; Pred. No. 1.2e-34;
RESULT 815
ID ABK40074 standard; DNA; 8899 BP.
DE Human chemically pretreated gene sequence #78 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 134; DB 6; Length 8899;
Best Local Similarity 100.0%; Pred. No. 1.2e-34;
RESULT 816
ID ABL32837 standard; DNA; 8899 BP.
DE Human immune system associated gene SEQ ID NO: 810.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 134; DB 6; Length 8899;
Best Local Similarity 100.0%; Pred. No. 1.2e-34;
RESULT 817
ID ABL32911 standard; DNA; 8946 BP.
DE Human immune system associated gene SEQ ID NO: 884.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 134; DB 6; Length 8946;
Best Local Similarity 100.0%; Pred. No. 1.2e-34;
RESULT 818
ID ADL26832 standard; cDNA; 12178 BP.
DE Rat L-NAME-related actin-associated cytoskeleton protein LACS CDNA.
PN WO2004022753-A1.
PD 18-MAR-2004.
PA (ANGE-) ANGES MG INC.
Query Match 4.7%; Score 134; DB 13; Length 12178;
Best Local Similarity 100.0%; Pred. No. 1.1e-34;
RESULT 819
ID AAV09036 standard; RNA; 12827 BP.
DE Equine arteritis virus partial RNA genome sequence.
PN WO9802549-A1.
PD 22-JAN-1998.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 4.7%; Score 134; DB 2; Length 12827;
Best Local Similarity 100.0%; Pred. No. 1.1e-34;
RESULT 820
ID AAV09039 standard; DNA; 15528 BP.
DE Equine arteritis virus expression vector pEAV030.
PN WO9802549-A1.
PD 22-JAN-1998.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 4.7%; Score 134; DB 2; Length 15528;
Best Local Similarity 100.0%; Pred. No. 1.1e-34;
RESULT 821
ID AAS45399 standard; DNA; 15832 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #52.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 134; DB 4; Length 15832;
Best Local Similarity 100.0%; Pred. No. 1.1e-34;
RESULT 822
ID ABL33343 standard; DNA; 15832 BP.
DE Human immune system associated gene SEQ ID NO: 1316.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 134; DB 6; Length 15832;

Best Local Similarity 100.0%; Pred. No. 1.1e-34;
RESULT 823
ID AAL04801 standard; DNA; 148 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7489.
FN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 134; DB 6; Length 15832;
Best Local Similarity 100.0%; Pred. No. 1.1e-34;
RESULT 824
ID ABO67149 standard; DNA; 40324 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 179.
FN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 134; DB 6; Length 40324;
Best Local Similarity 100.0%; Pred. No. 8.4e-35;
RESULT 825
ID AAS35937 standard; DNA; 148 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1437.
FN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 826
ID AAK89970 standard; DNA; 148 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3546.
FN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 827
ID AA162624 standard; DNA; 148 BP.
DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 274.
FN WO200155324-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 828
ID AAK78753 standard; DNA; 148 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33565.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 829
ID AAK81310 standard; DNA; 148 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36122.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 830
ID AAK73937 standard; DNA; 148 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28749.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 831
ID AAK79569 standard; DNA; 148 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34381.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;

RESULT 832
ID AAL04801 standard; DNA; 148 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7489.
FN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 833
ID AAL06718 standard; DNA; 148 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9406.
FN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 834
ID AAL07121 standard; DNA; 148 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9809.
FN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 835
ID AAL05015 standard; DNA; 148 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7703.
FN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 836
ID ABA08155 standard; DNA; 148 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 950.
FN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 837
ID ABL97695 standard; DNA; 148 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2347.
FN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 838
ID ABL97908 standard; DNA; 148 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2560.
FN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 839
ID AAS29186 standard; DNA; 148 BP.
DE Genomic sequence #29 encoding novel human DNA-binding protein.
FN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 5; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 840
ID AAS29163 standard; DNA; 148 BP.
DE Genomic sequence #6 encoding novel human DNA-binding protein.
FN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 5; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 841

ID AAS29228 standard; DNA; 148 BP.
DE Genomic sequence #71 encoding novel human DNA-binding protein.
PN WO200155162-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 5; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 842
ID AAS29176 standard; DNA; 148 BP.
DE Genomic sequence #19 encoding novel human DNA-binding protein.
PN WO200155162-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 5; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 843
ID ABA17037 standard; DNA; 148 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9368.
PN WO200159063-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 5; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 844
ID AAD16668 standard; DNA; 148 BP.
DE Human pancreatic related protein-encoding exon, SEQ ID NO:32.
PN WO200155327-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 5; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 845
ID ABS68316 standard; DNA; 148 BP.
DE Human DNA-binding protein genomic DNA sequence #19.
PN US2002102638-A1.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.7%; Score 133; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 846
ID ABS68303 standard; DNA; 148 BP.
DE Human DNA-binding protein genomic DNA sequence #6.
PN US2002102638-A1.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.7%; Score 133; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 847
ID ABS68326 standard; DNA; 148 BP.
DE Human DNA-binding protein genomic DNA sequence #29.
PN US2002102638-A1.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.7%; Score 133; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 848
ID ABS68368 standard; DNA; 148 BP.
DE Human DNA-binding protein genomic DNA sequence #71.
PN US2002102638-A1.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.7%; Score 133; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 849
ID ADA41651 standard; DNA; 148 BP.

DE Human secreted protein related DNA.
PN WO2002102993-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 8; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 850
ID ADC25448 standard; CDNA; 148 BP.
DE Human cDNA from extracellular matrix gene 53 #4.
PN US2003049650-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 851
ID ADC25490 standard; CDNA; 148 BP.
DE Human cDNA from extracellular matrix gene 80 #2.
PN US2003049650-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 852
ID ADC25425 standard; CDNA; 148 BP.
DE Human cDNA from extracellular matrix gene 14 #3.
PN US2003049650-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 853
ID ADC25438 standard; CDNA; 148 BP.
DE Human cDNA from extracellular matrix gene 25 #2.
PN US2003049650-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 854
ID ADC74709 standard; DNA; 148 BP.
DE Human secreted protein-related DNA - SEQ ID 1342.
PN WO2003038063-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 855
ID ADE46631 standard; DNA; 148 BP.
DE Human cardiovascular system related genomic DNA #197.
PN US2003059908-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 856
ID ADA57783 standard; DNA; 148 BP.
DE BAC fragment containing human secreted protein gene #537.
PN WO2002102994-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 857
ID ADN41714 standard; DNA; 148 BP.
DE Novel human secreted protein polynucleotide seqid 836.
PN US2004044191-A1.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KIYAW/) KIYAW H.
PA (LIYY/) LI Y.

PA (ZENG/) ZENG Z.
PA (LAPL/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLUSE/) OLSEN H.
PA (EBNER/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 12; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 858
ID ADJ08049 standard; DNA; 148 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1437.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;
RESULT 859
ID AAF24360 standard; DNA; 160 BP.
DE Retroviral recombination assay coding sequence fragment #5.
PN WO200104360-A2.
PD 18-JAN-2001.
PA (UABR-) UAB RES FOUND.
PA (TRAN-) TRANZYME INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 5; Length 160;
Best Local Similarity 100.0%; Pred. No. 7e-34;
RESULT 860
ID AAF24365 standard; DNA; 172 BP.
DE Retroviral recombination assay coding sequence fragment #10.
PN WO200104360-A2.
PD 18-JAN-2001.
PA (UABR-) UAB RES FOUND.
PA (TRAN-) TRANZYME INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 5; Length 172;
Best Local Similarity 100.0%; Pred. No. 6.9e-34;
RESULT 861
ID AAF24361 standard; DNA; 178 BP.
DE Retroviral recombination assay coding sequence fragment #6.
PN WO200104360-A2.
PD 18-JAN-2001.
PA (UABR-) UAB RES FOUND.
PA (TRAN-) TRANZYME INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 5; Length 178;
Best Local Similarity 100.0%; Pred. No. 6.8e-34;
RESULT 862
ID AAT13475 standard; RNA; 191 BP.
DE Capture probe for detection of target sequence by chimeraic probe.
PN EP707076-A1.
PD 17-APR-1996.
PA (STAD) AMOCO CORP.
Query Match
Best Local Similarity 4.7%; Score 133; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 6.7e-34;
RESULT 863
ID ACA25512 standard; DNA; 195 BP.
DE Prokaryotic essential gene #7169.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 8; Length 195;
Best Local Similarity 100.0%; Pred. No. 6.7e-34;
RESULT 864
ID ADP85921 standard; DNA; 196 BP.
DE Synthetic construct #5.
PN US2004110205-A1.
PD 10-JUN-2004.
PA (WANG/) WANG H.
Query Match
Best Local Similarity 4.7%; Score 133; DB 12; Length 196;
Best Local Similarity 100.0%; Pred. No. 6.7e-34;
RESULT 865
ID AA41451 standard; cDNA; 202 BP.
DE Nucleotide sequence of the 3' portion of the BL229_22 clone.
PN WO9821332-A2.
PD 22-MAY-1998.

PA (GEMY) GENETICS INST INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 6.6e-34;
RESULT 866
ID AAF98423 standard; cDNA; 202 BP.
DE Human cDNA clone BL229_22 3' sequence SEQ ID 81.
PN WO200119988-A1.
PD 22-MAR-2001.
PA (GEMY) GENETICS INST INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 5; Length 202;
Best Local Similarity 100.0%; Pred. No. 6.6e-34;
RESULT 867
ID AAF24363 standard; DNA; 208 BP.
DE Retroviral recombination assay coding sequence fragment #8.
PN WO200104360-A2.
PD 18-JAN-2001.
PA (UABR-) UAB RES FOUND.
PA (TRAN-) TRANZYME INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 5; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.6e-34;
RESULT 868
ID AEX49357 standard; cDNA; 220 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #14522.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 4.7%; Score 133; DB 8; Length 220;
Best Local Similarity 100.0%; Pred. No. 6.5e-34;
RESULT 869
ID AAC98734 standard; cDNA; 225 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:744.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.4e-34;
RESULT 870
ID AAT76782 standard; DNA; 240 BP.
DE Staphylococcus aureus exfoliative toxin A gene capture probe.
PN US5627054-A.
PD 06-MAY-1997.
PA (USSA) US SEC OF ARMY.
Query Match
Best Local Similarity 4.7%; Score 133; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 6.3e-34;
RESULT 871
ID ABX38708 standard; cDNA; 242 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3873.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 4.7%; Score 133; DB 8; Length 242;
Best Local Similarity 100.0%; Pred. No. 6.3e-34;
RESULT 872
ID ABX48177 standard; cDNA; 286 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13342.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 4.7%; Score 133; DB 8; Length 286;
Best Local Similarity 100.0%; Pred. No. 6.1e-34;
RESULT 873
ID ADL35477 standard; DNA; 305 BP.
DE Human filamin A alpha-related functional screen hit DNA 3.
PN WO2004019893-A2.

PD 11-MAR-2004.
PA (RIGE-) RIGEL PHARM INC. 4.7%; Score 133; DB 12; Length 305;
Query Match
Best Local Similarity 100.0%; Pred. No. 6e-34;
RESULT 874
ID ABV44994 standard; cDNA; 309 BP.
DE Human prostate expression marker CDNA 44985.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.9e-34;
RESULT 875
ID ACN58609 standard; cDNA; 313 BP.
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-010-Q6-N6-C11, SEQ:13390.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.9e-34;
RESULT 876
ID ACN51559 standard; cDNA; 318 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-004-Q1-N6-B3, SEQ:6340.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.9e-34;
RESULT 877
ID ACN53877 standard; cDNA; 325 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-C7, SEQ:8658.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.9e-34;
RESULT 878
ID ABX39465 standard; cDNA; 327 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4630.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.9e-34;
RESULT 879
ID ACN45670 standard; cDNA; 341 BP.
DE Cotton primed seed EST Clone ID: LIB3825-007-Q1-K6-C8, SEQ:451.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e-34;
RESULT 880
ID ADL43689 standard; DNA; 351 BP.
DE Human ovarian cancer DNA marker #17579.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e-34;
RESULT 881
ID ABX43106 standard; cDNA; 365 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #8271.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.7e-34;
RESULT 882
ID ABV44911 standard; cDNA; 375 BP.
DE Human prostate expression marker CDNA 44902.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.7e-34;
RESULT 883
ID AAI87526 standard; cDNA; 382 BP.
DE Human polynucleotide SEQ ID NO 7586.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
RESULT 884
ID AAI85202 standard; cDNA; 390 BP.
DE Human polynucleotide SEQ ID NO 5262.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
RESULT 885
ID ABV13564 standard; cDNA; 394 BP.
DE Human prostate expression marker CDNA 13555.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
RESULT 886
ID AAF94862 standard; cDNA; 396 BP.
DE Human ovarian cancer associated coding sequence SEQ ID NO: 53.
PN WO200118046-A2.
PD 15-MAR-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
RESULT 887
ID ABL48812 standard; cDNA; 396 BP.
DE Ovarian carcinoma sequence isolate 24368.
PN US200204491-A1.
PD 10-JAN-2002.
PA (XUJ/) XU J.
PA (STOL/) STOLK J A.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
RESULT 888
ID ABT03129 standard; cDNA; 396 BP.
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 53.
PN WO200239885-A2.
PD 23-MAY-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
RESULT 889

ID ADM10722 standard; cDNA; 396 BP.
DE Human ovarian carcinoma-associated cDNA 24368.
PN US2003206918-A1.
PD 06-NOV-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.7%; Score 133; DB 11; Length 396;
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
RESULT 890
ID ADJ11052 standard; cDNA; 396 BP.
DE Representative human ovarian carcinoma cDNA SeqID 53.
PN US2003232056-A1.
PD 18-DEC-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.7%; Score 133; DB 12; Length 396;
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
RESULT 891
ID ADM43313 standard; cDNA; 396 BP.
DE Human ovarian carcinoma cDNA #53.
PN US2003129192-A1.
PD 10-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.7%; Score 133; DB 12; Length 396;
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
RESULT 892
ID AA188388 standard; cDNA; 398 BP.
DE Human polynucleotide SEQ ID NO 8448.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 133; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
RESULT 893
ID ACN53082 standard; cDNA; 398 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-021-Q1-N6-F7, SEQ:7863.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 398;
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
RESULT 894
ID AD137305 standard; DNA; 406 BP.
DE Human ovarian cancer DNA marker #11195.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 133; DB 5; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
RESULT 895
ID AD172158 standard; DNA; 406 BP.
DE Human ovarian cancer DNA marker #4900.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 133; DB 5; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
RESULT 896
ID ABV43535 standard; cDNA; 408 BP.
DE Human prostate expression marker cDNA 43526.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 133; DB 5; Length 408;
Best Local Similarity 100.0%; Pred. No. 5.5e-34;
RESULT 897
ID ABV34679 standard; cDNA; 408 BP.
DE Human prostate expression marker cDNA 34670.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 133; DB 5; Length 408;

Best Local Similarity 100.0%; Pred. No. 5.5e-34;
RESULT 898
ID ACN52913 standard; cDNA; 411 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-019-Q1-N6-D10, SEQ:7694.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 411;
Best Local Similarity 100.0%; Pred. No. 5.5e-34;
RESULT 899
ID ACN52877 standard; cDNA; 421 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-N6-H7, SEQ:7658.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 421;
Best Local Similarity 100.0%; Pred. No. 5.5e-34;
RESULT 900
ID ACN56895 standard; cDNA; 435 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-011-Q6-N6-E2, SEQ:11676.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 435;
Best Local Similarity 100.0%; Pred. No. 5.5e-34;
RESULT 901
ID ACN52033 standard; cDNA; 443 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-H4, SEQ:6814.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 443;
Best Local Similarity 100.0%; Pred. No. 5.4e-34;
RESULT 902
ID ABX38235 standard; cDNA; 446 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3400.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.7%; Score 133; DB 8; Length 446;
Best Local Similarity 100.0%; Pred. No. 5.4e-34;
RESULT 903
ID AA183052 standard; cDNA; 452 BP.
DE Human polynucleotide SEQ ID NO 3112.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 133; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 5.4e-34;
RESULT 904
ID ACN49987 standard; cDNA; 452 BP.
DE Cotton primed seed EST Clone ID: LIB3825-033-Q6-N6-F5, SEQ:4768.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.

Query Match 4.7%; Score 133; DB 13; Length 452;
Best Local Similarity 100.0%; Pred. No. 5.4e-34;
RESULT 905
ID AAI80464 standard; cDNA; 456 BP.
DE Human polynucleotide SEQ ID NO 524.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 133; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 5.4e-34;
RESULT 906
ID ABX4494 standard; cDNA; 456 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #9659.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.7%; Score 133; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 5.4e-34;
RESULT 907
ID ACN62049 standard; cDNA; 469 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-024-Q6-N6-E4, SEQ:16830.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 469;
Best Local Similarity 100.0%; Pred. No. 5.4e-34;
RESULT 908
ID ACN58522 standard; cDNA; 476 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-010-Q6-K6-Cl1, SEQ:13303.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 476;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
RESULT 909
ID ACN51993 standard; cDNA; 478 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-E1, SEQ:6774.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 478;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
RESULT 910
ID ABV56248 standard; cDNA; 481 BP.
DE Human prostate expression marker cDNA 56239.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 133; DB 5; Length 481;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
RESULT 911
ID ACN53393 standard; cDNA; 485 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-007-Q1-K6-C5, SEQ:8174.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;

RESULT 912
ID ACN52021 standard; cDNA; 485 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-G4, SEQ:6802.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
RESULT 913
ID ACN53606 standard; cDNA; 486 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-K6-F5, SEQ:8387.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 486;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
RESULT 914
ID ACN48060 standard; cDNA; 487 BP.
DE Cotton primed seed EST Clone ID: LIB3825-018-Q1-N6-F4, SEQ:2841.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 487;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
RESULT 915
ID ACN54384 standard; cDNA; 489 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-004-Q1-K6-F9, SEQ:9165.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 489;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
RESULT 916
ID ACN49736 standard; cDNA; 489 BP.
DE Cotton primed seed EST Clone ID: LIB3825-026-Q6-N6-B11, SEQ:4517.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 489;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
RESULT 917
ID ACN61416 standard; cDNA; 490 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-015-Q1-N6-H1, SEQ:16197.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 490;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
RESULT 918
ID ACN47898 standard; cDNA; 495 BP.
DE Cotton primed seed EST Clone ID: LIB3825-016-Q1-N6-E4, SEQ:2679.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E. 4.7%; Score 133; DB 13; Length 495;
Query Match 100.0%; Pred. No. 5.3e-34;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
RESULT 919
ID ACN62281 standard; cDNA; 496 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-027-Q6-N6-E4, SEQ:17062.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 496;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
RESULT 920
ID ACN46935 standard; cDNA; 499 BP.
DE Cotton primed seed EST Clone ID: LIB3825-005-Q1-N6-D10, SEQ:1716.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 499;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
RESULT 921
ID ABV59092 standard; cDNA; 501 BP.
DE Human prostate expression marker cDNA 59083.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MTLL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 133; DB 5; Length 501;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
RESULT 922
ID ACN56650 standard; cDNA; 502 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-001-Q1-N6-H7, SEQ:11431.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 502;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
RESULT 923
ID ACN47530 standard; cDNA; 506 BP.
DE Cotton primed seed EST Clone ID: LIB3825-012-Q1-K6-F1, SEQ:2311.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 506;
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
RESULT 924
ID ADR64316 standard; cDNA; 510 BP.
DE Cotton cDNA sequence, SEQ ID 5097.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match 4.7%; Score 133; DB 13; Length 510;
Best Local Similarity 100.0%; Pred. No. 5.2e-34;
RESULT 925
ID ACN55753 standard; cDNA; 516 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-N6-B12, SEQ:10534.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E. 4.7%; Score 133; DB 13; Length 516;
Query Match 100.0%; Pred. No. 5.2e-34;
Best Local Similarity 100.0%; Pred. No. 5.2e-34;
RESULT 926
ID ACN55333 standard; cDNA; 517 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-K6-E7, SEQ:10114.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 517;
Best Local Similarity 100.0%; Pred. No. 5.2e-34;
RESULT 927
ID ACN46088 standard; cDNA; 522 BP.
DE Cotton primed seed EST Clone ID: LIB3825-015-Q1-K6-A5, SEQ:869.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 522;
Best Local Similarity 100.0%; Pred. No. 5.2e-34;
RESULT 928
ID ACN61425 standard; cDNA; 527 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-015-Q1-N6-H7, SEQ:16206.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 527;
Best Local Similarity 100.0%; Pred. No. 5.2e-34;
RESULT 929
ID ACN47028 standard; cDNA; 528 BP.
DE Cotton primed seed EST Clone ID: LIB3825-006-Q1-N6-B12, SEQ:1809.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 528;
Best Local Similarity 100.0%; Pred. No. 5.2e-34;
RESULT 930
ID ACN53350 standard; cDNA; 528 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-006-Q1-N6-F8, SEQ:8131.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 528;
Best Local Similarity 100.0%; Pred. No. 5.2e-34;
RESULT 931
ID ACN46089 standard; cDNA; 538 BP.
DE Cotton primed seed EST Clone ID: LIB3825-015-Q1-K6-A6, SEQ:870.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 133; DB 13; Length 538;
Best Local Similarity 100.0%; Pred. No. 5.2e-34;
RESULT 932
ID ACN57165 standard; cDNA; 541 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-014-Q6-N6-G1, SEQ:11946.

PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 541;
100.0%; Pred. No. 5.2e-34;
RESULT 933
ID ACN521102 standard; cDNA; 542 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-E12, SEQ:6883.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 542;
100.0%; Pred. No. 5.2e-34;
RESULT 934
ID ACN521108 standard; cDNA; 545 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-F7, SEQ:6889.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 545;
100.0%; Pred. No. 5.2e-34;
RESULT 935
ID ACN51414 standard; cDNA; 547 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-K6-G6, SEQ:6195.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 547;
100.0%; Pred. No. 5.2e-34;
RESULT 936
ID ACN62109 standard; cDNA; 547 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-025-Q6-N6-C2, SEQ:16890.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 547;
100.0%; Pred. No. 5.2e-34;
RESULT 937
ID ACN53890 standard; cDNA; 547 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-F10, SEQ:8671.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 547;
100.0%; Pred. No. 5.2e-34;
RESULT 938
ID ACN52320 standard; cDNA; 549 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-B10, SEQ:7101.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 549;
100.0%; Pred. No. 5.2e-34;

Best Local Similarity 100.0%; Pred. No. 5.2e-34;
RESULT 939
ID ACN62570 standard; cDNA; 552 BP.
DE Cotton developing fibre EST Clone ID: LIB3830-001-Q1-N6-A1, SEQ:17351.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 552;
100.0%; Pred. No. 5.1e-34;
RESULT 940
ID ACN49708 standard; cDNA; 554 BP.
DE Cotton primed seed EST Clone ID: LIB3825-025-Q6-N6-F6, SEQ:4489.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 554;
100.0%; Pred. No. 5.1e-34;
RESULT 941
ID ACN47785 standard; cDNA; 557 BP.
DE Cotton primed seed EST Clone ID: LIB3825-015-Q1-N6-A5, SEQ:2566.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 557;
100.0%; Pred. No. 5.1e-34;
RESULT 942
ID ACN47472 standard; cDNA; 560 BP.
DE Cotton primed seed EST Clone ID: LIB3825-011-Q1-N6-C9, SEQ:2253.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 560;
100.0%; Pred. No. 5.1e-34;
RESULT 943
ID ABV57899 standard; cDNA; 565 BP.
DE Human prostate expression marker cDNA 57890.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 565;
100.0%; Pred. No. 5.1e-34;
RESULT 944
ID ACN56344 standard; cDNA; 565 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-034-Q6-N6-B10, SEQ:11125.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 565;
100.0%; Pred. No. 5.1e-34;
RESULT 945
ID ACN53459 standard; cDNA; 567 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-008-Q1-K6-A7, SEQ:8240.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.

Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 567;
RESULT 946
ID ACN87735 standard; DNA; 599 BP.
DE Breast cancer related marker, seq id 8885.
PN US2003099974-A1.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 5; Length 570;
RESULT 947
ID ACN52090 standard; cDNA; 571 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-B9, SEQ:6871.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 571;
RESULT 948
ID ACN52610 standard; cDNA; 574 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-N6-G6, SEQ:7391.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 574;
RESULT 949
ID ACN51300 standard; cDNA; 583 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-C2, SEQ:6081.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 583;
RESULT 950
ID ACN58226 standard; cDNA; 591 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-008-Q6-K6-G6, SEQ:13007.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 591;
RESULT 951
ID ACN87190 standard; DNA; 592 BP.
DE Breast cancer related marker, seq id 8340.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 11; Length 592;
RESULT 952
ID ACN49504 standard; cDNA; 593 BP.
DE Cotton primed seed EST Clone ID: LIB3825-034-Q6-K6-G11, SEQ:4285.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 593;
RESULT 953
ID ACN87735 standard; DNA; 599 BP.
DE Breast cancer related marker, seq id 8885.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 11; Length 599;
RESULT 954
ID ACN45292 standard; cDNA; 627 BP.
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-K6-A11, SEQ:73.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 627;
RESULT 955
ID ACN54072 standard; cDNA; 640 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-020-Q1-K6-G11, SEQ:8853.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 640;
RESULT 956
ID AAC80551 standard; cDNA; 658 BP.
DE Human secreted protein gene 21 SEQ ID NO:31.
PN WO200058467-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 3; Length 658;
RESULT 957
ID AAC59098 standard; cDNA; 667 BP.
DE Human secreted protein coding sequence SEQ ID NO: 60.
PN WO200055171-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 3; Length 667;
RESULT 958
ID AAD05318 standard; cDNA; 671 BP.
DE Human secreted protein-encoding gene 19 cDNA clone HWLF064, SEQ ID NO:29.
PN WO200134626-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 4; Length 671;
RESULT 959
ID AAS62239 standard; cDNA; 681 BP.
DE cDNA sequence #26 encoding novel human secreted protein.
PN WO200177291-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 6; Length 681;
RESULT 960
ID AAK8206 standard; cDNA; 698 BP.
DE Human digestive system antigen coding sequence SEQ ID NO: 522.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 4; Length 698;
RESULT 961
ID AAS29150 standard; cDNA; 698 BP.
DE cDNA encoding for human DNA-binding protein #121.

Query Match
Best Local Similarity 4.7%; Score 133; DB 11; Length 599;
RESULT 954
ID ACN45292 standard; cDNA; 627 BP.
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-K6-A11, SEQ:73.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 627;
RESULT 955
ID ACN54072 standard; cDNA; 640 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-020-Q1-K6-G11, SEQ:8853.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 4.7%; Score 133; DB 13; Length 640;
RESULT 956
ID AAC80551 standard; cDNA; 658 BP.
DE Human secreted protein gene 21 SEQ ID NO:31.
PN WO200058467-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 3; Length 658;
RESULT 957
ID AAC59098 standard; cDNA; 667 BP.
DE Human secreted protein coding sequence SEQ ID NO: 60.
PN WO200055171-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 3; Length 667;
RESULT 958
ID AAD05318 standard; cDNA; 671 BP.
DE Human secreted protein-encoding gene 19 cDNA clone HWLF064, SEQ ID NO:29.
PN WO200134626-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 4; Length 671;
RESULT 959
ID AAS62239 standard; cDNA; 681 BP.
DE cDNA sequence #26 encoding novel human secreted protein.
PN WO200177291-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 6; Length 681;
RESULT 960
ID AAK8206 standard; cDNA; 698 BP.
DE Human digestive system antigen coding sequence SEQ ID NO: 522.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.7%; Score 133; DB 4; Length 698;
RESULT 961
ID AAS29150 standard; cDNA; 698 BP.
DE cDNA encoding for human DNA-binding protein #121.

PN WO200155162-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 5; Length 698;
 RESULT 962
 ID AAD16659 standard; cDNA; 698 BP.
 DE Human novel protein-encoding cDNA clone HVAET61, SEQ ID NO:13.
 PN WO200155327-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 5; Length 698;
 RESULT 963
 ID ABS68290 standard; cDNA; 698 BP.
 DE cDNA encoding human DNA-binding protein #121.
 PN US2002102638-A1.
 PD 01-AUG-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 6; Length 698;
 RESULT 964
 ID ADC25284 standard; cDNA; 698 BP.
 DE Human cDNA from extracellular matrix gene 121.
 PN US2003049650-A1.
 PD 13-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 10; Length 698;
 RESULT 965
 ID ACD92384 standard; cDNA; 700 BP.
 DE Human colon cancer cell expressed cDNA #796.
 PN US2002155438-A1.
 PD 24-OCT-2002.
 PA (SIMP/) SIMPSON A J G.
 PA (NETO/) NETO E D.
 PA (BRENT/) BRENTANI R R.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 10; Length 700;
 RESULT 966
 ID ADP23585 standard; cDNA; 733 BP.
 DE PRO polypeptide encoding cDNA SEQ ID NO:763.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 13; Length 733;
 RESULT 967
 ID ABV29481 standard; cDNA; 760 BP.
 DE Human prostate expression marker cDNA 29472.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 5; Length 760;
 RESULT 968
 ID ADX57243 standard; DNA; 774 BP.
 DE Plant DNA sequence which confers altered metabolic characteristic #4626.
 PN WO2003020936-A1.
 PD 13-MAR-2003.
 PA (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 10; Length 774;
 RESULT 969
 ID AAA64638 standard; DNA; 801 BP.
 DE Partial sequence MEL3 associated with melanoma and thyroid tumors.
 PN WO200050595-A2.
 PD 31-AUG-2000.
 PA (GOUT/) GOUT I.
 PA (RODN/) RODNIN N.

PA (FILO/) FILOENKO V.
 PA (MATS/) MATSUKA G.
 PA (SCAN/) SCANLAN M.
 PA (OLDL/) OLD L.
 PA (BILY/) BILYNSKY B.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 3; Length 801;
 RESULT 970
 ID AB282489 standard; cDNA; 805 BP.
 DE Human secreted protein cDNA #SEQ ID 36.
 PN WO200268628-A1.
 PD 06-SEP-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 6; Length 805;
 RESULT 971
 ID AAF31060 standard; cDNA; 872 BP.
 DE Rat clone 701291473H1 coding sequence.
 PN WO200102557-A1.
 PD 11-JAN-2001.
 PA (JANC) JANSSEN PHARM NV.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 4; Length 872;
 RESULT 972
 ID ADF81828 standard; DNA; 873 BP.
 DE Leukaemia-related DNA sequence #2384.
 PN WO2003039443-A2.
 PD 15-MAY-2003.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
 PA (HAPE/) HAPERLACH T.
 PA (SCHO/) SCHOCH C.
 PA (KERN/) KERN W.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 10; Length 873;
 RESULT 973
 ID AAC59297 standard; cDNA; 887 BP.
 DE Human secreted protein cDNA #21.
 PN WO200056753-A1.
 PD 28-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 3; Length 887;
 RESULT 974
 ID AAI87708 standard; cDNA; 903 BP.
 DE Human polynucleotide SEQ ID NO 7768.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 4; Length 903;
 RESULT 975
 ID AAA64642 standard; DNA; 905 BP.
 DE Partial sequence MEL7 associated with melanoma and thyroid tumors.
 PN WO200050595-A2.
 PD 31-AUG-2000.
 PA (GOUT/) GOUT I.
 PA (RODN/) RODNIN N.
 PA (FILO/) FILOENKO V.
 PA (MATS/) MATSUKA G.
 PA (SCAN/) SCANLAN M.
 PA (OLDL/) OLD L.
 PA (BILY/) BILYNSKY B.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 3; Length 905;
 RESULT 976
 ID AAZ06226 standard; DNA; 936 BP.
 DE Human secreted protein gene NO. 8.
 PN WO9935158-A1.
 PD 15-JUL-1999.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; Score 133; DB 2; Length 936;
 RESULT 977

RESULT 977
ID AAD07722 standard; cDNA; 938 BP.
DE Human secreted protein-encoding gene 18 cDNA clone HLYDU43, SEQ ID NO:28.
PN WO200134800-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 5; Length 938;
Best Local Similarity 100.0%; Pred. No. 4.5e-34;
RESULT 978
ID ADQ62833 standard; RNA; 1000 BP.
DE Homopoly-A contaminant for RNaseH activity assay.
PN WO2004059012-A1.
PD 15-JUL-2004.
PA (AMHP) WYETH.
Query Match 4.7%; Score 133; DB 12; Length 1000;
Best Local Similarity 100.0%; Pred. No. 4.4e-34;
RESULT 979
ID ADQ62832 standard; RNA; 1000 BP.
DE Homopoly-U contaminant for RNaseH activity assay.
PN WO2004059012-A1.
PD 15-JUL-2004.
PA (AMHP) WYETH.
Query Match 4.7%; Score 133; DB 12; Length 1000;
Best Local Similarity 100.0%; Pred. No. 4.4e-34;
RESULT 980
ID ADB40468 standard; DNA; 1047 BP.
DE Human granzyme H (gene ID 1793) DNA.
PN WO2003070883-A2.
PD 28-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.7%; Score 133; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 4.4e-34;
RESULT 981
ID ABV78042 standard; DNA; 1071 BP.
DE Hypoxia-regulated protein coding sequence #62.
PN WO200246465-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 4.7%; Score 133; DB 6; Length 1071;
Best Local Similarity 100.0%; Pred. No. 4.4e-34;
RESULT 982
ID ADM19286 standard; cDNA; 1167 BP.
DE Novel human channel/transporter gene #83.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 5; Length 1167;
Best Local Similarity 100.0%; Pred. No. 4.3e-34;
RESULT 983
ID AAF91902 standard; cDNA; 1198 BP.
DE Human secreted protein-encoding gene 45 cDNA clone HRACI26, SEQ ID NO:55.
PN WO200118022-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 1198;
Best Local Similarity 100.0%; Pred. No. 4.2e-34;
RESULT 984
ID AD22434 standard; DNA; 1215 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5254.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.7%; Score 133; DB 12; Length 1215;
Best Local Similarity 100.0%; Pred. No. 4.2e-34;
RESULT 985
ID ADP85917 standard; DNA; 1300 BP.
DE Synthetic construct #1.
PN US2004110205-A1.
PD 10-JUN-2004.
PA (WANG/) WANG H.
Query Match 4.7%; Score 133; DB 12; Length 1300;
Best Local Similarity 100.0%; Pred. No. 4.2e-34;
RESULT 986

ID ADD9623 standard; cDNA; 1343 BP.
DE Human REMAP cDNA - SEQ ID 52.
PN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.7%; Score 133; DB 10; Length 1343;
Best Local Similarity 100.0%; Pred. No. 4.1e-34;
RESULT 987
ID ADM47812 standard; DNA; 1383 BP.
DE Polynucleotide sequence #230 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 4.7%; Score 133; DB 12; Length 1383;
Best Local Similarity 100.0%; Pred. No. 4.1e-34;
RESULT 988
ID ADN39370 standard; cDNA; 1416 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:B54.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.7%; Score 133; DB 11; Length 1416;
Best Local Similarity 100.0%; Pred. No. 4.1e-34;
RESULT 989
ID ACN41008 standard; cDNA; 1416 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA327030, SEQ ID NO:6163.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 4.7%; Score 133; DB 13; Length 1416;
Best Local Similarity 100.0%; Pred. No. 4.1e-34;
RESULT 990
ID ADR62569 standard; cDNA; 1423 BP.
DE Cotton cDNA sequence, SEQ ID 3350.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match 4.7%; Score 133; DB 13; Length 1423;
Best Local Similarity 100.0%; Pred. No. 4.1e-34;
RESULT 991
ID ADD9624 standard; cDNA; 1464 BP.
DE Human REMAP cDNA - SEQ ID 53.
PN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.7%; Score 133; DB 10; Length 1464;
Best Local Similarity 100.0%; Pred. No. 4e-34;
RESULT 992
ID AAD50017 standard; cDNA; 1696 BP.
DE Human secreted protein cDNA.
PN WO200283914-A2.
PD 24-OCT-2002.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 133; DB 8; Length 1696;
Best Local Similarity 100.0%; Pred. No. 3.9e-34;
RESULT 993
ID AAS20587 standard; cDNA; 1798 BP.
DE Human methionine aminopeptidase protease cDNA.
PN US6329188-B1.
PD 11-DEC-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 133; DB 6; Length 1798;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
RESULT 994
ID ABX92004 standard; cDNA; 1808 BP.
DE Lung specific nucleic acid (LSNA) #46.
PN WO200268633-A2.
PD 06-SEP-2002.
PA (DIAD-) DIADEXUS INC.

Query Match 4.7%; Score 133; DB 6; Length 1808;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
RESULT 995
ID AAQ04690 standard; cDNA; 1834 BP.
DE Encodes Mammalian amino acid dehydrogenase activating factor-eta.
PN JP02111796-A.
PD 24-APR-1990.
PA (TOFU) TOA NENRYO KOGYO KK.
Query Match 4.7%; Score 133; DB 2; Length 1834;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
RESULT 996
ID AD143478 standard; DNA; 1875 BP.
DE Plant transcription factor polynucleotide #1329.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER) SHERMAN B K.
PA (RIEC) RIECHMANN J L.
PA (JIAN) JIANG C.
PA (HEAR) HEARD J E.
PA (HAAK) HAAKE V.
PA (CREE) CREELMAN R A.
PA (RATC) RATCLIFFE O.
PA (ADAM) ADAM L J.
PA (REUB) REUBER T L.
PA (KEDD) KEDDIE J.
PA (BROU) BROUN P E.
PA (PILG) PILGRIM M L.
PA (DUBE) DUBELL A N.
PA (PINE) PINEDA O.
PA (YUGG) YU G.
Query Match 4.7%; Score 133; DB 12; Length 1875;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
RESULT 997
ID ADN05367 standard; cDNA; 1913 BP.
DE Antiporiatric cDNA sequence #906.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 133; DB 12; Length 1913;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
RESULT 998
ID AA23442 standard; cDNA; 1933 BP.
DE cDNA encoding human secreted protein vc52_1, SEQ ID NO:39.
PN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 4.7%; Score 133; DB 3; Length 1933;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
RESULT 999
ID AA23441 standard; cDNA; 1954 BP.
DE cDNA encoding human secreted protein vc51_1, SEQ ID NO:37.
PN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 4.7%; Score 133; DB 3; Length 1954;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
RESULT 1000
ID AB159287 standard; cDNA; 1957 BP.
DE Nucleotide sequence of AA233368 protein (from first ORF).
PN WO200246362-A2.
PD 13-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (NITSB) JAPAN TOBACCO INC.
Query Match 4.7%; Score 133; DB 6; Length 1957;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
RESULT 1001
ID ABL59288 standard; cDNA; 1957 BP.
DE Nucleotide sequence of AA233368 protein (from second ORF).
PN WO200246362-A2.
PD 13-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (NITSB) JAPAN TOBACCO INC.
Query Match 4.7%; Score 133; DB 6; Length 1957;

Best Local Similarity 100.0%; Pred. No. 3.8e-34;
RESULT 1002
ID AAF72803 standard; DNA; 2057 BP.
DE Secreted protein gene #5.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 4; Length 2057;
Best Local Similarity 100.0%; Pred. No. 3.7e-34;
RESULT 1003
ID AA252560 standard; cDNA; 2262 BP.
DE Human secreted protein clone ye7_1 nucleotide sequence SEQ ID NO:171.
PN WO958642-A2.
PD 18-NOV-1999.
PA (GEMY) GENETICS INST INC.
Query Match 4.7%; Score 133; DB 3; Length 2262;
Best Local Similarity 100.0%; Pred. No. 3.6e-34;
RESULT 1004
ID AAV54587 standard; cDNA; 2447 BP.
DE Human secretory protein encoding cDNA clone CO1020-1.
PN WO9833916-A2.
PD 06-AUG-1998.
PA (GEMY) GENETICS INST INC.
Query Match 4.7%; Score 133; DB 2; Length 2447;
Best Local Similarity 100.0%; Pred. No. 3.6e-34;
RESULT 1005
ID AA225607 standard; cDNA; 2447 BP.
DE Human secreted protein clone CO1020_1 nucleotide sequence.
PN US9565397-A.
PD 12-OCT-1999.
PA (GEMY) GENETICS INST INC.
Query Match 4.7%; Score 133; DB 2; Length 2447;
Best Local Similarity 100.0%; Pred. No. 3.6e-34;
RESULT 1006
ID AB210078 standard; DNA; 2501 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #218.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 8; Length 2501;
Best Local Similarity 100.0%; Pred. No. 3.5e-34;
RESULT 1007
ID AB210224 standard; DNA; 2501 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #364.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 8; Length 2501;
Best Local Similarity 100.0%; Pred. No. 3.5e-34;
RESULT 1008
ID ADQ29621 standard; DNA; 2566 BP.
DE Human colorectal cancer-associated protein coding sequence #43.
PN EPI439393-A2.
PD 21-JUN-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 4.7%; Score 133; DB 12; Length 2566;
Best Local Similarity 100.0%; Pred. No. 3.5e-34;
RESULT 1009
ID ADQ24863 standard; DNA; 2575 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7683.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.7%; Score 133; DB 12; Length 2575;
Best Local Similarity 100.0%; Pred. No. 3.5e-34;
RESULT 1010
ID AAA48576 standard; cDNA; 2604 BP.
DE cDNA encoding wheat protein phosphatase 2A regulatory subunit A.
PN WO200036121-A2.
PD 22-JUN-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.7%; Score 133; DB 3; Length 2604;

Best Local Similarity 100.0%; Pred. No. 3.5e-34;
RESULT 1011
ID AA243781 standard; cDNA; 2685 BP.
DE Human fetal brain cDNA clone vb6_1.
PN WO9955721-A1.
PD 04-NOV-1999.
PA (ALPH-) ALPHAGENE INC.
Query Match 4.7%; Score 133; DB 3; Length 2685;
Best Local Similarity 100.0%; Pred. No. 3.5e-34;
RESULT 1012
ID AD022306 standard; DNA; 2700 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5126.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.7%; Score 133; DB 12; Length 2700;
Best Local Similarity 100.0%; Pred. No. 3.5e-34;
RESULT 1013
ID AAC77829 standard; cDNA; 2921 BP.
DE Human cancer associated gene sequence SEQ ID NO:223.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 133; DB 3; Length 2921;
Best Local Similarity 100.0%; Pred. No. 3.4e-34;
RESULT 1014
ID ABV23160 standard; cDNA; 2922 BP.
DE Human prostate expression marker cDNA 23151.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 133; DB 5; Length 2922;
Best Local Similarity 100.0%; Pred. No. 3.4e-34;
RESULT 1015
ID ADQ08601 standard; DNA; 3030 BP.
DE Ciona intestinalis nervous system associated gene SeqID3.
PN JP2004057127-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 4.7%; Score 133; DB 12; Length 3030;
Best Local Similarity 100.0%; Pred. No. 3.4e-34;
RESULT 1016
ID ADK00688 standard; DNA; 3226 BP.
DE HOMO protein encoding sequence #33.
PN WO2004014946-A1.
PD 19-FEB-2004.
PA (NEWO-) NEWORGEN LTD.
Query Match 4.7%; Score 133; DB 12; Length 3226;
Best Local Similarity 100.0%; Pred. No. 3.3e-34;
RESULT 1017
ID ADI18906 standard; DNA; 3232 BP.
DE Human disease related protein DNA sequence SeqID238.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 4.7%; Score 133; DB 10; Length 3232;
Best Local Similarity 100.0%; Pred. No. 3.3e-34;
RESULT 1018
ID ADQ23592 standard; DNA; 3454 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6412.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.7%; Score 133; DB 12; Length 3454;
Best Local Similarity 100.0%; Pred. No. 3.3e-34;
RESULT 1019
ID ADJ48200 standard; DNA; 3505 BP.
DE Maize oil-associated gene #18.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR-) LAURIE C C.
PA (RAVA-) RAVANELLO M.
PA (SAVA-) SAVAGE T.

PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 4.7%; Score 133; DB 12; Length 3505;
Best Local Similarity 100.0%; Pred. No. 3.3e-34;
RESULT 1020
ID ABL32171 standard; DNA; 3973 BP.
DE Human immune system associated gene SEQ ID NO: 144.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 3973;
Best Local Similarity 100.0%; Pred. No. 3.2e-34;
RESULT 1021
ID ABK33928 standard; DNA; 4001 BP.
DE Human DNA for staging of Astrocytomas, complement, #5.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 4001;
Best Local Similarity 100.0%; Pred. No. 3.1e-34;
RESULT 1022
ID ADA20431 standard; DNA; 4001 BP.
DE Prostate tumour related genomic DNA complement sample #48.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 8; Length 4001;
Best Local Similarity 100.0%; Pred. No. 3.1e-34;
RESULT 1023
ID ADA84238 standard; DNA; 4001 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:96.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 8; Length 4001;
Best Local Similarity 100.0%; Pred. No. 3.1e-34;
RESULT 1024
ID ABO92014 standard; cDNA; 4236 BP.
DE Human polynucleotide SEQ ID NO 11.
PN US2002065394-A1.
PD 30-MAY-2002.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (SPAU/) SPAULDING V.
Query Match 4.7%; Score 133; DB 6; Length 4236;
Best Local Similarity 100.0%; Pred. No. 3.1e-34;
RESULT 1025
ID AA61487 standard; cDNA; 4237 BP.
DE Human secreted protein fe366_1 cDNA.
PN WO9841539-A2.
PD 24-SEP-1998.
PA (GEMV) GENETICS INST INC.
Query Match 4.7%; Score 133; DB 2; Length 4237;
Best Local Similarity 100.0%; Pred. No. 3.1e-34;
RESULT 1026
ID ABK40004 standard; DNA; 5586 BP.
DE Human chemically pretreated gene sequence #43 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 5586;
Best Local Similarity 100.0%; Pred. No. 2.9e-34;
RESULT 1027
ID ABQ67140 standard; DNA; 6134 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 170.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 4.7%; Score 133; DB 6; Length 6134;
Best Local Similarity 100.0%; Pred. No. 2.8e-34;
RESULT 1028
ID ABL32411 standard; DNA; 6161 BP.
DE Human immune system associated gene SEQ ID NO: 384.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 6161;
Best Local Similarity 100.0%; Pred. No. 2.8e-34;
RESULT 1029
ID AC62785 standard; DNA; 7369 BP.
DE Colon cancer analysis related genomic DNA SEQ ID NO:34.
PN WO2003014388-A2.
PD 20-FEB-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 8; Length 7369;
Best Local Similarity 100.0%; Pred. No. 2.7e-34;
RESULT 1030
ID AB209991 standard; DNA; 7369 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #131.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 8; Length 7369;
Best Local Similarity 100.0%; Pred. No. 2.7e-34;
RESULT 1031
ID ABL92313 standard; DNA; 8079 BP.
DE Chemically treated DNA repair gene fragment complementary to #61.
PN WO2003181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 8079;
Best Local Similarity 100.0%; Pred. No. 2.6e-34;
RESULT 1032
ID AAS46303 standard; DNA; 10369 BP.
DE Tumour suppressor gene derived chemically modified sequence #25.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 4; Length 10369;
Best Local Similarity 100.0%; Pred. No. 2.5e-34;
RESULT 1033
ID ABL32392 standard; DNA; 10369 BP.
DE Human immune system associated gene SEQ ID NO: 365.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 10369;
Best Local Similarity 100.0%; Pred. No. 2.5e-34;
RESULT 1034
ID ABL32118 standard; DNA; 11416 BP.
DE Human immune system associated gene SEQ ID NO: 91.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 11416;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 1035
ID ABL70135 standard; DNA; 11416 BP.
DE Chemically treated cell signalling DNA sequence #13.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 11416;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 1036
ID AAS61063 standard; DNA; 11416 BP.
DE Human gene regulation-associated gene oligonucleotide #18.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 11416;

Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 1037
ID ABL32895 standard; DNA; 11729 BP.
DE Human immune system associated gene SEQ ID NO: 868.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 11729;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 1038
ID ABL32717 standard; DNA; 12007 BP.
DE Human immune system associated gene SEQ ID NO: 690.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 12007;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
RESULT 1039
ID ABL33032 standard; DNA; 14798 BP.
DE Human immune system associated gene SEQ ID NO: 1005.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 14798;
Best Local Similarity 100.0%; Pred. No. 2.3e-34;
RESULT 1040
ID ABL33404 standard; DNA; 16033 BP.
DE Human immune system associated gene SEQ ID NO: 1377.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 16033;
Best Local Similarity 100.0%; Pred. No. 2.2e-34;
RESULT 1041
ID ABN79984 standard; DNA; 16633 BP.
DE Human chemically modified disease associated gene SEQ ID NO 1.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 6; Length 16633;
Best Local Similarity 100.0%; Pred. No. 2.1e-34;
RESULT 1042
ID AAS46815 standard; DNA; 21354 BP.
DE Tumour suppressor gene derived chemically modified sequence #512.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 4; Length 21354;
Best Local Similarity 100.0%; Pred. No. 2.1e-34;
RESULT 1043
ID AB209958 standard; DNA; 35962 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #98.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 8; Length 35962;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
RESULT 1044
ID AB210104 standard; DNA; 35962 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #244.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 133; DB 8; Length 35962;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
RESULT 1045
ID ACN59858 standard; cDNA; 531 BP.
DE Cotton gynoecium tissue EST Clone ID: LFB3829-035-Q1-K6-D8, SEQ:14639.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.

PA (ZIEGLER) ZIEGLER T E. 4.6%; Score 132; DB 13; Length 531;
 Query Match
 Best Local Similarity 100.0%; Pred. No. 1.1e-33;
 RESULT 1046
 ID ABV56662 standard; cDNA; 549 BP.
 DE Human prostate expression marker cDNA 56653.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 1.1e-33;
 RESULT 1047
 ID ACN53254 standard; cDNA; 578 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-004-Q1-N6-F11, SEQ:8035.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEGLER) ZIEGLER T E.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 1.1e-33;
 RESULT 1048
 ID ADG79210 standard; cDNA; 896 BP.
 DE Human secreted protein cDNA of the invention SEQ ID NO:16.
 PN WO200268638-A1.
 PD 06-SEP-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 1.1e-33;
 RESULT 1049
 ID ABQ54211 standard; cDNA; 970 BP.
 DE Human ovarian antigen HHFBV53 cDNA, SEQ ID NO:91.
 PN WO200200677-A1.
 PD 03-JAN-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 9.7e-34;
 RESULT 1050
 ID ADP04748 standard; cDNA; 1352 BP.
 DE Sea squirt cDNA with tissue specific expression in development Seq 343.
 PN JP2004057129-A.
 PD 26-FEB-2004.
 PA (KAGU-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 8.7e-34;
 RESULT 1051
 ID ADQ22502 standard; DNA; 1389 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5322.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 8.7e-34;
 RESULT 1052
 ID ACC50413 standard; cDNA; 1663 BP.
 DE Human secreted protein coding sequence, SEQ ID 80.
 PN WO200295010-A2.
 PD 28-NOV-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 8.3e-34;
 RESULT 1053
 ID ABZ71230 standard; cDNA; 1663 BP.
 DE Human secreted protein-encoding gene 41 cDNA clone HDP5H53, SEQ ID NO:51.
 PN WO200276488-A1.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 8.3e-34;
 RESULT 1054
 ID ADP91122 standard; cDNA; 1663 BP.
 DE Human secreted protein cDNA #SEQ ID 68.

PN WO2003004622-A2.
 PD 16-JAN-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 8.3e-34;
 RESULT 1055
 ID ADC73466 standard; DNA; 1663 BP.
 DE Human secreted protein-related DNA - SEQ ID 99.
 PN WO2003038063-A2.
 PD 08-MAY-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 8.3e-34;
 RESULT 1056
 ID ADN04959 standard; cDNA; 1999 BP.
 DE Antipsoriatic cDNA sequence #694.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 7.9e-34;
 RESULT 1057
 ID AAF97906 standard; cDNA; 2394 BP.
 DE Human secreted protein cDNA, SEQ ID NO: 33.
 PN WO200121658-A1.
 PD 29-MAR-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 7.6e-34;
 RESULT 1058
 ID ADH61306 standard; DNA; 3420 BP.
 DE INTSIG encoding DNA 7512389CBI, SEQ ID 23.
 PN WO2004001005-A2.
 PD 31-DEC-2003.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 6.9e-34;
 RESULT 1059
 ID ABO67159 standard; DNA; 6775 BP.
 DE Human angiogenesis associated polynucleotide SEQ ID NO 189.
 PN WO200246454-A2.
 PD 13-JUN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 5.9e-34;
 RESULT 1060
 ID ADS89685 standard; DNA; 8900 BP.
 DE Oligonucleotide of the invention SEQ ID NO:701.
 PN WO2004035803-A2.
 PD 29-APR-2004.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 5.5e-34;
 RESULT 1061
 ID ADS89411 standard; DNA; 8900 BP.
 DE Oligonucleotide of the invention SEQ ID NO:427.
 PN WO2004035803-A2.
 PD 29-APR-2004.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 5.5e-34;
 RESULT 1062
 ID ADG33178 standard; DNA; 1381 BP.
 DE Human DNA differentially expressed in patients with SLE SeqID502.
 PN WO2003090694-A2.
 PD 06-NOV-2003.
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 Query Match
 Best Local Similarity 100.0%; Pred. No. 1.8e-33;
 RESULT 1063
 ID ADR44025 standard; DNA; 1806 BP.
 DE Human colon tumour associated gene clone-36 SEQ ID NO:35.
 PN WO2004074506-A2.

PD 02-SEP-2004.
PA (MORG-) MERGEN LTD.
Query Match 4.6%; Score 131; DB 13; Length 1806;
Best Local Similarity 100.0%; Pred. No. 1.7e-33;
RESULT 1064
ID ABV23003 standard; cDNA; 2827 BP.
DE Human prostate expression marker cDNA 22994.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.6%; Score 131; DB 5; Length 2827;
Best Local Similarity 100.0%; Pred. No. 1.5e-33;
RESULT 1065
ID ABV28839 standard; cDNA; 2827 BP.
DE Human prostate expression marker cDNA 28830.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.6%; Score 131; DB 5; Length 2827;
Best Local Similarity 100.0%; Pred. No. 1.5e-33;
RESULT 1066
ID ADG32917 standard; cDNA; 4670 BP.
DE Human DNA differentially expressed in patients with SLE SeqID241.
PN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 4.6%; Score 131; DB 10; Length 4670;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
RESULT 1067
ID ADQ19630 standard; cDNA; 4670 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2449.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.6%; Score 131; DB 12; Length 4670;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
RESULT 1068
ID ADQ23804 standard; cDNA; 4672 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6624.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.6%; Score 131; DB 12; Length 4672;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
RESULT 1069
ID ABN80102 standard; cDNA; 8712 BP.
DE Human chemically modified disease associated gene SEQ ID NO 119.
PN WO20020927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.6%; Score 131; DB 6; Length 8712;
Best Local Similarity 100.0%; Pred. No. 1.2e-33;
RESULT 1070
ID ACN53490 standard; cDNA; 468 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-008-Q1-K6-D3, SEQ:8271.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.6%; Score 130; DB 13; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.1e-33;
RESULT 1071
ID ACN56061 standard; cDNA; 474 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-031-Q6-N6-F7, SEQ:10842.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.6%; Score 130; DB 13; Length 474;

Best Local Similarity 100.0%; Pred. No. 5.1e-33;
RESULT 1072
ID ACN56273 standard; cDNA; 517 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-N6-E7, SEQ:11054.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.6%; Score 130; DB 13; Length 517;
Best Local Similarity 100.0%; Pred. No. 5e-33;
RESULT 1073
ID ACN51185 standard; cDNA; 603 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-B6, SEQ:5966.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.6%; Score 130; DB 13; Length 603;
Best Local Similarity 100.0%; Pred. No. 4.8e-33;
RESULT 1074
ID AAC74364 standard; cDNA; 639 BP.
DE Human secreted protein gene 28 SEQ ID NO:38.
PN WO200058340-A2.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.6%; Score 130; DB 3; Length 639;
Best Local Similarity 100.0%; Pred. No. 4.7e-33;
RESULT 1075
ID ABX15834 standard; cDNA; 1447 BP.
DE cDNA encoding soybean sterol C5 desaturase protein #2.
PN US6465717-B1.
PD 15-OCT-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.6%; Score 130; DB 8; Length 1447;
Best Local Similarity 100.0%; Pred. No. 3.9e-33;
RESULT 1076
ID ADI19006 standard; cDNA; 1447 BP.
DE Soybean sterol-C5-desaturase cDNA #2.
PN US200322914-A1.
PD 11-DEC-2003.
PA (FAMO/) FAMODU O O.
PA (OROZ/) OROZCO E M.
PA (RAFA/) RAFALSKI J A.
PA (SHEN/) SHEN J B.
Query Match 4.6%; Score 130; DB 12; Length 1447;
Best Local Similarity 100.0%; Pred. No. 3.9e-33;
RESULT 1077
ID AAF91859 standard; cDNA; 3436 BP.
DE Human secreted protein-encoding gene 2 cDNA clone HDPFB02, SEQ ID NO:12.
PN WO200118022-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.6%; Score 130; DB 4; Length 3436;
Best Local Similarity 100.0%; Pred. No. 3.1e-33;
RESULT 1078
ID AAS00767 standard; cDNA; 3436 BP.
DE Human B7-H3 cDNA clone.
PN WO200118021-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MAYO-) MAYO CLINIC.
Query Match 4.6%; Score 130; DB 4; Length 3436;
Best Local Similarity 100.0%; Pred. No. 3.1e-33;
RESULT 1079
ID ADA39737 standard; cDNA; 3436 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 4.6%; Score 130; DB 8; Length 3436;
Best Local Similarity 100.0%; Pred. No. 3.1e-33;
RESULT 1080
ID ADC73453 standard; DNA; 3436 BP.
DE Human secreted protein-related DNA - SEQ ID 86.
FN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.6%; Score 130; DB 10; Length 3436;
Best Local Similarity 100.0%; Pred. No. 3.1e-33;
RESULT 1081
ID ABX45893 standard; cDNA; 160 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11058.
FN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.5%; Score 129; DB 8; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.4e-32;
RESULT 1082
ID ABX38052 standard; cDNA; 242 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3217.
FN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.5%; Score 129; DB 8; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.3e-32;
RESULT 1083
ID ACN48604 standard; cDNA; 249 BP.
DE Cotton primed seed EST Clone ID: LIB3825-023-Q6-K6-G7, SEQ:3385.
FN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.5%; Score 129; DB 13; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.3e-32;
RESULT 1084
ID ACN50243 standard; cDNA; 368 BP.
DE Cotton non-primed seed EST Clone ID: LIB3826-002-Q1-K6-B12, SEQ:5024.
FN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.5%; Score 129; DB 13; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
RESULT 1085
ID ABX39555 standard; cDNA; 383 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4720.
FN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.5%; Score 129; DB 8; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
RESULT 1086
ID ABX43354 standard; cDNA; 395 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #8519.
FN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.

PA (WARR/) WARREN W C.
Query Match 4.5%; Score 129; DB 8; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
RESULT 1087
ID ADG37731 standard; DNA; 408 BP.
DE Aspergillus solid-culture DNA #442.
FN JP2003180365-A.
PD 02-JUL-2003.
PA (DOKU-) DOKURITSU GYOSEI HOJIN SHURUI SOGO KENKY.
Query Match 4.5%; Score 129; DB 10; Length 408;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
RESULT 1088
ID ABX44057 standard; cDNA; 421 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #9222.
FN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.5%; Score 129; DB 8; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
RESULT 1089
ID ABX39788 standard; cDNA; 460 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4953.
FN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.5%; Score 129; DB 8; Length 460;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
RESULT 1090
ID ABV57765 standard; cDNA; 502 BP.
DE Human prostate expression marker cDNA 57756.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.5%; Score 129; DB 5; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
RESULT 1091
ID ACN61238 standard; cDNA; 548 BP.
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-034-Q1-N6-C12, SEQ:16019.
FN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.5%; Score 129; DB 13; Length 548;
Best Local Similarity 100.0%; Pred. No. 1e-32;
RESULT 1092
ID ACN57821 standard; cDNA; 560 BP.
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-006-Q6-K6-C12, SEQ:12602.
FN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.5%; Score 129; DB 13; Length 560;
Best Local Similarity 100.0%; Pred. No. 1e-32;
RESULT 1093
ID ACN53147 standard; cDNA; 578 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-022-Q1-N6-E3, SEQ:7928.
FN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.5%; Score 129; DB 13; Length 578;

Best Local Similarity 100.0%; Pred. No. 1e-32;
RESULT 1094
ID ADR59449 standard; cDNA; 639 BP.
DE Cotton cDNA sequence, SEQ ID 230.
FN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA// KOVALIC D K.
PA (ZHOU// ZHOU Y.
PA (CAOY// CAO Y.
Query Match 4.5%; Score 129; DB 13; Length 639;
Best Local Similarity 100.0%; Pred. No. 1e-32;
RESULT 1095
ID AA291918 standard; cDNA; 1051 BP.
DE Murine mahogany protein coding sequence akml004.
FN WO200005373-A2.
PD 03-FEB-2000.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 4.5%; Score 129; DB 3; Length 1051;
Best Local Similarity 100.0%; Pred. No. 8.9e-33;
RESULT 1096
ID ADF94940 standard; cDNA; 1311 BP.
DE Human gene 8-derived ACRP30-like cDNA, SEQ ID NO:36.
FN WO2003031586-A2.
PD 17-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (BLON// BLONDEL O.
PA (RUBE// RUBEN S M.
Query Match 4.5%; Score 129; DB 10; Length 1311;
Best Local Similarity 100.0%; Pred. No. 8.4e-33;
RESULT 1097
ID ABL39587 standard; cDNA; 1615 BP.
DE Human cancer suppressing gene PP432 encoding cDNA SEQ ID NO:12.
FN CN133318-A.
PD 19-SEP-2001.
PA (SHAN-) SHANGHAI INST ONCOLOGY.
Query Match 4.5%; Score 129; DB 6; Length 1615;
Best Local Similarity 100.0%; Pred. No. 8e-33;
RESULT 1098
ID ADM67116 standard; DNA; 2090 BP.
DE Human homologue of murine adipocyte specific DNA SeqID 252.
FN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMG-) HMGNE INC.
Query Match 4.5%; Score 129; DB 12; Length 2090;
Best Local Similarity 100.0%; Pred. No. 7.5e-33;
RESULT 1099
ID AAQ04107 standard; cDNA; 2427 BP.
DE Human pro-urokinase cDNA of clone pcuk176.
FN EP365894-A.
PD 02-MAY-1990.
PA (FARM) FARMITALIA ERBA SPA CARLO.
Query Match 4.5%; Score 129; DB 2; Length 2427;
Best Local Similarity 100.0%; Pred. No. 7.2e-33;
RESULT 1100
ID ABN80138 standard; DNA; 6484 BP.
DE Human chemically modified disease associated gene SEQ ID NO 155.
FN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.5%; Score 129; DB 6; Length 6484;
Best Local Similarity 100.0%; Pred. No. 5.6e-33;
RESULT 1101
ID ABL33356 standard; DNA; 6577 BP.
DE Human immune system associated gene SEQ ID NO: 1329.
FN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.5%; Score 129; DB 6; Length 6577;
Best Local Similarity 100.0%; Pred. No. 5.6e-33;
RESULT 1102
ID ABL70561 standard; DNA; 6577 BP.
DE Chemically treated cell signalling DNA sequence#226.
FN WO200202807-A2.

PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.5%; Score 129; DB 6; Length 6577;
Best Local Similarity 100.0%; Pred. No. 5.6e-33;
RESULT 1103
ID AAS61221 standard; DNA; 6577 BP.
DE Human gene regulation-associated gene oligonucleotide #176.
FN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.5%; Score 129; DB 6; Length 6577;
Best Local Similarity 100.0%; Pred. No. 5.6e-33;
RESULT 1104
ID ABX41830 standard; cDNA; 152 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6995.
FN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT// BYATT J C.
PA (MATH// MATHIALAGAN N.
PA (TAON// TAO N.
PA (WARR// WARREN W C.
Query Match 4.5%; Score 128; DB 8; Length 152;
Best Local Similarity 100.0%; Pred. No. 3e-32;
RESULT 1105
ID ABX40291 standard; cDNA; 365 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #5456.
FN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT// BYATT J C.
PA (MATH// MATHIALAGAN N.
PA (TAON// TAO N.
PA (WARR// WARREN W C.
Query Match 4.5%; Score 128; DB 8; Length 365;
Best Local Similarity 100.0%; Pred. No. 2.4e-32;
RESULT 1106
ID AAL84786 standard; cDNA; 414 BP.
DE Human polynucleotide SEQ ID NO 4846.
FN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.5%; Score 128; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 2.4e-32;
RESULT 1107
ID ABX45932 standard; cDNA; 429 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11097.
FN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT// BYATT J C.
PA (MATH// MATHIALAGAN N.
PA (TAON// TAO N.
PA (WARR// WARREN W C.
Query Match 4.5%; Score 128; DB 8; Length 429;
Best Local Similarity 100.0%; Pred. No. 2.3e-32;
RESULT 1108
ID ACN60066 standard; cDNA; 556 BP.
DE Cotton gynocium tissue EST Clone ID: LIB3829-017-Q6-K6-E3, SEQ:14847.
FN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK// DEIKMAN J.
PA (FENG// FENG P C C.
PA (FINC// FINCHER K L.
PA (ZIEG// ZIEGLER T E.
Query Match 4.5%; Score 128; DB 13; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.2e-32;
RESULT 1109
ID ACN45381 standard; cDNA; 577 BP.
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-C7, SEQ:162.
FN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK// DEIKMAN J.
PA (FENG// FENG P C C.
PA (FINC// FINCHER K L.
PA (ZIEG// ZIEGLER T E.

Query Match
Best Local Similarity 4.5%; Score 128; DB 13; Length 577;
RESULT 1110 100.0%; Pred. No. 2.2e-32;
ID ABV58690 standard; cDNA; 579 BP.
DE Human prostate expression marker cDNA 58681.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 5; Length 579;
RESULT 1111 100.0%; Pred. No. 2.2e-32;
ID ACN51614 standard; cDNA; 584 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-005-Q1-N6-C5, SEQ:6395.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 4.5%; Score 128; DB 13; Length 584;
RESULT 1112 100.0%; Pred. No. 2.2e-32;
ID ACC60574 standard; cDNA; 878 BP.
DE Polynucleotide relating to the invention SEQ ID NO: 151.
PN WO200257460-A2.
PD 25-JUL-2002.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 4.5%; Score 128; DB 6; Length 878;
RESULT 1113 100.0%; Pred. No. 2e-32;
ID AA243798 standard; cDNA; 1936 BP.
DE Human fetal brain cDNA clone vc26_1.
PN WO955721-A1.
PD 04-NOV-1999.
PA (ALPH-) ALPHAGENE INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 3; Length 1936;
RESULT 1114 100.0%; Pred. No. 1.6e-32;
ID AAC59406 standard; cDNA; 1985 BP.
DE Human secreted protein cDNA #15.
PN WO200056765-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 3; Length 1985;
RESULT 1115 100.0%; Pred. No. 1.6e-32;
ID AAF72410 standard; cDNA; 1985 BP.
DE Human PRO271 cDNA.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 4; Length 1985;
RESULT 1116 100.0%; Pred. No. 1.6e-32;
ID AA245938 standard; cDNA; 1985 BP.
DE Human DNA encoding PRO polypeptide sequence #14.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 4; Length 1985;
RESULT 1117 100.0%; Pred. No. 1.6e-32;
ID ACA60174 standard; cDNA; 1985 BP.
DE Human cDNA for secreted/transmembrane protein PRO271.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1118 100.0%; Pred. No. 1.6e-32;
ID ACA89388 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003036141-A1.

PD 20-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1119 100.0%; Pred. No. 1.6e-32;
ID ACA73398 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1120 100.0%; Pred. No. 1.6e-32;
ID ACA05713 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1121 100.0%; Pred. No. 1.6e-32;
ID ACA66547 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO protein #14.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1122 100.0%; Pred. No. 1.6e-32;
ID ACD07574 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1123 100.0%; Pred. No. 1.6e-32;
ID ACF20122 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1124 100.0%; Pred. No. 1.6e-32;
ID ACF19508 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1125 100.0%; Pred. No. 1.6e-32;
ID ACD21796 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1126 100.0%; Pred. No. 1.6e-32;
ID ACF12961 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1127 100.0%; Pred. No. 1.6e-32;
ID ACD25064 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1128 100.0%; Pred. No. 1.6e-32;
ID ACF00113 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003054474-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1129
 ID ACA72170 standard; cDNA; 1985 BP.
 DE Novel human secreted and transmembrane protein PRO271 cDNA.
 PN US2003032114-A1.
 PD 13-FEB-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1130
 ID AC004694 standard; cDNA; 1985 BP.
 DE Novel human secreted and transmembrane protein PRO271 cDNA.
 PN US2003032101-A1.
 PD 13-FEB-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1131
 ID AC008155 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003036124-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1132
 ID AC008162 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003040054-A1.
 PD 27-FEB-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1133
 ID ABX71622 standard; cDNA; 1985 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO271.
 PN US2002132240-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1134
 ID ACA88596 standard; cDNA; 1985 BP.
 DE Novel human secreted and transmembrane protein PRO271 cDNA.
 PN US2003036133-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1135
 ID ACA70038 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003036134-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1136
 ID ACD12260 standard; cDNA; 1985 BP.
 DE Novel human secreted and transmembrane protein PRO271 cDNA.
 PN US2003022294-A1.
 PD 30-JAN-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1137
 ID ACC74175 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003027275-A1.
 PD 06-FEB-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1138
 ID ACD15803 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003027324-A1.

PD 06-FEB-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1139
 ID ACD25371 standard; cDNA; 1985 BP.
 DE Novel human secreted and transmembrane protein PRO271 cDNA.
 PN US2003036118-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1140
 ID ACD17848 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003036123-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1141
 ID ACC8135 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003036148-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1142
 ID ACD21489 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003040060-A1.
 PD 27-FEB-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1143
 ID ACD18556 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003044916-A1.
 PD 06-MAR-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1144
 ID ACH06954 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane polypeptide PRO271 cDNA.
 PN US2003044839-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1145
 ID ABX98166 standard; cDNA; 1985 BP.
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 27.
 PN US2003036156-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1146
 ID ACD13917 standard; cDNA; 1985 BP.
 DE Human PRO polynucleotide #14.
 PN US2003032117-A1.
 PD 13-FEB-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1147
 ID ACD09697 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003036128-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
 RESULT 1148
 ID ACC88442 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003027266-A1.
 PD 06-FEB-2003.

Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1149
ID ACD211182 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1150
ID ABX75354 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO271.
FN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1151
ID ABX97757 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003032102-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1152
ID ACA97233 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
FN US2003036117-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1153
ID ACA57696 standard; cDNA; 1985 BP.
DE Human PRO271 cDNA.
FN US2003036143-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1154
ID ACD14224 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003032130-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1155
ID ACC91007 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1156
ID ACC88749 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003036132-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1157
ID ACD06946 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1158
ID ACA67397 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003017542-A1.
PD 23-JAN-2003.

Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1159
ID ACC81452 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1160
ID ACC89056 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1161
ID ACC86412 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1162
ID ACC89670 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1163
ID ACC92849 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1164
ID ACA72477 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1165
ID ACA88995 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1166
ID ACA69731 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1167
ID ACA96874 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
FN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1168
ID ACA90870 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
FN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;
RESULT 1169
ID ACA67397 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003017542-A1.
PD 23-JAN-2003.

RESULT 1169
ID ACA70652 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1170
ID ACA95162 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1171
ID ACC86105 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1172
ID ACC89977 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1173
ID ACD12585 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1174
ID ACF19815 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1175
ID ABX76759 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1176
ID ABX96191 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1177
ID ACA73091 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1178
ID ACA05512 standard; cDNA; 1985 BP.
DE cDNA encoding human secreted protein PRO271.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;

RESULT 1179
ID ACA68634 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1180
ID ACA74478 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1181
ID ACA70345 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1182
ID ACD14531 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1183
ID ACD20179 standard; cDNA; 1985 BP.
DE Human secreted / transmembrane polypeptide PRO271 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1184
ID ACA68203 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1185
ID ABX98668 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1186
ID ACC81145 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1187
ID ACA95469 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1188
ID ACD04387 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1189
ID ACC87828 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1190
ID ACF12490 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1191
ID ACA96205 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1192
ID ACA64979 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1193
ID ACA73705 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1194
ID ACA74117 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1195
ID ACA96512 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1196
ID ACD10618 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1197
ID ACC91314 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1198
ID ACD02649 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1199
ID ACC87214 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036165-A1.

PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1200
ID ACC85798 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1201
ID ACA65286 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1202
ID ACA94103 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1203
ID ACA97847 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1204
ID ACA91349 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1205
ID ACA90563 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1206
ID ACD16110 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1207
ID ACD17271 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1208
ID ACC91928 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1209
ID ACA74785 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;

Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1210
ID ACA91656 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1211
ID ACA71300 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1212
ID ACC90700 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1213
ID ACA65710 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO protein #14.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1214
ID ACA54982 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1215
ID ACA94855 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1216
ID ACD16417 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1217
ID ACD15496 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1218
ID ABX16599 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 8; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1219
ID ACA97540 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;

RESULT 1220
ID ACA98989 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1221
ID ACC91621 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1222
ID ACD11032 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1223
ID ACD14882 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1224
ID ACD19817 standard; cDNA; 1985 BP.
DE Human secreted / transmembrane polypeptide PRO271 cDNA.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1225
ID ACD11646 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1226
ID ACC95775 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1227
ID ACF16338 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1228
ID ACF02456 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1229
ID ACF02763 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049743-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1230
ID ACF211350 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1231
ID ACF10034 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1232
ID ACF7927 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1233
ID ACD46632 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1234
ID ACD49395 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1235
ID ACF28162 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1236
ID ACD88852 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1237
ID ACD84247 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1238
ID ACD99021 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1239
ID ADA77779 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1240
ID ACF48763 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1241
ID ADB29417 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1242
ID ACD09083 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1243
ID ACF11876 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1244
ID ACF41110 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1245
ID ACF15724 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1246
ID ACF16031 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1247
ID ACD31858 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1248
ID ACF18666 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1249
ID ACF09113 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1250
ID ACF78234 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1251
ID ACF51833 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1252
ID ACF26320 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1253
ID ACF24113 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1254
ID ACF63424 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1255
ID ACF50298 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1256
ID ACH07769 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1257
ID ACF13575 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064462-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1258
ID ACD41501 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1259
ID ACF31914 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1260
ID ACF23192 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1261
ID ACF39882 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1262
ID ACD45404 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1263
ID ACF53061 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1264
ID ACF27241 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1265
ID ACF45079 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;
RESULT 1266
ID ACF29697 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1267 100.0%; Pred. No. 1.6e-32;
ID ACD89773 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1268 100.0%; Pred. No. 1.6e-32;
ID ACD84554 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1269 100.0%; Pred. No. 1.6e-32;
ID ACD98714 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1270 100.0%; Pred. No. 1.6e-32;
ID ACF77006 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003082717-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1271 100.0%; Pred. No. 1.6e-32;
ID ACF76699 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1272 100.0%; Pred. No. 1.6e-32;
ID ACF49684 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003104542-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1273 100.0%; Pred. No. 1.6e-32;
ID ACF49991 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003104543-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1274 100.0%; Pred. No. 1.6e-32;
ID ACD09390 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003036127-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1275 100.0%; Pred. No. 1.6e-32;
ID ACD08469 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003040061-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1276 100.0%; Pred. No. 1.6e-32;
ID ACF12183 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003036130-A1.

PD 20-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1277 100.0%; Pred. No. 1.6e-32;
ID ACC94691 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1278 100.0%; Pred. No. 1.6e-32;
ID ACD22410 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1279 100.0%; Pred. No. 1.6e-32;
ID ACF15110 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003044917-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1280 100.0%; Pred. No. 1.6e-32;
ID ACC97205 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003044929-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1281 100.0%; Pred. No. 1.6e-32;
ID ADA18273 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
FN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1282 100.0%; Pred. No. 1.6e-32;
ID ACD66964 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO271.
FN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1283 100.0%; Pred. No. 1.6e-32;
ID ACC92235 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1284 100.0%; Pred. No. 1.6e-32;
ID ACF13882 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1285 100.0%; Pred. No. 1.6e-32;
ID ACF14189 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
RESULT 1286 100.0%; Pred. No. 1.6e-32;

RESULT 1286
ID ACF09420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1287
ID ACF45711 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1288
ID ACF47860 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1289
ID ACF67591 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1290
ID ACF25399 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1291
ID ACF29083 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1292
ID ACF84861 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1293
ID ACF83940 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1294
ID ACF87931 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1295

ID ACF30618 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1296
ID ACF32221 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1297
ID ACF11881 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1298
ID ACF12188 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1299
ID ACF40580 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1300
ID ACF18052 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1301
ID ACF08499 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1302
ID ACF31300 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1303
ID ACF52140 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1304
ID ACF50009 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.

PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1305
ID ACF38712 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1306
ID ACF26627 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1307
ID ACF24727 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1308
ID ACF46307 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1309
ID ACF27855 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1310
ID ACD89159 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1311
ID ACF63731 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1312
ID ACF60371 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003083734-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1313
ID ACHI2495 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049773-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1314
ID ACH09918 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1315
ID ACD03773 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1316
ID ACD10311 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1317
ID ACD11953 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1318
ID ACD83125 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1319
ID ACF42338 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1320
ID ADA16248 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1321
ID ACF18359 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1322
ID ACF02149 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1323

ID ACF21657 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003049770-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1324
 ID ACF10341 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003073169-A1.
 PD 17-APR-2003.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1325
 ID ACF33793 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003064457-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1326
 ID ACF44755 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003068711-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1327
 ID ACD9387 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003049745-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1328
 ID ACD91000 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003049751-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1329
 ID ACF30311 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003067478-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1330
 ID ACD87010 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003068773-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1331
 ID ACF60064 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003073185-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1332
 ID ACF46614 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003087373-A1.
 PD 08-MAY-2003.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1333
 ID ACF75471 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003096353-A1.
 PD 22-MAY-2003.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1334
 ID ADA79571 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003073173-A1.
 PD 17-APR-2003.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1335
 ID ACF17131 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003054458-A1.
 PD 20-MAR-2003.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1336
 ID ACF22885 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003059886-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1337
 ID ACF07885 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003049758-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1338
 ID ACF08192 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003049772-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1339
 ID ACF40496 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003064448-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1340
 ID ACF53675 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
 PN US2003064456-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1341
 ID ACD46939 standard; cDNA; 1985 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #14.
 PN US2003068693-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.5%; Score 128; DB 9; Length 1985;
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;
 RESULT 1342
 ID ACF46614 standard; cDNA; 1985 BP.
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

RESULT 1342
ID ACF47842 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1343
ID ACF47228 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1344
ID ACF46000 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1345
ID ACD86089 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1346
ID ACF52447 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1347
ID ACF52754 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1348
ID ACF64747 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1349
ID ACF76392 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1350
ID ACF61292 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1351
ID ACF61599 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1352
ID ACD30630 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1353
ID ACD31551 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1354
ID ACD32472 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1355
ID ACF17438 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1356
ID ACF07271 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1357
ID ACF20429 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1358
ID ACF21043 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1359
ID ACF20736 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1360
ID ACD47553 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;

RESULT 1361
ID ACF47535 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1362
ID ACF53368 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1363
ID ACD86703 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1364
ID ACH04951 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1365
ID ACF44448 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1366
ID ADA42393 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1367
ID ADA81298 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1368
ID ACD22103 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1369
ID ACD24450 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1370
ID ACD39653 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.

PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1371
ID ACD39960 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1372
ID ACF13268 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1373
ID ACF03070 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1374
ID ACD23303 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1375
ID ACF78541 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1376
ID ACF11262 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1377
ID ACF50605 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1378
ID ACF34100 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1379
ID ACD46325 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;

Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1380
ID ACD48167 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1381
ID ACF27548 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1382
ID ACF24420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1383
ID ACD85475 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1384
ID ACD90080 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1385
ID ACD83633 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1386
ID ACF49070 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1387
ID ACF07155 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1388
ID ACH07462 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1389

ID ACH08076 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1390
ID ACH11267 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1391
ID ACH11574 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1392
ID ACH10225 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1393
ID ACF01228 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1394
ID ACF40803 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1395
ID ACD24143 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1396
ID ACD31244 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1397
ID ACF17745 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1398
ID ACF32528 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003064445-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1399
ID ACF40189 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1400
ID ACF48149 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1401
ID ACF38098 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1402
ID ACF25034 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1403
ID ACF26934 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1404
ID ACF29390 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1405
ID ACD87624 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1406
ID ACF76085 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1407
ID ACF49377 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1408

ID ACF43834 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1409
ID ACH06179 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1410
ID ACH06486 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1411
ID ADA83096 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1412
ID ACC92542 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1413
ID ACC93156 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1414
ID ACF19201 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1415
ID ACD12892 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1416
ID ACF06350 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1417
ID ACC94384 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;

Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1418
ID ACC97812 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003044932-A1.
PD 06-MAR-2003.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1419
ID ACC94077 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003027270-A1.
PD 06-FEB-2003.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1420
ID ACF42031 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1421
ID ACD30937 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003032126-A1.
PD 13-FEB-2003.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1422
ID ACD42966 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1423
ID ACD43273 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1424
ID ACF14803 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1425
ID ACF01535 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003049738-A1.
PD 13-MAR-2003.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1426
ID ACF31607 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1427
ID ACD67284 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003064453-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1428
ID ACD48474 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1429
ID ACD48781 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1430
ID ACF51219 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1431
ID ACF53982 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1432
ID ACF25706 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1433
ID ACF39019 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1434
ID ACF28776 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1435
ID ACD90693 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1436
ID ACD86396 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003068765-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1437
ID ACH05258 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1438
ID ACF65054 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1439
ID ADB20139 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1440
ID ACF43527 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1441
ID ACH08997 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1442
ID ACH09304 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1443
ID ADA78391 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1444
ID ACF09727 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1445
ID ACF50912 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match

Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1446
ID ACF23806 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1447
ID ACD88238 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1448
ID ACH09611 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1449
ID ACH10532 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1450
ID ACD11339 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1451
ID ACC96389 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1452
ID ACC98419 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1453
ID ADA16672 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1454
ID ACF41724 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1455
ID ACF16645 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040073-A1.

PD 27-FEB-2003.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1456
ID ADAL1301 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1457
ID ACD32165 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1458
ID ACD30323 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1459
ID ACD41194 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1460
ID ACF07578 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1461
ID ACF30993 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1462
ID ACF77313 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1463
ID ACF10955 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1464
ID ACF32835 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;

RESULT 1465
ID ACF26013 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1466
ID ACD83326 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1467
ID ACF23499 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1468
ID ACF42913 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1469
ID ACF43320 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1470
ID ACH05872 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1471
ID ACH08690 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1472
ID ADA41969 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1473
ID ACC90284 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 128; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
RESULT 1474
ID ACF10648 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036119-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
PD 10-FEB-2003.

RESULT 1475
ID AC93463 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036120-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
PD 10-FEB-2003.

RESULT 1476
ID AC96082 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036161-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
PD 10-FEB-2003.

RESULT 1477
ID ACD24757 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044921-A1.
PD 06-MAR-2003.

Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
PD 06-MAR-2003.

RESULT 1478
ID ADA1716 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003017498-A1.
PD 23-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
PD 23-JAN-2003.

RESULT 1479
ID ACF01842 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049739-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
PD 13-MAR-2003.

RESULT 1480
ID ACF21964 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059882-A1.
PD 27-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
PD 27-MAR-2003.

RESULT 1481
ID ACF22578 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059884-A1.
PD 27-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
PD 27-MAR-2003.

RESULT 1482
ID ACF08806 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068687-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
PD 10-APR-2003.

RESULT 1483
ID ACF33142 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073186-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.

RESULT 1493
ID ADA42819 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
100.0%; Pred. No. 1.6e-32;
RESULT 1494
ID ACD10004 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
100.0%; Pred. No. 1.6e-32;
RESULT 1495
ID ACD16729 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
100.0%; Pred. No. 1.6e-32;
RESULT 1496
ID ACC99026 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
100.0%; Pred. No. 1.6e-32;
RESULT 1497
ID ACF00420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
100.0%; Pred. No. 1.6e-32;
RESULT 1498
ID ACD40887 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
100.0%; Pred. No. 1.6e-32;
RESULT 1499
ID ACF14496 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
100.0%; Pred. No. 1.6e-32;
RESULT 1500
ID ACF22271 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;
100.0%; Pred. No. 1.6e-32;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2005, 11:21:33 ; Search time 5970 Seconds
(without alignments)
18145.881 Million cell updates/sec

Title: US-10-063-692-37
Perfect score: 2846
Sequence: 1 cgtcggccaccgcccggc.....aaaaaaaaaaaaaaaaaaaaa 2846

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsl1:*

9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2468	86.7	3165	3	HSM806734
2	2394	84.1	2650	3	AF370388
3	1130	39.7	2214	9	AY406074
C 4	889	31.2	1100	5	BX337780
C 5	786	27.6	897	5	BX434191
6	724	25.4	795	6	CD655367
7	706	24.8	1049	5	BX399905
C 8	691	24.3	1008	5	BX399904
9	685	24.1	879	6	CD514783
C 10	677	23.8	952	5	BX439313
11	672	23.6	723	5	BQ014545
C 12	647	22.7	886	5	BX337781
13	640	22.5	645	4	BM728083
C 14	640	22.5	645	5	BM930545
C 15	640	22.5	722	5	BU742056
C 16	638	22.4	740	5	BQ008840
C 17	636	22.3	645	4	BM683392
C 18	636	22.3	650	4	BM684138
C 19	630	22.1	722	5	BQ014522
C 20	589	20.7	633	2	AW957662
21	589	20.7	645	5	BM929554
22	578	20.3	626	5	BF381335
23	566	19.9	566	5	BP289572
C 24	560	19.7	649	4	BM680642

AI954161	1	19.6	557	AI954161
BX350293	5	19.5	555	BX350293
CO394970	27	19.1	851	CO394970
BM998737	C 28	18.3	586	BM998737
BP205877	C 29	514	584	BP205877
AI671186	C 30	507	574	AI671186
CF125161	C 31	491	571	CF125161
BX282717	718	17.3	718	BX282717
BE048236	742	16.7	476	BE048236
AI920243	452	15.9	452	AI920243
AI920243	2	15.6	449	AI920243
AI823626	449	15.6	449	AI823626
AI088620	1	14.9	449	AI088620
BF197805	449	14.9	449	BF197805
AI624892	428	14.7	428	AI624892
AW340294	415	14.4	415	AW340294
BM724013	472	14.4	472	BM724013
AA812954	630	14.3	630	AA812954
AA460698	397	13.9	397	AA460698
AA460698	557	13.6	557	AA460698
AL048495	715	13.5	715	AL048495
AI432522	433	13.4	433	AI432522
AA708420	419	13.0	419	AA708420
AI057206	367	12.9	367	AI057206
AA045104	545	12.8	545	AA045104
CD707019	382	12.5	382	CD707019
CN334668	348	12.2	348	CN334668
AW028008	447	12.1	447	AW028008
BM929450	400	11.9	400	BM929450
BU742789	401	11.9	401	BU742789
AA433935	337	11.8	337	AA433935
AW206753	404	11.7	404	AW206753
AI420902	325	11.4	325	AI420902
BP312143	584	11.2	584	BP312143
AI579963	315	11.1	315	AI579963
BG403264	773	10.8	773	BG403264
CN296855	492	10.4	492	CN296855
CN334669	756	9.9	756	CN334669
AY406075	2214	9.7	2214	AY406075
AI583699	330	9.6	330	AI583699
CN296856	9.2	9.2	411	CN296856
AI824672	274	9.0	274	AI824672
AA430705	436	8.9	436	AA430705
AL701986	258	8.9	258	AL701986
AW511691	406	8.9	406	AW511691
AA989716	237	8.3	237	AA989716
TS2085	8.1	8.1	333	TS2085
BP216550	583	6.8	583	BP216550
AA460872	491	6.6	491	AA460872
CR772910	381	6.4	381	CR772910
AW340199	359	6.3	359	AW340199
CN334667	163	5.7	163	CN334667
N94393	356	5.3	356	N94393
CA819677	410	5.3	410	CA819677
AV711924	228	5.0	228	AV711924
CR629263	674	4.9	674	CR629263
BX489675	409	4.8	409	BX489675
BX499601	194	4.8	194	BX499601
BX507033	393	4.8	393	BX507033
BF981774	418	4.8	418	BF981774
CD641072	738	4.8	738	CD641072
CD108244	850	4.8	850	CD108244
BU555370	865	4.8	865	BU555370
BU529694	870	4.8	870	BU529694
BC021396	2417	4.8	2417	BC021396
BJ704049	164	4.8	164	BJ704049
CO193787	243	4.8	243	CO193787
CF212786	245	4.8	245	CF212786
CO416891	273	4.8	273	CO416891
BM341777	276	4.8	276	BM341777
CK385496	276	4.8	276	CK385496
AL589270	286	4.8	286	AL589270
CO417291	291	4.8	291	CO417291
CO183642	331	4.8	331	CO183642

98	136	4.8	346	7	CV525623	CV525623	Mdlv4012b	171	135	4.7	370	4	BG610096	BG610096	324577	MA
99	136	4.8	353	6	CD678777	CD678777	hpl3d03.y	172	135	4.7	373	7	CK429577	CK429577	oj38e03.y	
c 100	136	4.8	388	9	CNS02026	AL175479	Tetraodon	173	135	4.7	388	7	CV524829	CV524829	Mdlv2_402	
101	136	4.8	425	7	CN831880	CN831880	AGENCOURT	174	135	4.7	389	7	CK430907	CK430907	oj55d10.y	
102	136	4.8	472	7	CK241530	CK241530	rx30f12.y	175	135	4.7	395	7	CO184785	CO184785	EST1546.z	
103	136	4.8	474	2	BF726322	BF726322	by04h07.y	176	135	4.7	409	6	CD052287	CD052287	EST1546.z	
104	136	4.8	556	7	CK791071	CK791071	AGENCOURT	c 177	135	4.7	409	9	CNS02V5X	AL215358	Tetraodon	
105	136	4.8	614	1	AV717179	AV717179	AGENCOURT	c 178	135	4.7	411	2	BF781925	BF781925	602105876	
106	136	4.8	705	5	BUS54894	BUS54894	AGENCOURT	179	135	4.7	442	6	CD679816	CD679816	lab08f08	
107	136	4.8	820	7	CO403732	CO403732	AGENCOURT	180	135	4.7	462	6	CA334925	CA334925	NISC_lc03	
108	136	4.8	854	5	BUS55510	BUS55510	AGENCOURT	181	135	4.7	462	9	CNS04PPQ	AL301607	Tetraodon	
109	136	4.8	953	5	BUI159214	BUI159214	AGENCOURT	182	135	4.7	463	6	CB445238	CB445238	696490	MA
c 110	136	4.8	1026	8	AZ546693	AZ546693	ENTR96TF	183	135	4.7	466	7	CO168381	CO168381	Mdfx3014j	
111	135	4.7	160	5	BU761067	BU761067	sae62e05.y	184	135	4.7	469	7	CK429230	CK429230	oj33h02.y	
112	135	4.7	167	7	CR557934	CR557934	DKF2p468P	185	135	4.7	481	7	CN838053	CN838053	AGENCOURT	
113	135	4.7	170	7	CR559085	CR559085	DKF2p468C	186	135	4.7	485	7	CR767537	CR767537	DKF2p468C	
114	135	4.7	172	1	AA638754	AA638754	vm94b12.r	187	135	4.7	487	1	AV755581	AV755581	AV755581	
115	135	4.7	172	9	CNS020RQ	AL175967	Tetraodon	188	135	4.7	494	9	CR128493	CR128493	Forward s	
116	135	4.7	178	7	CO180729	CO180729	EC03492.5	189	135	4.7	509	6	CA374148	CA374148	648459	NC
117	135	4.7	180	7	CO192489	CO192489	EC033879.5	190	135	4.7	533	1	AV756477	AV756477	AV756477	
118	135	4.7	183	1	AJ796704	AJ796704	AGENCOURT	c 191	135	4.7	536	9	CNS037X4	AL231189	Tetraodon	
c 119	135	4.7	188	4	BF971016	BF971016	602270336	192	135	4.7	551	4	BG926438	BG926438	HNC62-1-B	
120	135	4.7	188	6	CA935203	CA935203	sau50c03.y	193	135	4.7	593	5	BP743369	BP743369	BP743369	
121	135	4.7	192	7	CR539079	CR539079	DKF2p459A	194	135	4.7	606	7	CO098232	CO098232	Mdfx3021m	
122	135	4.7	192	7	CR559081	CR559081	DKF2p468C	195	135	4.7	611	7	CV064412	CV064412	WNEl10f4	
c 123	135	4.7	195	5	BQ389262	BQ389262	NISC_mc06	196	135	4.7	623	7	CK005475	CK005475	AGENCOURT	
124	135	4.7	196	6	CA819430	CA819430	sau78c12.y	197	135	4.7	623	6	CD770235	CD770235	AGENCOURT	
125	135	4.7	197	2	AW100960	AW100960	sd63906.y	198	135	4.7	635	6	CD773201	CD773201	AGENCOURT	
126	135	4.7	198	7	CR766521	CR766521	DKF2p469L	199	135	4.7	650	6	CD773004	CD773004	AGENCOURT	
127	135	4.7	208	4	BI901084	BI901084	ib84g08.y	200	135	4.7	651	6	CD433621	CD433621	EL01N0313	
128	135	4.7	216	4	BJ311098	BJ311098	AGENCOURT	201	135	4.7	661	6	CD641297	CD641297	AGENCOURT	
129	135	4.7	216	6	CB073167	CB073167	taa29c09.y	202	135	4.7	671	4	BG029399	BG029399	602296828	
130	135	4.7	217	7	CR545913	CR545913	DKF2p470D	203	135	4.7	730	2	BE613622	BE613622	601504411	
131	135	4.7	220	7	CK727624	CK727624	UMC-bend	c 204	135	4.7	738	7	CF285052	CF285052	AGENCOURT	
c 132	135	4.7	226	6	CA819138	CA819138	sau69f11.y	c 205	135	4.7	756	7	CF290080	CF290080	AGENCOURT	
133	135	4.7	228	7	CF216003	CF216003	CAS70002	c 206	135	4.7	788	7	CF285572	CF285572	AGENCOURT	
134	135	4.7	230	7	CO180224	CO180224	EC01250.5	c 207	135	4.7	792	2	BE967113	BE967113	601660642	
135	135	4.7	234	7	CK430621	CK430621	oj51g01.y	208	135	4.7	793	5	BUS55575	BUS55575	AGENCOURT	
136	135	4.7	257	5	BK476287	BK476287	DKF2p686F	209	135	4.7	823	5	BUS44017	BUS44017	AGENCOURT	
137	135	4.7	259	2	AW100693	AW100693	sd58909.y	210	135	4.7	832	5	BUS29282	BUS29282	AGENCOURT	
138	135	4.7	259	5	BK250050	BK250050	bx250050.y	c 211	135	4.7	837	9	CNS060EL	AL407971	T3 end of	
139	135	4.7	262	7	CF804520	CF804520	lad74e09.y	212	135	4.7	844	5	BU603787	BU603787	AGENCOURT	
c 140	135	4.7	263	7	CO989546	CO989546	UMC-pd3en	213	135	4.7	847	5	BU954608	BU954608	AGENCOURT	
141	135	4.7	265	4	BI674494	BI674494	sah96g05.y	c 214	135	4.7	847	7	CK196959	CK196959	FGA500542	
142	135	4.7	267	7	CO184366	CO184366	EC27977.5	215	135	4.7	848	7	CV064704	CV064704	WNEl14b12	
143	135	4.7	269	6	CD638413	CD638413	AGENCOURT	c 216	135	4.7	863	2	BE964633	BE964633	601658560	
144	135	4.7	270	2	AW101788	AW101788	sd70d09.y	217	135	4.7	863	5	BUS42140	BUS42140	AGENCOURT	
145	135	4.7	272	7	CK655115	CK655115	AGENCOURT	218	135	4.7	868	5	BU955256	BU955256	AGENCOURT	
146	135	4.7	278	7	CO192919	CO192919	EC34778.5	219	135	4.7	868	7	CN385261	CN385261	LE2TR03C0	
147	135	4.7	289	7	CK429678	CK429678	oj39g11.y	220	135	4.7	877	6	CD517184	CD517184	AGENCOURT	
c 148	135	4.7	290	7	CR771988	CR771988	DKF2p4680	221	135	4.7	898	6	CD251269	CD251269	AGENCOURT	
149	135	4.7	295	2	BF883916	BF883916	ILJ3-ET011	222	135	4.7	913	5	BUS63702	BUS63702	AGENCOURT	
150	135	4.7	297	7	CO180424	CO180424	EC01537.5	223	135	4.7	916	5	BUS88527	BUS88527	AGENCOURT	
151	135	4.7	298	7	CO184759	CO184759	EC28526.5	c 224	135	4.7	918	7	CV069762	CV069762	WPA8huk15	
152	135	4.7	301	7	CV042729	CV042729	dba10g08.y	225	135	4.7	924	5	BQ960177	BQ960177	AGENCOURT	
153	135	4.7	302	2	AW100887	AW100887	sd62f09.y	226	135	4.7	940	5	BUS55708	BUS55708	AGENCOURT	
154	135	4.7	303	7	CO752990	CO752990	Mdfx3022e	c 227	135	4.7	941	8	AZ539217	AZ539217	ENTR348TF	
155	135	4.7	307	7	CV525614	CV525614	Mdlv40120	228	135	4.7	943	4	BF968041	BF968041	602269570	
156	135	4.7	308	5	BX506616	BX506616	DKF2p779D	229	135	4.7	945	6	CB202961	CB202961	AGENCOURT	
157	135	4.7	310	4	BJ703028	BJ703028	AGENCOURT	230	135	4.7	948	6	CA476817	CA476817	AGENCOURT	
158	135	4.7	312	7	CK900688	CK900688	TSL9 Taiwan	231	135	4.7	975	5	BUS55889	BUS55889	AGENCOURT	
159	135	4.7	313	5	BM897446	BM897446	pha1e09.y	c 232	135	4.7	983	6	CD386907	CD386907	AGENCOURT	
160	135	4.7	315	9	CNS022RL	AL178534	Tetraodon	233	135	4.7	989	6	BM415116	BM415116	OP20188.M	
c 161	135	4.7	317	5	BQ599878	BQ599878	MI-P-E6-a	234	135	4.7	995	6	CA476250	CA476250	AGENCOURT	
162	135	4.7	319	1	AL121270	AL121270	DKF2p7621	235	135	4.7	1016	5	BQ718364	BQ718364	AGENCOURT	
163	135	4.7	320	5	BQ261271	BQ261271	fz72a05.y	236	135	4.7	1022	3	BC050966	BC050966	Mus muscu	
164	135	4.7	323	4	BI709353	BI709353	fs63e06.y	237	135	4.7	1065	6	CA476982	CA476982	AGENCOURT	
165	135	4.7	324	5	BUS88095	BUS88095	AGENCOURT	c 238	135	4.7	1071	6	CD050614	CD050614	AGENCOURT	
166	135	4.7	339	7	CO192197	CO192197	EC33332.5	239	135	4.7	1079	9	CNS035IX	AL228786	Tetraodon	
167	135	4.7	351	7	CK378884	CK378884	la127f04.y	240	135	4.7	1101	9	CNS02021J	AL061936	Drosophil	
168	135	4.7	356	6	CB722234	CB722234	jnn609B07	241	135	4.7	1134	4	BM804069	BM804069	AGENCOURT	
169	135	4.7	361	7	CK005157	CK005157	AGENCOURT	242	135	4.7	1165	9	CL082700	CL082700	CH216-169	
170	135	4.7	364	7	CK430797	CK430797	oj54a08.y	243	135	4.7	1189	5	BQ049769	BQ049769	AGENCOURT	

C 244	135	4.7	1211	5	BQ929879	AGENCY	C 317	134	4.7	212	4	BM638146	BM638146
245	135	4.7	1213	5	BQ718626	AGENCY	318	134	4.7	214	5	BU760607	BU760607
246	135	4.7	1214	5	BU167807	AGENCY	319	134	4.7	215	6	CA819195	CA819195
247	135	4.7	1225	9	CL078581	CH216-151	320	134	4.7	216	2	BR048071	BR048071
248	135	4.7	1226	9	AG365340	Mus muscu	321	134	4.7	217	7	CR765974	CR765974
249	135	4.7	1280	9	AG347131	Mus muscu	322	134	4.7	218	5	BM645556	BM645556
250	135	4.7	1316	9	AG381842	Mus muscu	323	134	4.7	219	1	AI945904	AI945904
251	135	4.7	1324	9	CL078591	CH216-151	324	134	4.7	219	4	BM361185	BM361185
252	135	4.7	1390	9	CL647502	CH213-139	325	134	4.7	219	5	BM255540	BM255540
253	135	4.7	1409	6	CD049654	AGENCY	326	134	4.7	221	7	CR290189	CR290189
254	135	4.7	1430	4	BM805984	AGENCY	327	134	4.7	222	1	AI868831	AI868831
255	135	4.7	1550	3	BC049704	Mus muscu	328	134	4.7	222	4	BM047503	BM047503
256	135	4.7	1596	8	CC293489	CH261-62N	329	134	4.7	222	4	BM186176	BM186176
257	135	4.7	1654	9	CL118709	ISB1-7211	330	134	4.7	222	5	BQ085944	BQ085944
258	135	4.7	1761	8	CL188336	CH261-70H	331	134	4.7	222	6	CA935086	CA935086
259	135	4.7	1899	3	BC061196	Mus muscu	332	134	4.7	223	1	AL697974	AL697974
260	135	4.7	2007	3	HSM807665	BM647519 Homo sapi	333	134	4.7	224	5	BU927029	BU927029
261	135	4.7	2596	3	BC053452	Mus muscu	334	134	4.7	224	6	CA935085	CA935085
262	135	4.7	3028	3	HSM801560	AL136586 Homo sapi	335	134	4.7	224	6	CD721912	CD721912
263	135	4.7	3145	3	BC027896	BC027896 Homo sapi	336	134	4.7	225	4	BM155365	BM155365
264	135	4.7	3226	3	CR627326	CR627326 Homo sapi	337	134	4.7	225	4	BM186096	BM186096
265	135	4.7	3870	3	CR749650	CR749650 Homo sapi	338	134	4.7	225	4	BM811854	BM811854
266	135	4.7	4643	3	CR749348	CR749348 Homo sapi	339	134	4.7	225	7	CR547597	CR547597
267	135	4.7	4793	3	CR749666	CR749666 Homo sapi	340	134	4.7	226	4	BM533163	BM533163
268	135	4.7	8296	3	CR749511	CR749511 Homo sapi	341	134	4.7	229	4	BM532465	BM532465
269	134	4.7	150	2	BE964700	BE964700 601658238	342	134	4.7	230	5	BQ075932	BQ075932
270	134	4.7	152	7	CR933635	CR933635 CGF100428	343	134	4.7	232	4	BM155357	BM155357
271	134	4.7	156	6	CA335198	CA335198 NISC 1c07	344	134	4.7	232	4	BM181343	BM181343
272	134	4.7	157	5	BM475990	BM475990 NISC 1c07	345	134	4.7	232	7	CO753858	CO753858
273	134	4.7	160	5	BM645532	BM645532 DXP72781J	346	134	4.7	232	2	AW733931	AW733931
274	134	4.7	161	7	CR557780	CR557780 DXP72686F	347	134	4.7	232	2	BE190203	BE190203
275	134	4.7	162	4	BT745065	BT745065 rK9508.Y	348	134	4.7	232	4	BM155357	BM155357
276	134	4.7	163	1	AL697695	AL697695 DXP72686F	349	134	4.7	232	7	CO181343	CO181343
277	134	4.7	163	9	CRNS01762	CRNS01762 Tetraodon	350	134	4.7	236	1	AI443075	AI443075
278	134	4.7	164	4	BM539426	BM539426 hb09c07.g	351	134	4.7	238	2	AW101785	AW101785
279	134	4.7	167	6	CR045764	CR045764 NISC_gcl12	352	134	4.7	238	5	BM476126	BM476126
280	134	4.7	169	7	CR791760	CR791760 DXP72686F	353	134	4.7	238	6	CB079729	CB079729
281	134	4.7	177	2	BE964812	BE964812 601658467	354	134	4.7	239	2	BE013300	BE013300
282	134	4.7	178	5	BM888959	BM888959 kb03c03.Y	355	134	4.7	239	7	CK376983	CK376983
283	134	4.7	179	5	BM956705	BM956705 DXP72781M	356	134	4.7	240	7	CR766048	CR766048
284	134	4.7	182	1	AL697655	AL697655 DXP72686A	357	134	4.7	241	6	CR044549	CR044549
285	134	4.7	183	7	CO893077	CO893077 Bovsen.21	358	134	4.7	242	2	BE059705	BE059705
286	134	4.7	185	6	CA935285	CA935285 sau51f03.	359	134	4.7	242	7	CR629082	CR629082
287	134	4.7	186	6	CA935579	CA935579 sau56c05.	360	134	4.7	243	7	CO747844	CO747844
288	134	4.7	187	6	CA674774	CA674774 wlsu2.pk0	361	134	4.7	244	4	BM154314	BM154314
289	134	4.7	187	6	CR099929	CR099929 py18h06.Y	362	134	4.7	244	4	BM573234	BM573234
290	134	4.7	187	7	CR771877	CR771877 DXP72686C	363	134	4.7	244	6	CB938710	CB938710
291	134	4.7	188	6	CA819358	CA819358 sau77b11.	364	134	4.7	244	7	CO182898	CO182898
292	134	4.7	189	1	AJ798430	AJ798430 AJ798430	365	134	4.7	245	4	BI840174	BI840174
293	134	4.7	189	6	CA935078	CA935078 sau64a10.	366	134	4.7	245	4	BM342819	BM342819
294	134	4.7	190	4	BG036846	BG036846 602326790	367	134	4.7	245	5	BM3951835	BM3951835
295	134	4.7	192	4	BM093800	BM093800 sah20h11.	368	134	4.7	247	4	BM745342	BM745342
296	134	4.7	192	7	CF3227002	CF3227002 NACL--01-	369	134	4.7	248	1	AJ768204	AJ768204
297	134	4.7	193	4	BG156523	BG156523 sab10e12.	370	134	4.7	248	4	BM154574	BM154574
298	134	4.7	193	5	BM955696	BM955696 DXP72781C	371	134	4.7	249	6	BM187301	BM187301
299	134	4.7	193	6	CA819599	CA819599 sau73b02.	372	134	4.7	249	6	CA935136	CA935136
300	134	4.7	195	4	BM186912	BM186912 fv79e10.Y	373	134	4.7	251	4	BM573771	BM573771
301	134	4.7	196	2	BM795712	BM795712 602259590	374	134	4.7	251	4	CF212181	CF212181
302	134	4.7	198	5	BM667440	BM667440 pb61e09.Y	375	134	4.7	252	7	CR525101	CR525101
303	134	4.7	201	6	CB045621	CB045621 NISC_gcl1	376	134	4.7	255	7	CO168373	CO168373
304	134	4.7	201	7	CF613757	CF613757 CES008061	377	134	4.7	256	7	BM582842	BM582842
305	134	4.7	203	2	AI100931	AI100931 sd63d04.Y	378	134	4.7	257	4	BM804375	BM804375
306	134	4.7	203	5	BM470454	BM470454 DXP72686A	379	134	4.7	257	7	CF804375	CF804375
307	134	4.7	206	7	CO938248	CO938248 UMC-pd14c	380	134	4.7	261	2	BF724691	BF724691
308	134	4.7	207	1	AI433376	AI433376 til2c12.X	381	134	4.7	261	4	BM154485	BM154485
309	134	4.7	207	6	CB721787	CB721787 op01e04.f	382	134	4.7	261	6	CF071153	CF071153
310	134	4.7	208	1	AL697778	AL697778 DXP72686P	383	134	4.7	261	7	CK937009	CK937009
311	134	4.7	208	6	CA802715	CA802715 sau41a12.	384	134	4.7	263	5	BM900884	BM900884
312	134	4.7	209	7	CF804603	CF804603 lad76b09.	385	134	4.7	263	6	CB722227	CB722227
313	134	4.7	209	7	CO417475	CO417475 Mdf+3012j	386	134	4.7	265	7	CM275140	CM275140
314	134	4.7	211	7	CM549956	CM549956 Q0244.B3	387	134	4.7	266	4	BM154640	BM154640
315	134	4.7	212	2	AW101775	AW101775 sd70b04.Y	388	134	4.7	268	4	BM154858	BM154858
316	134	4.7	212	4	BM599268	BM599268 170006690	389	134	4.7	269	7	CR766078	CR766078

330	134	4.7	271	7	CF755569 lae43all.	463	134	4.7	333	7	CO184639	CO184639 EC28357.5
331	134	4.7	272	1	AJ799419	464	134	4.7	334	2	BE806983	BE806983 se09e10.y
332	134	4.7	272	2	CF510988	C 465	134	4.7	334	4	BM496453	BM496453 IPQGBr2.1
333	134	4.7	272	7	CK428530	C 466	134	4.7	339	5	EX551395	EX551395 BX551395
334	134	4.7	272	7	COL84738	467	134	4.7	339	7	CO182353	CO182353 EC22486.5
335	134	4.7	272	7	CR630238	468	134	4.7	341	5	EX953635	EX953635 DKF2p781M
336	134	4.7	273	2	BE013312	C 469	134	4.7	342	6	CB080456	CB080456 hp86h08.b
337	134	4.7	273	7	CF633575	470	134	4.7	343	7	CV525143	CV525143 Md1v4010m
338	134	4.7	274	5	BQ298677	471	134	4.7	344	6	CB721972	CB721972 jnn603C04
339	134	4.7	277	7	CO185085	472	134	4.7	346	6	CO416889	CO416889 Mdf30119
400	134	4.7	279	4	B1671444	473	134	4.7	347	2	BE785905	BE785905 601477905
401	134	4.7	279	5	BQ242916	474	134	4.7	347	5	EX506028	EX506028 DKF2p686P
402	134	4.7	280	4	BM532335	475	134	4.7	348	4	BJ696950	BJ696950 BJ696950
403	134	4.7	280	6	CA802930	476	134	4.7	348	6	CB704555	CB704555 AMGNNUC.N
404	134	4.7	280	7	CK975391	477	134	4.7	348	7	CO191264	CO191264 EC30590.5
405	134	4.7	281	6	CA934992	478	134	4.7	352	5	BU760774	BU760774 sas8c11.
406	134	4.7	282	1	AJ774701	479	134	4.7	353	5	BU081852	BU081852 ear01d06.
407	134	4.7	282	7	CR559176	480	134	4.7	358	5	EX505899	EX505899 DKF2p686P
408	134	4.7	285	6	CA334895	481	134	4.7	363	6	CB468702	CB468702 734551.MA
409	134	4.7	285	7	CR791521	C 482	134	4.7	364	6	CB409286	CB409286 NISC.nc04
410	134	4.7	287	5	BX503626	483	134	4.7	364	7	CK375041	CK375041 lai44b01.
411	134	4.7	287	7	CO748478	484	134	4.7	364	7	CR789952	CR789952 DKF2p459L
412	134	4.7	289	7	CR559200	485	134	4.7	365	5	BM966550	BM966550 ko09a03.y
413	134	4.7	291	2	AW459750	C 486	134	4.7	369	6	CD638357	CD638357 AGENCOURT
414	134	4.7	291	4	BJ697356	487	134	4.7	369	6	CF644109	CF644109 K17.A10.F
415	134	4.7	292	5	BU760770	488	134	4.7	369	7	BE057180	BE057180 sm97f06.y
416	134	4.7	292	7	CO191848	489	134	4.7	373	2	BE057180	BE057180 hq16a10.b
417	134	4.7	293	2	BE023554	C 490	134	4.7	376	6	CB084484	CB084484 hq16a10.b
418	134	4.7	294	1	AL706899	491	134	4.7	377	7	CK004038	CK004038 AGENCOURT
419	134	4.7	294	1	AL725181	C 492	134	4.7	377	1	AI1863014	AI1863014 wm45c09.x
420	134	4.7	294	2	AW101221	493	134	4.7	378	1	AV762488	AV762488 AV762488
421	134	4.7	294	6	CB045066	494	134	4.7	378	2	AW117882	AW117882 xe38c06.x
422	134	4.7	295	2	BE013898	495	134	4.7	379	7	CK937918	CK937918 QGF100448
423	134	4.7	295	6	CB641171	496	134	4.7	380	6	CD243157	CD243157 AGENCOURT
424	134	4.7	299	1	AJ798370	497	134	4.7	380	7	CK933848	CK933848 GGF100427
425	134	4.7	299	5	BU760890	498	134	4.7	386	6	CB939082	CB939082 IPQGBx13
426	134	4.7	300	7	CK429583	499	134	4.7	387	7	CF426295	CF426295 lad2b03.
427	134	4.7	301	6	CA802821	500	134	4.7	388	6	CA345950	CA345950 676724.NC
428	134	4.7	302	7	CF253048	501	134	4.7	388	6	CD640168	CD640168 AGENCOURT
429	134	4.7	302	7	CN831978	502	134	4.7	389	3	BC022358	BC022358 Homo.sapi
430	134	4.7	305	6	CD672586	C 503	134	4.7	389	6	CB044164	CB044164 NISC.gc02
431	134	4.7	306	4	B1945447	504	134	4.7	389	7	CR537555	CR537555 DKF2p459J
432	134	4.7	307	6	CD722153	505	134	4.7	390	4	BG896775	BG896775 HOA50-1.A
433	134	4.7	307	6	CD722153	C 506	134	4.7	391	1	AI690751	AI690751 tx88h11.x
434	134	4.7	309	4	BM874527	C 507	134	4.7	391	5	BQ527112	BQ527112 NISC.nc02
435	134	4.7	309	7	CA414161	508	134	4.7	391	6	CB721942	CB721942 jnn602H03
436	134	4.7	310	7	CR559169	509	134	4.7	392	7	CO370974	CO370974 tah7g904.
437	134	4.7	310	7	CR559169	C 510	134	4.7	394	5	EX473239	EX473239 DKF2p686N
438	134	4.7	311	4	BM154732	511	134	4.7	396	1	AV711509	AV711509 AV711509
439	134	4.7	311	4	BM154818	512	134	4.7	396	2	BE048081	BE048081 tz47g03.y
440	134	4.7	311	7	CF321259	513	134	4.7	398	6	CB722395	CB722395 jnn612A04
441	134	4.7	311	7	CO182176	514	134	4.7	398	7	CK375940	CK375940 lah76h05.
442	134	4.7	314	1	AL697923	C 515	134	4.7	399	1	AI226246	AI226246 ue88h04.y
443	134	4.7	314	2	BE047863	516	134	4.7	399	6	CD673835	CD673835 fs05b06.x
444	134	4.7	316	6	CD639207	517	134	4.7	400	4	BG553256	BG553256 dac23h02.
445	134	4.7	318	5	BX500893	518	134	4.7	402	1	AL698015	AL698015 DKF2p686N
446	134	4.7	319	5	BX489110	519	134	4.7	402	2	BF726297	BF726297 by04e10.y
447	134	4.7	320	2	AW509353	520	134	4.7	402	7	CR791705	CR791705 DKF2p468P
448	134	4.7	320	9	CNS01E1H	521	134	4.7	403	6	CB768447	CB768447 AMGNNUC.M
449	134	4.7	321	7	CO417155	522	134	4.7	403	6	CK263662	CK263662 mj21a12.y
450	134	4.7	323	4	BG237484	C 523	134	4.7	405	1	AI567632	AI567632 tp62c08.x
451	134	4.7	323	6	CB410191	C 524	134	4.7	406	5	BQ526114	BQ526114 NISC.no14
452	134	4.7	323	6	CB430419	525	134	4.7	408	7	CR770942	CR770942 DKF2p469G
453	134	4.7	326	4	BM154967	C 526	134	4.7	409	6	CB054205	CB054205 NISC.gn03
454	134	4.7	326	6	CD723900	527	134	4.7	410	7	CK983358	CK983358 re24a04.y
455	134	4.7	327	6	CB721391	528	134	4.7	411	4	BM532515	BM532515 fy09b01.y
456	134	4.7	328	7	CR767432	529	134	4.7	413	5	EX953260	EX953260 DKF2p781H
457	134	4.7	329	7	CO183457	530	134	4.7	414	7	CO871032	CO871032 rt66g04.y
458	134	4.7	330	7	CK623571	531	134	4.7	415	7	CO192413	CO192413 EC33671.5
459	134	4.7	331	4	BG155453	532	134	4.7	416	7	CB834026	CB834026 AGENCOURT
460	134	4.7	331	5	BU860679	C 533	134	4.7	417	6	CB053341	CB053341 NISC.g113
461	134	4.7	332	4	CO185234	534	134	4.7	419	7	CF511730	CF511730 CABud0002
462	134	4.7	332	7	CV122318	C 535	134	4.7	421	5	BQ396582	BQ396582 NISC.ng21

536	134	4.7	424	1	AV682809	AV682809	AV682809	CD678845	hp01b11.x	611	134	4.7	535	5	BQ527144	NISC_no2
537	134	4.7	426	6	CD678845	iqp2ic10.b	610	134	4.7	538	7	CFY52656	Mdfr30255			
538	134	4.7	429	6	CD997642	2p2ic10.b	611	134	4.7	540	7	CFI23120	UI-HF-CH0			
539	134	4.7	431	6	COA10125	NISC_nc09	612	134	4.7	542	6	CD796549	EST667910			
540	134	4.7	431	7	CO191531	EC31328.5	613	134	4.7	545	7	CV223275	taj59h05			
541	134	4.7	433	7	CN835159	AGENCOURT	614	134	4.7	546	7	CF370112	tg48cl0.y			
542	134	4.7	435	7	CR753204	DKFzp4680	615	134	4.7	549	6	CB523098	UI-M-GK0-			
543	134	4.7	436	6	CB817673	d3o23pz.f	616	134	4.7	549	7	CF754275	EST-77-2-			
544	134	4.7	436	7	CF358365	rm89f08.y	617	134	4.7	550	7	CS397597	170004243			
545	134	4.7	437	7	CV525154	Mdlv4010a	618	134	4.7	552	7	CK426429	rx15c08.y			
546	134	4.7	438	6	CB075288	hz42a10.b	619	134	4.7	557	6	CB089052	f09c01.b			
547	134	4.7	441	7	CK428352	laj14g06.	620	134	4.7	557	7	CO752812	Mdfr30255			
548	134	4.7	443	5	BQ637878	hd15fil.y	621	134	4.7	558	7	CK118076	218d01.p1			
549	134	4.7	447	6	CB723709	UI-M-GK0-	622	134	4.7	559	6	CB376949	H502A03.L			
550	134	4.7	451	7	CV525442	Mdlv4011d	623	134	4.7	564	7	CO722540	Mdfr30171			
551	134	4.7	452	3	BC050981	Mus_muscu	624	134	4.7	565	5	BX549733	BX549733			
552	134	4.7	453	7	CK005374	AGENCOURT	625	134	4.7	565	7	CF612717	lae95gl2.			
553	134	4.7	459	5	BX953619	DKFzp781K	626	134	4.7	568	4	BG929104	HNC33-1-H			
554	134	4.7	461	5	BX472677	DKFzp6861	627	134	4.7	569	7	CV222905	taj54d02			
555	134	4.7	462	6	CA394496	ce52bl12.y	628	134	4.7	575	6	CB054849	NISC_gm06			
556	134	4.7	463	7	FR790920	DKFzp4691	629	134	4.7	577	6	CB044223	NISC_gc03			
557	134	4.7	464	6	CF041960	QC132b12.	630	134	4.7	578	6	CB051669	NISC_gl02			
558	134	4.7	466	6	CB044446	NISC_gc04	631	134	4.7	580	6	CB088637	if03f11.b			
559	134	4.7	468	6	CB721944	jnm602H05	632	134	4.7	580	7	CV223330	taj60g10.			
560	134	4.7	470	5	BX554535	BX554535	633	134	4.7	581	7	CO067712	Mdfr3014P			
561	134	4.7	471	5	BQ523226	NISC_n121	634	134	4.7	582	4	BG925169	HNC39-1-G			
562	134	4.7	475	6	CB089293	qs07d05.b	635	134	4.7	582	7	CV222884	taj54b02.			
563	134	4.7	476	5	BG939811	NISC_mp05	636	134	4.7	583	2	BF673434	602136211			
564	134	4.7	477	6	CD677843	ho23j03.y	637	134	4.7	585	7	CO403863	AGENCOURT			
565	134	4.7	478	7	CO722515	Mdfr3017C	638	134	4.7	587	3	AF116639	Homo_sapi			
566	134	4.7	479	6	CA335089	NISC_lt06	639	134	4.7	589	1	A1207510	HA2865_Hu			
567	134	4.7	480	7	CO191784	EC31982.5	640	134	4.7	590	6	CB937830	IPCQJx13			
568	134	4.7	482	7	MD122300	Mdlv4003a	641	134	4.7	594	7	CO065309	WNEL20h4-			
569	134	4.7	486	6	CB044432	NISC_gc04	642	134	4.7	594	7	CV507247	kc13ell.y			
570	134	4.7	486	7	CK379180	lai31g06.	643	134	4.7	596	7	CV199662	km18b02.y			
571	134	4.7	488	7	CP755040	laes1g03.	644	134	4.7	600	5	BQ391797	NISC_mq20			
572	134	4.7	489	7	CO417069	Mdfr30111	645	134	4.7	602	7	CO315672	Mdfr3007b			
573	134	4.7	491	5	BQ525482	NISC_no10	646	134	4.7	606	7	CK619769	KM28b09.y			
574	134	4.7	491	6	CD722238	oj07b10.y	647	134	4.7	608	4	BG678047	602625771			
575	134	4.7	491	7	CF123399	UI-HF-CH0	648	134	4.7	613	7	CV12121985	Mdlv4002b			
576	134	4.7	491	7	CO866143	Mdf3020c	649	134	4.7	618	6	CD676511	hm01n07.x			
577	134	4.7	491	9	CN80359Q		650	134	4.7	620	5	BQ393958	NISC_ng06			
578	134	4.7	494	7	CV525345	Mdlv40111	651	134	4.7	626	6	CD771746	AGENCOURT			
579	134	4.7	495	5	BX504818	DKFzp686K	652	134	4.7	626	7	CO069285	Mdfr30159			
580	134	4.7	495	6	CD236950	FNPAAEGL1	653	134	4.7	627	7	CK837813	4063204.B			
581	134	4.7	495	7	CO752765	Mdfr3025b	654	134	4.7	630	4	BI651834	603299838			
582	134	4.7	499	1	AL119748		655	134	4.7	631	7	CF330508	NACL--06-			
583	134	4.7	501	5	BP742677	BP742677	656	134	4.7	634	7	CK120520	AGENCOURT			
584	134	4.7	501	5	BQ392601	NISC_mq25	657	134	4.7	634	7	CN322082	AGENCOURT			
585	134	4.7	501	5	BQ396639	NISC_ng22	658	134	4.7	635	6	CD638395	AGENCOURT			
586	134	4.7	503	6	CA376868	655327_NC	659	134	4.7	637	6	CD766445	AGENCOURT			
587	134	4.7	503	6	CB350381	ACHG165_H	660	134	4.7	637	7	CK005551	AGENCOURT			
588	134	4.7	503	7	CO417413	Mdf30121	661	134	4.7	639	1	AI969601	wz69b11.x			
589	134	4.7	504	5	BQ524016	NISC_no02	662	134	4.7	639	7	CK459607	929814_MA			
590	134	4.7	504	5	BQ526248	NISC_no15	663	134	4.7	640	7	CV065863	WNEL27f11			
591	134	4.7	504	7	CF513671	Cabud0007	664	134	4.7	645	6	CD773631	AGENCOURT			
592	134	4.7	506	7	CK430668	oj52c07.y	665	134	4.7	647	7	CV222879	taj54a09.			
593	134	4.7	507	4	BI437760	ic83d10.y	666	134	4.7	656	7	CV064567	WNEL12e4			
594	134	4.7	510	5	BQ748115	UI-M-FA0-	667	134	4.7	659	6	CD640691	AGENCOURT			
595	134	4.7	510	7	CV057219	ENEL25C9	668	134	4.7	659	7	CV491566	AGENCOURT			
596	134	4.7	512	5	BQ266641	NISC_ff14	669	134	4.7	661	6	CD640938	AGENCOURT			
597	134	4.7	512	5	BQ523234	NISC_n121	670	134	4.7	663	7	CK242290	rx08a11.y			
598	134	4.7	512	5	BX568557	BX568557	671	134	4.7	667	6	CD638527	AGENCOURT			
599	134	4.7	512	6	CB095854	ie95e09.b	672	134	4.7	669	6	CD638433	AGENCOURT			
600	134	4.7	513	7	CO417018	Mdfr3011b	673	134	4.7	670	6	CD642160	AGENCOURT			
601	134	4.7	516	1	AV757012	AV757012	674	134	4.7	671	7	CO898117	Mdfr3020d			
602	134	4.7	523	6	CB083179	hn67f10.b	675	134	4.7	673	4	CG871128	rt68c01.y			
603	134	4.7	523	7	CV525558	Mdlv4012k	676	134	4.7	674	4	BG259801	602371947			
604	134	4.7	527	7	CV072206	EST4367_Z	677	134	4.7	679	7	CN843802	AGENCOURT			
605	134	4.7	529	1	AV758217	AV758217	678	134	4.7	680	7	CO074617	GR_Ea34N			
606	134	4.7	532	1	AJ658998	AJ658998	679	134	4.7	680	7	CO095071	GR_Ea171			
607	134	4.7	534	6	CA336360	NISC_lu12	680	134	4.7	683	1	AV682672	AV682672			
608	134	4.7	535	1	AV757455	AV757455	681	134	4.7	688	7	CO074646	GR_Ea34N			

682	134	4.7	689	7	CK003202	AGENCOURT	755	134	4.7	871	5	BUS29398	AGENCOURT
683	134	4.7	690	7	CK065814	WNEl27a11	756	134	4.7	872	5	BUS29249	AGENCOURT
684	134	4.7	691	7	CK005554	AGENCOURT	757	134	4.7	872	5	BUS87868	AGENCOURT
685	134	4.7	693	6	CK641480	AGENCOURT	758	134	4.7	872	5	BUS88646	AGENCOURT
686	134	4.7	701	7	CV520583	0089P0047	759	134	4.7	873	6	CD520987	AGENCOURT
687	134	4.7	702	7	CK065824	WNEl27b1	760	134	4.7	873	7	CN385475	AGENCOURT
688	134	4.7	707	6	CD640765	AGENCOURT	761	134	4.7	874	7	CN390078	AGENCOURT
689	134	4.7	708	6	CD237931	FNPARF04	C 762	134	4.7	874	7	CF783995	AGENCOURT
690	134	4.7	710	2	AG349204	GM210004A	C 763	134	4.7	875	7	BUS55372	AGENCOURT
691	134	4.7	712	4	BG739805	602630530	764	134	4.7	878	5	BUS68606	f2 new ch
692	134	4.7	713	1	AV733819	AV733819	765	134	4.7	878	7	CK790722	AGENCOURT
693	134	4.7	713	7	CK0870545	rlc60809.Y	766	134	4.7	884	5	BUS36542	AGENCOURT
C 694	134	4.7	714	6	CB339355	CA23E1031	767	134	4.7	885	5	BUS36542	AGENCOURT
695	134	4.7	714	7	CK064496	WNEl11f11	768	134	4.7	888	5	BUS65751	AGENCOURT
696	134	4.7	722	6	CD639592	AGENCOURT	769	134	4.7	888	5	BUS55497	AGENCOURT
697	134	4.7	724	7	CK460466	930744_MA	770	134	4.7	889	5	BUS50913	AGENCOURT
698	134	4.7	726	6	CD639437	AGENCOURT	771	134	4.7	889	5	BUS63271	AGENCOURT
C 699	134	4.7	728	5	BUS030396	AGENCOURT	772	134	4.7	890	5	BUS63755	AGENCOURT
700	134	4.7	729	6	CD640222	AGENCOURT	773	134	4.7	893	5	BUS851134	AGENCOURT
701	134	4.7	731	4	BM367453	NXlV_049	774	134	4.7	894	5	BQ441805	AGENCOURT
702	134	4.7	738	4	BG284611	602408778	775	134	4.7	894	5	BUS88228	AGENCOURT
703	134	4.7	739	1	AV726951	AV726951	776	134	4.7	895	5	BQ942584	AGENCOURT
704	134	4.7	748	5	BUS421419	AGENCOURT	C 777	134	4.7	895	7	CK068617	f2 new ch
C 705	134	4.7	754	7	CO395166	AGENCOURT	C 778	134	4.7	897	4	BM415645	OP20723 M
706	134	4.7	754	7	BUS37812	AGENCOURT	779	134	4.7	899	5	BQ218921	AGENCOURT
707	134	4.7	769	7	CF547327	AGENCOURT	780	134	4.7	899	5	BUS88232	AGENCOURT
708	134	4.7	769	7	CK064941	WNEl17c10	781	134	4.7	905	6	CB946345	AGENCOURT
709	134	4.7	770	5	BUS37695	AGENCOURT	782	134	4.7	907	6	CA977049	AGENCOURT
710	134	4.7	771	5	BUS943072	AGENCOURT	783	134	4.7	909	5	BUS87993	AGENCOURT
711	134	4.7	773	7	CV064559	WNEl12d8	784	134	4.7	913	5	BQ952206	AGENCOURT
C 712	134	4.7	776	5	BUS55076	AGENCOURT	785	134	4.7	914	5	BUS851349	AGENCOURT
C 713	134	4.7	778	7	CK068825	f2 new ch	786	134	4.7	921	6	CB844970	M2PN-0536
714	134	4.7	782	4	BI861670	603389343	787	134	4.7	923	5	BUS960730	AGENCOURT
715	134	4.7	785	7	CK790726	AGENCOURT	C 788	134	4.7	924	4	BM415316	OP20389 M
716	134	4.7	793	6	CD298877	AGENCOURT	C 789	134	4.7	926	7	CK068623	f2 new ch
717	134	4.7	801	5	BUS40225	AGENCOURT	790	134	4.7	927	6	CA455489	AGENCOURT
718	134	4.7	802	5	BUS851163	AGENCOURT	791	134	4.7	930	5	BUS58002	AGENCOURT
719	134	4.7	804	7	CK066336	WNEl32f2	792	134	4.7	931	5	BUS60826	AGENCOURT
720	134	4.7	805	5	BUS944935	AGENCOURT	C 793	134	4.7	932	4	BG033403	602301577
721	134	4.7	809	5	BUS58264	AGENCOURT	C 794	134	4.7	933	7	CV070185	WPAEhux15
722	134	4.7	809	6	CD559362	AGENCOURT	C 795	134	4.7	937	5	BUS193300	AGENCOURT
723	134	4.7	811	3	BC050987	Mus muscu	796	134	4.7	939	5	BQ434577	AGENCOURT
724	134	4.7	811	6	CD523425	AGENCOURT	C 797	134	4.7	939	7	CK068729	f2 new ch
725	134	4.7	813	5	BUS63257	AGENCOURT	C 798	134	4.7	942	5	BUS941184	AGENCOURT
726	134	4.7	813	7	CK794968	AGENCOURT	C 799	134	4.7	946	6	CA454659	AGENCOURT
727	134	4.7	814	5	BUS30990	AGENCOURT	C 800	134	4.7	946	7	CK068644	f2 new ch
728	134	4.7	814	5	BUS64423	AGENCOURT	C 801	134	4.7	947	5	BQ921561	AGENCOURT
729	134	4.7	814	5	BUS553115	AGENCOURT	C 802	134	4.7	952	7	CK151506	FGAS03407
730	134	4.7	816	5	BUS644811	AGENCOURT	C 803	134	4.7	955	5	BUS148296	AGENCOURT
731	134	4.7	817	8	BH156712	ENTSM49TF	C 804	134	4.7	961	4	BM416179	OP21266 M
C 732	134	4.7	819	5	BUS564488	AGENCOURT	C 805	134	4.7	965	5	BQ233225	AGENCOURT
733	134	4.7	821	5	BUS45039	AGENCOURT	C 806	134	4.7	966	4	BM415421	OP20495 M
734	134	4.7	826	5	BUS58181	AGENCOURT	C 807	134	4.7	969	5	BQ937042	AGENCOURT
735	134	4.7	830	5	BUS842943	AGENCOURT	C 808	134	4.7	971	5	BQ880542	AGENCOURT
736	134	4.7	830	5	BUS43607	AGENCOURT	C 809	134	4.7	972	7	CK068750	f2 new ch
737	134	4.7	831	7	CV490005	AGENCOURT	C 810	134	4.7	977	2	BE777769	601463009
738	134	4.7	832	5	BUS40111	AGENCOURT	C 811	134	4.7	979	5	BUS176137	AGENCOURT
739	134	4.7	835	7	CK799632	AGENCOURT	C 812	134	4.7	981	6	CD1513655	AGENCOURT
740	134	4.7	837	5	BUS36801	AGENCOURT	C 813	134	4.7	995	6	CB756884	AGENCOURT
741	134	4.7	840	5	BUS35967	AGENCOURT	C 814	134	4.7	996	6	CD050659	AGENCOURT
742	134	4.7	841	5	BUS962609	AGENCOURT	C 815	134	4.7	1008	6	CD246480	AGENCOURT
743	134	4.7	842	1	AV757327	AV757327	C 816	134	4.7	1012	4	BG121222	602320980
744	134	4.7	842	5	BUS87831	AGENCOURT	C 817	134	4.7	1017	4	BG108324	AGENCOURT
745	134	4.7	845	5	BUS441419	AGENCOURT	C 818	134	4.7	1020	6	CD050222	AGENCOURT
746	134	4.7	846	5	BUS37024	AGENCOURT	C 819	134	4.7	1025	3	BC027804	AGENCOURT
747	134	4.7	846	5	BUS851167	AGENCOURT	C 820	134	4.7	1025	3	BC027804	AGENCOURT
C 748	134	4.7	847	7	CK196235	FGAS00468	C 821	134	4.7	1026	5	BUS556025	AGENCOURT
749	134	4.7	848	7	CK068583	f2 new ch	C 822	134	4.7	1027	5	BUS59878	AGENCOURT
C 750	134	4.7	850	5	BUS89468	AGENCOURT	C 823	134	4.7	1036	9	CNS031WT	AGENCOURT
751	134	4.7	856	5	BUS34849	AGENCOURT	C 824	134	4.7	1037	4	BG104782	AGENCOURT
752	134	4.7	856	7	CV480269	AGENCOURT	C 825	134	4.7	1041	6	CD051043	AGENCOURT
753	134	4.7	863	6	CD107497	AGENCOURT	C 826	134	4.7	1052	5	BUS60001	AGENCOURT
754	134	4.7	868	5	BUS29631	AGENCOURT	C 827	134	4.7	1057	6	CD387510	AGENCOURT

828	134	4.7	1061	4	BM803249	AGENCOURT	901	133	4.7	142	4	BM014138	603639815
829	134	4.7	1063	4	BM469499	AGENCOURT	902	133	4.7	142	5	BU066696	1609_H09
830	134	4.7	1066	5	BU540067	AGENCOURT	c 903	133	4.7	143	7	CK615751	ou03c06.y
831	134	4.7	1067	6	CD386564	AGENCOURT	c 904	133	4.7	143	7	CK616902	ou29b11.y
c 832	134	4.7	1068	5	BU908068	AGENCOURT	c 905	133	4.7	143	7	CO478890	Q00177_B7
833	134	4.7	1077	5	BU540030	AGENCOURT	c 906	133	4.7	144	7	CF329001	NACL--04-
834	134	4.7	1081	6	CB182058	AGENCOURT	c 907	133	4.7	144	7	CK120535	20720.p1
835	134	4.7	1086	5	BU960798	AGENCOURT	c 908	133	4.7	145	7	CF308439	ABF--02-E
c 836	134	4.7	1097	4	BM464212	AGENCOURT	c 909	133	4.7	145	7	CF320486	HD--11-G
837	134	4.7	1099	4	BM457274	AGENCOURT	c 910	133	4.7	145	7	CK118018	207g21.p1
838	134	4.7	1109	5	BU530365	AGENCOURT	c 911	133	4.7	145	7	CK616841	ou27f08.y
839	134	4.7	1116	6	CA475599	AGENCOURT	c 912	133	4.7	148	7	CK616682	ou24a08.y
c 840	134	4.7	1139	4	BM476544	AGENCOURT	c 913	133	4.7	148	7	CO474093	Q0046.TB
841	134	4.7	1141	5	BM905793	AGENCOURT	c 914	133	4.7	149	5	BP454965	BP454965
c 842	134	4.7	1150	4	BM477385	AGENCOURT	c 915	133	4.7	149	6	CB089104	IF03h09.b
843	134	4.7	1150	5	BU902080	AGENCOURT	c 916	133	4.7	149	7	CK616434	ou18h11.y
844	134	4.7	1152	5	BO956600	AGENCOURT	c 917	133	4.7	150	7	CK616925	ou29g08.y
c 845	134	4.7	1188	4	BM458180	AGENCOURT	c 918	133	4.7	150	8	BZ239557	CH210-307
846	134	4.7	1200	5	BU508078	AGENCOURT	c 919	133	4.7	151	7	CK615670	ou01c04.y
c 847	134	4.7	1202	4	BM450025	AGENCOURT	c 920	133	4.7	152	2	BE877769	601486336
848	134	4.7	1213	3	BC029635	Mus muscu	c 921	133	4.7	152	7	CR557690	DKF2p4681
849	134	4.7	1234	4	BM460327	AGENCOURT	c 922	133	4.7	153	1	AL036396	DKF2p564H
850	134	4.7	1235	4	BM470058	AGENCOURT	c 923	133	4.7	153	4	BM033066	kh62g03.y
851	134	4.7	1251	4	BM453439	AGENCOURT	c 924	133	4.7	153	4	BM033228	kh64g07.y
852	134	4.7	1511	3	BC030320	AGENCOURT	c 925	133	4.7	153	5	BQ134995	IN111_2_H
853	134	4.7	1521	3	CR749559	AGENCOURT	c 926	133	4.7	153	6	CB409976	NISC.nc08
854	134	4.7	1534	5	BF342709	AGENCOURT	c 927	133	4.7	153	7	CK120779	206b23.p1
855	134	4.7	1611	4	BM466171	AGENCOURT	c 928	133	4.7	153	7	CR546234	DKF2p459B
856	134	4.7	1699	3	HSM801509	AGENCOURT	c 929	133	4.7	153	7	CR546234	DKF2p459B
857	134	4.7	1708	3	BC027831	AGENCOURT	c 930	133	4.7	154	2	BF422215	FM1_13_D1
858	134	4.7	1762	3	BC050651	AGENCOURT	c 931	133	4.7	155	4	BM155493	fw06g02.y
859	134	4.7	1782	3	CR749618	AGENCOURT	c 932	133	4.7	155	4	BM187047	ph81d02.y
860	134	4.7	1802	3	BC030213	AGENCOURT	c 933	133	4.7	155	5	BM896646	ph54a07.y
861	134	4.7	1840	3	BC036564	AGENCOURT	c 934	133	4.7	155	5	BM897043	ph55f05.y
862	134	4.7	1977	3	BC044307	AGENCOURT	c 935	133	4.7	155	5	BQ134923	IN111_1_H
863	134	4.7	1999	3	BC027914	AGENCOURT	c 936	133	4.7	155	7	CR772376	DKF2p4680
864	134	4.7	2001	3	BC032428	AGENCOURT	c 937	133	4.7	157	6	CB084762	hq22d11.b
865	134	4.7	2080	3	CR749502	AGENCOURT	c 938	133	4.7	157	6	BA493591	DKF2p781P
866	134	4.7	2084	3	BC025705	AGENCOURT	c 939	133	4.7	158	5	BA493591	DKF2p781P
867	134	4.7	2105	3	HSM803705	AGENCOURT	c 940	133	4.7	158	6	CB099755	py16e12.y
868	134	4.7	2286	3	AF116646	AGENCOURT	c 941	133	4.7	158	7	CF572034	MCSA032D0
869	134	4.7	2401	3	AF130075	AGENCOURT	c 942	133	4.7	159	4	BI783190	kh4Ba07.y
870	134	4.7	2500	3	BC026293	AGENCOURT	c 943	133	4.7	159	6	CB045580	NISC.g011
871	134	4.7	2623	3	HSM808057	AGENCOURT	c 944	133	4.7	159	6	CB046652	NISC_gf05
872	134	4.7	2700	3	BC036824	AGENCOURT	c 945	133	4.7	160	5	BI500352	rs71a10.y
873	134	4.7	2799	3	BC075812	AGENCOURT	c 946	133	4.7	160	5	BM896912	ph49f06.y
874	134	4.7	2949	3	BC075812	AGENCOURT	c 947	133	4.7	160	6	CB970716	CAB10004
875	134	4.7	3250	3	BC035530	AGENCOURT	c 948	133	4.7	160	6	CK615771	ou03g05.y
876	134	4.7	3645	3	HSM807326	AGENCOURT	c 949	133	4.7	161	4	BM155043	fv92g09.y
877	134	4.7	4195	3	HSM803410	AGENCOURT	c 950	133	4.7	162	1	AL696159	DKF2p686B
878	134	4.7	4712	3	CR749443	AGENCOURT	c 951	133	4.7	162	4	BG252929	602365530
879	134	4.7	5152	3	HSM803128	AGENCOURT	c 952	133	4.7	162	5	BA475911	DKF2p686E
880	134	4.7	5239	3	CR749475	AGENCOURT	c 953	133	4.7	162	7	CK616920	ou29f10.y
881	134	4.7	5940	3	CB627133	AGENCOURT	c 954	133	4.7	162	8	BH579624	BOGFV03TF
882	134	4.7	7420	3	CR749364	AGENCOURT	c 955	133	4.7	163	7	CR557869	DKF2p468H
883	134	4.7	7733	2	BE965556	AGENCOURT	c 956	133	4.7	163	4	BM154953	fv91f07.y
884	134	4.7	8133	7	CK616244	AGENCOURT	c 957	133	4.7	164	4	BM154953	ou03b09.y
885	134	4.7	8133	7	CK616732	AGENCOURT	c 958	133	4.7	164	7	CK615828	ou03b09.y
886	134	4.7	8133	7	CK617018	AGENCOURT	c 959	133	4.7	164	7	CK615828	ou03b09.y
887	134	4.7	8133	7	CK617288	AGENCOURT	c 960	133	4.7	165	4	BI498656	sai16h09.y
888	134	4.7	8133	7	CK120739	AGENCOURT	c 961	133	4.7	165	5	BM966627	ko10b04.y
889	134	4.7	8133	7	CK120739	AGENCOURT	c 962	133	4.7	166	5	BM966627	ko10b04.y
890	134	4.7	8133	7	CK120739	AGENCOURT	c 963	133	4.7	166	6	CA335025	NISC.lt04
891	134	4.7	8133	7	CK120739	AGENCOURT	c 964	133	4.7	166	6	CA335025	NISC.lt04
892	134	4.7	8133	7	CK120739	AGENCOURT	c 965	133	4.7	166	6	CA335025	NISC.lt04
893	134	4.7	8133	7	CK120739	AGENCOURT	c 966	133	4.7	166	6	CA335025	NISC.lt04
894	134	4.7	8133	7	CK120739	AGENCOURT	c 967	133	4.7	166	6	CA335025	NISC.lt04
895	134	4.7	8133	7	CK120739	AGENCOURT	c 968	133	4.7	166	6	CA335025	NISC.lt04
896	134	4.7	8133	7	CK120739	AGENCOURT	c 969	133	4.7	166	6	CA335025	NISC.lt04
897	134	4.7	8133	7	CK120739	AGENCOURT	c 970	133	4.7	167	1	AI433157	ti32b12.x
898	134	4.7	8133	7	CK120739	AGENCOURT	c 971	133	4.7	167	1	AI433157	ti32b12.x
899	134	4.7	8133	7	CK120739	AGENCOURT	c 972	133	4.7	167	7	CK120239	208b19.p1
900	134	4.7	8133	7	CK120739	AGENCOURT	c 973	133	4.7	167	7	CK120239	208b19.p1

974	133	4.7	168	7	CO194577	1047	133	4.7	186	2	BF343172	602015819
975	133	4.7	169	7	CR555269	1048	133	4.7	186	6	CA802489	sau37b06.
c 976	133	4.7	169	1	AL045500	1049	133	4.7	186	6	CA819169	sau370c02.
977	133	4.7	169	4	BI781645	1050	133	4.7	186	7	CK120313	208b05.pl
978	133	4.7	169	4	BI784430	c1051	133	4.7	186	7	CR753497	KRF2p465K
979	133	4.7	169	4	BI863663	1052	133	4.7	187	4	BI468624	sai01d03.
980	133	4.7	169	5	BM898046	1053	133	4.7	187	4	BI749319	ro76f11.y
c 981	133	4.7	169	6	BM898046	1054	133	4.7	187	6	CA802526	sau37g01.
c 982	133	4.7	169	7	CR518899	1055	133	4.7	187	6	CA802526	sau37g01.
c 983	133	4.7	170	2	CR536079	1056	133	4.7	187	7	CO191674	EC31648.5
c 984	133	4.7	170	2	AW268253	c1056	133	4.7	188	5	EX479066	KRF2p686L
985	133	4.7	170	4	BJ701151	1057	133	4.7	188	6	CA813174	sau70c07.
986	133	4.7	170	5	EX503607	1058	133	4.7	188	6	CK616430	ou18g09.y
987	133	4.7	170	6	CR072967	1059	133	4.7	189	1	AA590777	vm21b06.r
988	133	4.7	171	4	BI863546	1060	133	4.7	189	4	BM178937	saj61c09.
989	133	4.7	171	5	BM889202	c1061	133	4.7	189	5	BQ400307	NISC mp08
990	133	4.7	171	5	BU926898	1062	133	4.7	189	7	CO182475	EC22756.5
991	133	4.7	171	7	CR555329	c1063	133	4.7	189	7	CA747073	wri2a.pk0
992	133	4.7	172	1	AL697684	1064	133	4.7	190	6	CA802078	sau29g04.
993	133	4.7	172	4	BM874768	1065	133	4.7	191	1	AL696149	AL696149 KRF2p686B
994	133	4.7	172	6	CR075586	1066	133	4.7	191	5	BM965865	ko18c09.y
c 995	133	4.7	173	6	CB084519	1067	133	4.7	191	5	EX503634	KRF2p686L
c 996	133	4.7	174	1	AJ654741	1068	133	4.7	191	6	CA819538	sau80a11.
c 997	133	4.7	174	4	BM186145	c1069	133	4.7	191	7	CF214566	GGF100081
c 998	133	4.7	174	5	BM896563	c1070	133	4.7	191	7	CR789784	KRF2p459E
999	133	4.7	174	7	CR616865	1071	133	4.7	192	1	AI856699	sb43f11.y
c1000	133	4.7	174	9	CNS023TP	1072	133	4.7	192	4	BM154409	fv84g05.y
1001	133	4.7	175	4	BM318082	1073	133	4.7	192	6	CD570788	kb76f12.y
c1002	133	4.7	175	5	BM896455	1074	133	4.7	192	7	CR557731	KRF2p468K
1003	133	4.7	175	7	CF215776	1075	133	4.7	193	6	CA819381	sau77f02.
1004	133	4.7	175	7	CR7119906	1076	133	4.7	193	7	CO192922	EC34787.5
1005	133	4.7	175	7	CR771914	1077	133	4.7	194	4	BI783226	sk48f02.y
1006	133	4.7	176	4	BM155475	1078	133	4.7	194	4	BM308918	sk452b01.
1007	133	4.7	176	5	EX503619	c1079	133	4.7	195	1	AU060359	AU060359
c1008	133	4.7	176	6	CR045509	1080	133	4.7	195	4	BJ021877	BJ021877
c1009	133	4.7	176	7	CR045579	1081	133	4.7	195	4	BJ251931	BJ251931
1010	133	4.7	177	1	AL697773	c1082	133	4.7	195	5	EX956516	KRF2p781K
1011	133	4.7	177	4	BQ464649	c1083	133	4.7	195	6	CB817512	d3k21p2.f
c1012	133	4.7	177	4	BM155200	1084	133	4.7	195	7	CK120094	208p09.pl
c1013	133	4.7	177	6	CR045548	1085	133	4.7	196	1	AL712417	KRF2p686P
1014	133	4.7	177	7	CR712639	1086	133	4.7	196	6	CA339374	NISC_ly02
1015	133	4.7	177	7	CR771835	c1087	133	4.7	196	6	CB045738	NISC_gc12
1016	133	4.7	178	4	BJ696903	1088	133	4.7	196	6	CB073175	taa29d07.
1017	133	4.7	178	5	BM965687	c1090	133	4.7	196	6	BI799993	602329538
c1018	133	4.7	178	5	BQ391656	1091	133	4.7	197	4	BG179993	BO666607
c1019	133	4.7	178	6	CR192208	1092	133	4.7	197	5	BO666607	pb44e06.y
c1020	133	4.7	179	6	CA670281	c1093	133	4.7	197	5	EX484617	KRF2p686L
c1021	133	4.7	179	6	CB216118	c1094	133	4.7	197	6	CA670214	wlsul.pk0
1022	133	4.7	180	1	AV184931	1095	133	4.7	197	6	CA802643	sau39h03.
c1023	133	4.7	180	1	AV200626	1096	133	4.7	197	6	CA935345	sau52d04.
1024	133	4.7	180	6	CA819701	c1097	133	4.7	198	5	BQ392333	NISC mq23
1025	133	4.7	180	7	CK120267	1098	133	4.7	198	6	CA819320	sau72f08.
1026	133	4.7	181	4	BJ696904	1099	133	4.7	198	7	CO181348	EC14089.5
c1027	133	4.7	181	5	BM899727	1100	133	4.7	199	1	AU037638	AU037638
c1028	133	4.7	181	6	CR980398	1101	133	4.7	199	6	CB376865	CB376865
c1029	133	4.7	181	7	CR543183	1102	133	4.7	200	5	BQ667387	pb60g04.y
1030	133	4.7	181	8	CR791725	1103	133	4.7	200	5	EX503618	KRF2p686E
c1031	133	4.7	181	8	AZ062901	1104	133	4.7	200	6	CD724098	o3j0d06.y
1032	133	4.7	182	2	AW101133	1105	133	4.7	200	7	CK593192	lad41d04.
1033	133	4.7	182	4	BM155169	1106	133	4.7	200	7	CR559013	KRF2p468P
1034	133	4.7	182	4	BM155421	c1107	133	4.7	201	5	BQ523741	NISC_r123
c1035	133	4.7	182	5	BU801954	1108	133	4.7	201	5	EX474221	KRF2p686D
c1036	133	4.7	182	6	CA340216	1109	133	4.7	201	6	CA802122	sau30e05.
1037	133	4.7	182	6	CB101650	c1110	133	4.7	201	7	CR546762	KRF2p4700
1038	133	4.7	183	5	BQ740714	1111	133	4.7	201	7	CR765965	CR765965
1039	133	4.7	183	5	BM508387	1112	133	4.7	202	4	BG736221	tk53d03.y
1040	133	4.7	183	7	CR766049	1113	133	4.7	202	4	BM154309	fv84e04.y
1041	133	4.7	183	7	CR791704	1114	133	4.7	202	5	BM965808	ko18e03.y
1042	133	4.7	184	4	BI705276	1115	133	4.7	202	7	CK118991	214p04.pl
1043	133	4.7	184	6	CR721356	1116	133	4.7	202	7	CO168360	Mdf.r3001.i
1044	133	4.7	185	5	BQ077400	1117	133	4.7	202	7	CO185210	BC29934.5
1045	133	4.7	185	5	EX501448	c1118	133	4.7	203	5	BQ399198	NISC mp02
1046	133	4.7	185	7	CR772164	1119	133	4.7	203	7	CK428917	1aj19b11.

1120	133	4.7	203	7	CR546261	DKF2p459D	1193	133	4.7	220	7	CR630411	DKF2p469D
1121	133	4.7	204	1	AL712721	DKF2p686I	1194	133	4.7	220	9	CNS0148D	AL103831
1122	133	4.7	204	4	BM064528	KS01068C0	1195	133	4.7	220	9	CNS037J	AL231400
1123	133	4.7	204	5	BA756691	DKF2p686J	1196	133	4.7	221	4	BM532327	BM532327
1124	133	4.7	204	6	CA819112	saue69b11	1197	133	4.7	221	5	BU764039	saes1908
1125	133	4.7	204	7	CK120836	205n01.p1	1198	133	4.7	221	7	CO168252	Mdf-3013j
1126	133	4.7	205	1	AA153231	mn31b12.f	1199	133	4.7	221	7	CV192584	SNES7bab1
1127	133	4.7	205	4	BM155383	fw04a12.y	1200	133	4.7	221	7	CV193270	SNES7bab2
1128	133	4.7	205	6	CA819594	saue73a07	1201	133	4.7	222	1	AL696218	DKF2p686C
1129	133	4.7	205	6	CA935286	saue51f04	1202	133	4.7	222	4	BI863321	r103d06.y
1130	133	4.7	205	6	CA935286	saue51f04	1203	133	4.7	222	6	CA802046	saue29c08
1131	133	4.7	205	6	CA935286	saue51f04	1204	133	4.7	222	8	BZ043861	lkha1a01
1132	133	4.7	205	6	CA935286	saue51f04	1205	133	4.7	223	6	CA819345	saue77a09
1133	133	4.7	205	7	CR557702	DKF2p468I	1206	133	4.7	223	7	CR791578	DKF2p468D
1134	133	4.7	206	7	CF331225	NACL--07	1207	133	4.7	223	9	CNS027EU	AL184575
1135	133	4.7	207	4	BI709283	fs62e01.y	1208	133	4.7	224	5	BX5033628	DKF2p686H
1136	133	4.7	207	5	BO399361	BO399361	1209	133	4.7	224	6	CA935362	saue52f03
1137	133	4.7	207	6	CA808898	if07C06.b	1210	133	4.7	224	7	CR544817	CR544817
1138	133	4.7	207	7	CK119802	210107.p1	1211	133	4.7	224	7	CR768779	DKF2p468D
1139	133	4.7	207	7	CR524509	DKF2p470B	1212	133	4.7	225	2	AW100941	sd63e06.y
1140	133	4.7	208	6	CB410192	NISC nc10	1213	133	4.7	225	6	CA819034	saue67h08
1141	133	4.7	208	7	CO195491	EC40468.5	1214	133	4.7	226	6	CB093154	te81a11.b
1142	133	4.7	209	1	AA638753	vm93e12.x	1215	133	4.7	226	7	CF572350	MCSA037C0
1143	133	4.7	209	5	BQ825960	OK-YZ-B49	1216	133	4.7	226	9	CNS0486K	AL287957
1144	133	4.7	209	5	BA484868	DKF2p686N	1217	133	4.7	227	5	BU764188	saes3902
1145	133	4.7	209	6	CA819818	saue76e11	1218	133	4.7	227	6	CB285901	CMD26_H02
1146	133	4.7	209	6	CB337509	laa34g09	1219	133	4.7	228	7	CK119140	214c04.p1
1147	133	4.7	209	7	CK427762	la03e08	1220	133	4.7	228	9	CNS021AJ	AL176644
1148	133	4.7	209	7	CO732829	SL1L01b03	1221	133	4.7	229	1	AA734226	Tetraodon
1149	133	4.7	210	4	BM873785	laa03a07	1222	133	4.7	229	5	BQ075610	vt26a09.x
1150	133	4.7	210	6	CA935503	saue5a10	1223	133	4.7	229	6	CA802763	fz06g08.y
1151	133	4.7	210	7	CK121439	203b24.p1	1224	133	4.7	229	7	CF929107	saue1906
1152	133	4.7	211	4	BI748687	RO81a03.y	1225	133	4.7	230	4	BI784178	kh31h01.y
1153	133	4.7	211	4	BJ680884	BJ680884	1226	133	4.7	230	4	BM595688	170006874
1154	133	4.7	211	6	CA935582	saue56c12	1227	133	4.7	230	6	CA936756	saue23a12
1155	133	4.7	211	6	CB722487	oj10d01.y	1228	133	4.7	230	6	CB287035	CMD51_F02
1156	133	4.7	211	7	CK120334	207m23.p1	1229	133	4.7	230	7	CF572716	MCSA053G0
1157	133	4.7	212	5	BU760971	saes1b04	1230	133	4.7	231	2	AW164838	se78f04.y
1158	133	4.7	212	7	CO195530	EC40529.5	1231	133	4.7	231	5	BM644880	DKF2p781D
1159	133	4.7	213	4	BG168696	602319949	1232	133	4.7	231	7	CO181733	EC14891.5
1160	133	4.7	213	6	CA935478	saue54f06	1233	133	4.7	232	7	CR537572	DKF2p459K
1161	133	4.7	214	1	AL703357	AL703357	1234	133	4.7	233	2	BE030380	128430_MA
1162	133	4.7	214	7	CR630363	DKF2p469J	1235	133	4.7	233	5	BM502988	DKF2p779D
1163	133	4.7	215	4	BG731047	dae09h01	1236	133	4.7	233	6	CB079472	hp71905.b
1164	133	4.7	215	4	BG893071	daa3e09	1237	133	4.7	233	6	CF722270	jnn609G08
1165	133	4.7	215	6	BI100794	kl61h01.y	1238	133	4.7	233	7	CF124181	UI-HF-CH0
1166	133	4.7	215	7	CF207515	CAB20001	1239	133	4.7	234	4	BM154438	fv85b03.y
1167	133	4.7	215	7	CF214757	CGF100082	1240	133	4.7	234	4	BM873724	laa02c06
1168	133	4.7	215	7	CF425648	lad42d03	1241	133	4.7	234	6	CD722269	oj07e09.y
1169	133	4.7	216	6	CA935095	saue64D09	1242	133	4.7	235	2	AW101589	sd66c02.y
1170	133	4.7	216	6	CA935420	saue53f05	1243	133	4.7	235	4	BI749483	ro78f07.y
1171	133	4.7	216	7	CF970477	la03g09	1244	133	4.7	235	4	BJ081948	BJ081948
1172	133	4.7	217	1	AI500077	tn71c02.x	1245	133	4.7	235	6	CB051841	NISC_g103
1173	133	4.7	217	1	BZ251664	BU251664	1246	133	4.7	235	6	CD577826	23_B04_23
1174	133	4.7	217	7	CR524654	DKF2p470I	1247	133	4.7	235	7	CF925885	la93b05
1175	133	4.7	217	7	AL666596	AL666596	1248	133	4.7	235	7	CO195635	EC40706.5
1176	133	4.7	218	4	BM154944	fv91e06.y	1249	133	4.7	236	6	CA339334	NISC_ly01
1177	133	4.7	218	6	CA935222	saue50e10	1250	133	4.7	236	6	CB948928	AGENCOURT
1178	133	4.7	218	7	CF426331	lad22h07	1251	133	4.7	236	7	CO180970	EC13263.5
1179	133	4.7	218	7	CK377805	lal08g07	1252	133	4.7	237	5	BQ128671	ii21g02.y
1180	133	4.7	218	7	CO727269	UMC-bend	1253	133	4.7	237	7	CK616649	ou23d05.y
1181	133	4.7	219	4	BI791181	id02g09.y	1254	133	4.7	237	7	CR543081	DKF2p470G
1182	133	4.7	219	4	BM587451	170006873	1255	133	4.7	237	7	CR791203	DKF2p468F
1183	133	4.7	219	6	CA818936	saue6d11	1256	133	4.7	238	7	CO184969	EC29002.5
1184	133	4.7	219	6	CA818959	saue6g10	1257	133	4.7	238	7	CO983126	GM8901782
1185	133	4.7	219	6	CB975278	CAB30006	1258	133	4.7	239	5	BQ094174	saes13C02
1186	133	4.7	219	7	CO182437	EC22654.5	1259	133	4.7	239	5	BM503636	DKF2p686J
1187	133	4.7	220	4	BI705030	fr62b01.y	1260	133	4.7	239	6	CA782245	saue32h02
1188	133	4.7	220	4	BM573836	fy04f07.y	1261	133	4.7	239	6	CA802785	saue42b04
1189	133	4.7	220	5	BU764212	saes4a06	1262	133	4.7	239	7	CO184329	EC27920.5
1190	133	4.7	220	6	CA819276	saue71g12	1263	133	4.7	240	1	AV184850	AV184850
1191	133	4.7	220	7	CF424575	lad32g04	1264	133	4.7	240	2	BE417917	SC1011.B0
1192	133	4.7	220	7	CK429243	oj34a08.y	1265	133	4.7	240	6	CB020904	px92c08.y

c1266	133	4.7	240	6	CB0433994	CB0433994	NISC gc01	1339	133	4.7	257	7	CV193143	CV193143	SNESBab2
1267	133	4.7	240	6	CD520495	AGENCOURT	CD520495	1340	133	4.7	258	4	BG735588	BG735588	rk41c01.Y
1268	133	4.7	240	6	CR774358	KFP2p459P	CR774358	1341	133	4.7	259	1	AL697721	AL697721	KFP2p686I
1269	133	4.7	241	4	B1863365		B1863365	1342	133	4.7	259	1	AL707050	AL707050	KFP2p686M
1270	133	4.7	241	4	B1863432		B1863432	1343	133	4.7	259	7	CK624985	CK624985	mi27905.Y
1271	133	4.7	242	1	AL036146	KFP2p564D	AL036146	1344	133	4.7	259	7	CO159753	CO159753	FLD1_15.D
1272	133	4.7	242	1	AL697724	KFP2p686I	AL697724	1345	133	4.7	260	4	BN307865	BN307865	sak39a09.
1273	133	4.7	242	6	CA802129	sau30f01.	CA802129	1346	133	4.7	260	7	CK377340	CK377340	lai02e06.
1274	133	4.7	243	2	B8057234	sm99c12.Y	BE057234	1347	133	4.7	260	7	CO988045	CO988045	Mdf13020e
1275	133	4.7	243	4	BG237165	sab04d10.	BG237165	1348	133	4.7	260	7	CR772316	CR772316	KFP2p468L
1276	133	4.7	243	4	B1142830	rk74f05.Y	B1142830	1349	133	4.7	260	9	CNS02QNR	AL209520	Tetraodon
1277	133	4.7	243	6	CD578259	21_H11_21	CD578259	1350	133	4.7	261	4	BJ469921	BJ469921	BJ469921
1278	133	4.7	243	7	CO752945	Mdf13022i	CO752945	1351	133	4.7	261	6	CA802634	CA802634	sau39g05.
1279	133	4.7	243	7	CO905671	SNESBbaa4	CO905671	1352	133	4.7	261	7	CV280938	CV280938	WS0138.B2
1280	133	4.7	244	6	CR721659	jnn613D09	CR721659	1353	133	4.7	262	7	CK593385	CK593385	tad39f12.
1281	133	4.7	244	7	CK430436	oj49d02.Y	CK430436	1354	133	4.7	262	7	CR791700	CR791700	KFP2p468P
1282	133	4.7	245	2	AW100988	sd64b09.Y	AW100988	c1355	133	4.7	263	6	CF040070	CF040070	QCH8d09.Y
1283	133	4.7	245	5	BX476550	KFP2p686O	BX476550	1356	133	4.7	263	7	CO982740	CO982740	GM89016B1
1284	133	4.7	246	1	AL696192	AL696192	AL696192	1357	133	4.7	264	7	CF317367	CF317367	HD--07-A1
1285	133	4.7	246	4	BG237816	sab08e11.	BG237816	1358	133	4.7	265	2	AW185173	AW185173	se87h05.Y
1286	133	4.7	246	5	BQ394140		BQ394140	1359	133	4.7	265	6	CA935083	CA935083	sau64b05.
1287	133	4.7	246	6	CA802566		CA802566	c1361	133	4.7	265	7	CN411756	CN411756	170005322
1288	133	4.7	246	6	CA802581	sau38g01.	CA802581	1360	133	4.7	265	7	CR766084	CR766084	KFP2p468I
1289	133	4.7	246	6	CB092960	hk40g05.g	CB092960	1362	133	4.7	266	5	BQ842918	BQ842918	ID_269_Su
c1290	133	4.7	246	7	CF214774	CGF100082	CF214774	1363	133	4.7	266	5	BX504760	BX504760	KFP2p686E
1291	133	4.7	246	7	CR559419	KFP2p468I	CR559419	1364	133	4.7	266	6	CD640467	CD640467	AGENCOURT
c1292	133	4.7	246	9	CNS013NL	Drosophi1	AL103083	1365	133	4.7	266	6	CD678505	CD678505	hp08g11.Y
1293	133	4.7	247	4	BJ701295		BJ701295	1366	133	4.7	267	5	BU703468	BU703468	UI-N-F00-
1294	133	4.7	247	4	BM187242	fw13g02.Y	BM187242	1367	133	4.7	267	5	BU703468	BU703468	UI-N-F00-
1295	133	4.7	248	1	AL712394	KFP2p686M	AL712394	1368	133	4.7	268	1	AL135661	AL135661	KFP2p762M
1296	133	4.7	248	4	BM521849	sak76g12.	BM521849	1369	133	4.7	268	4	BG058208	BG058208	nah22b05.
c1297	133	4.7	248	5	BQ265006	NISC ff02	BQ265006	1370	133	4.7	268	6	CD640467	CD640467	AGENCOURT
1298	133	4.7	248	5	BU721072	SJM2BJD06	BU721072	1371	133	4.7	268	7	CK430337	CK430337	oj48b09.Y
1299	133	4.7	248	5	BX507072	KFP2p779G	BX507072	1372	133	4.7	269	1	AL708133	AL708133	KFP2p686D
1300	133	4.7	248	6	CA935253	sau51b05.	CA935253	1373	133	4.7	269	5	EX474011	EX474011	KFP2p686L
c1301	133	4.7	248	6	CB977176	CAB40003	CB977176	1374	133	4.7	269	7	CO416572	CO416572	Mdf130081
1302	133	4.7	248	7	CR078154	BovGen_06	CR078154	1375	133	4.7	270	1	AV836739	AV836739	AV836739
1303	133	4.7	248	7	CR772335	KFP2p468M	CR772335	1376	133	4.7	270	4	BG737252	BG737252	rk68h06.Y
1304	133	4.7	249	2	B8059724	sn36a12.Y	BE059724	1377	133	4.7	270	4	BJ686519	BJ686519	KJ686519
1305	133	4.7	249	4	BM493181		BM493181	1378	133	4.7	270	4	BJ696724	BJ696724	BJ696724
1306	133	4.7	249	5	BQ785446	saq77h12.Y	BQ785446	1379	133	4.7	270	4	BM281117	BM281117	ki08f12.Y
1307	133	4.7	249	7	CR559477	KFP2p468J	CR559477	1380	133	4.7	270	5	BM882656	BM882656	rb28b09.Y
c1308	133	4.7	250	5	BQ395199	NISC ng13	BQ395199	1381	133	4.7	270	5	BU721775	BU721775	SJM2CBF02
1309	133	4.7	250	7	CA429184	oj33c07.Y	CA429184	1382	133	4.7	270	5	BX503644	BX503644	KFP2p686N
1310	133	4.7	251	5	BX503645		BX503645	c1383	133	4.7	270	7	CN266212	CN266212	170004251
1311	133	4.7	251	7	CK121775		CK121775	1384	133	4.7	270	7	CO979289	CO979289	GM89004A2
1312	133	4.7	251	7	COL80942	EC13208.5	COL80942	1385	133	4.7	271	6	CA802092	CA802092	sau30a04.
1313	133	4.7	252	6	CA336435	NISC 1v01	CA336435	1386	133	4.7	271	6	CA802549	CA802549	sau38b03.
c1314	133	4.7	252	6	CB043981	NISC gc01	CB043981	1387	133	4.7	271	7	CR629027	CR629027	KFP2p468O
1315	133	4.7	252	6	CB409398	NISC nc05	CB409398	1388	133	4.7	272	4	BI142828	BI142828	rk74e10.Y
1316	133	4.7	252	7	CO415260	Mdf13006k	CO415260	1389	133	4.7	272	5	BX507023	BX507023	KFP2p779A
c1317	133	4.7	252	7	CR545848		CR545848	1390	133	4.7	272	6	CA935343	CA935343	sau52d02.
1318	133	4.7	252	7	CR771899	KFP2p468C	CR771899	1391	133	4.7	272	6	CD520705	CD520705	AGENCOURT
1319	133	4.7	253	6	CD241885	AGENCOURT	CD241885	1392	133	4.7	272	7	CO069398	CO069398	Mdf13015k
1320	133	4.7	253	9	CNS0149M		AL103876	1393	133	4.7	273	7	CR763153	CR763153	KFP2p470L
1321	133	4.7	254	2	B8057342	Drosophi1	BE057342	1394	133	4.7	273	6	CB945895	CB945895	AGENCOURT
1322	133	4.7	254	4	B1705355	fr57g11.Y	BI705355	1395	133	4.7	273	7	CN266183	CN266183	170004250
c1323	133	4.7	254	5	BX493069	KFP2p781N	BR493069	1396	133	4.7	274	5	BQ385858	BQ385858	NISC ma14
1324	133	4.7	254	7	CR559205	KFP2p468M	CR559205	1397	133	4.7	274	6	CA934958	CA934958	sau61f10.
1325	133	4.7	254	7	CR559920	KFP2p459M	CR559920	1398	133	4.7	275	4	BM522686	BM522686	sae96b08.
1326	133	4.7	255	4	BG879342	ib62g05.Y	BG879342	1399	133	4.7	275	7	CF612545	CF612545	lae11h04.
1327	133	4.7	255	6	CA335171	NISC 1t07	CA335171	1400	133	4.7	275	9	CR675233	CR675233	KFP2p468K
1328	133	4.7	255	6	CA802891	sau43g09.	CA802891	c1401	133	4.7	275	9	CNS034C8	AL227249	Tetraodon
c1329	133	4.7	255	7	CF519323	AGENCOURT	CF519323	1402	133	4.7	276	4	BG736627	BG736627	rk60b07.Y
1330	133	4.7	256	7	CO066438	Mdf13004O	CO066438	1403	133	4.7	276	7	CN550423	CN550423	QQ0243.B3
1331	133	4.7	256	6	CB088964	1f08a08.b	CB088964	c1404	133	4.7	277	4	BM644186	BM644186	170006873
1332	133	4.7	256	7	CO183275	EC25346.5	CO183275	1405	133	4.7	279	6	CD721804	CD721804	oj01f10.Y
1333	133	4.7	256	7	CO195335	EC40072.5	CO195335	1406	133	4.7	279	7	CF400770	CF400770	RTW1_7.D
1334	133	4.7	257	1	AL731976		AL731976	1407	133	4.7	280	1	AJ769221	AJ769221	AJ769221
1335	133	4.7	257	4	BG894303	rk51a05.Y	BG894303	1408	133	4.7	280	4	BJ019482	BJ019482	BJ019482
1336	133	4.7	257	6	CB191298	py30e08.Y	CB191298	1409	133	4.7	280	7	CK593941	CK593941	tad16b05.
1337	133	4.7	257	7	CO065740	Mdf13015J	CO065740	1410	133	4.7	281	4	BM261286	BM261286	dai16d01.
1338	133	4.7	257	7	CO982751	GM89016B1	CO982751	c1411	133	4.7	281	5	BQ392472	BQ392472	NISC mq24

1412	133	4.7	282	1	AL712459	AL712459	DKFZp686D	1485	133	4.7	306	4	BJ678742	BJ678742	BJ678742	BJ678742
1413	133	4.7	282	4	BG735988	BG735988	rk46b09.y	1486	133	4.7	306	6	CD052334	CD052334	CD052334	EST1593.2
1414	133	4.7	282	6	CB711645	AMGNNUC.N		1487	133	4.7	306	6	CD250397	CD250397	AGENCOURT	AGENCOURT
1415	133	4.7	282	6	CD641456	AGENCOURT		1488	133	4.7	306	7	CF424510	CF424510	lad31g07.	lad31g07.
1416	133	4.7	282	7	CO417188	Mdfc3012a		c1489	133	4.7	307	5	BX472583	DKFZp686N	DKFZp686N	DKFZp686N
1417	133	4.7	282	7	CR750600	DKFZp470H		1490	133	4.7	309	9	CNS0606H	T3 end of	T3 end of	T3 end of
1418	133	4.7	283	4	BT324331	rk7f811.y		1491	133	4.7	310	5	EX476425	DKFZp686A	DKFZp686A	DKFZp686A
1419	133	4.7	283	5	EX644833	DKFZp781M		c1492	133	4.7	311	5	BQ389350	NISC.mq07	NISC.mq07	NISC.mq07
1420	133	4.7	283	6	CB288125	CMD74.E02		1493	133	4.7	311	6	CD678330	hpo5h10.y	hpo5h10.y	hpo5h10.y
1421	133	4.7	283	7	CR765052	DKFZp470P		1494	133	4.7	311	7	CO067761	Mdfc3014j	Mdfc3014j	Mdfc3014j
1422	133	4.7	283	9	CNS01TV3	Tetraodon		1495	133	4.7	311	7	CR543039	DKFZp470B	DKFZp470B	DKFZp470B
1423	133	4.7	284	4	BG736811	rk62f11.y		1496	133	4.7	312	4	BM154503	fv85h09.y	fv85h09.y	fv85h09.y
1424	133	4.7	284	7	CF124689	UI-HF-CHO		1497	133	4.7	312	4	BM181161	fv94h12.y	fv94h12.y	fv94h12.y
1425	133	4.7	285	6	CD219274	EST0171.2		1498	133	4.7	312	6	CD723029	oj17b05.y	oj17b05.y	oj17b05.y
1426	133	4.7	285	6	CD521457	AGENCOURT		1499	133	4.7	312	7	CK625997	mj16h04.y	mj16h04.y	mj16h04.y
1427	133	4.7	285	9	CNS0216T	Tetraodon		1500	133	4.7	312	7	CO191506	EC31225.5	EC31225.5	EC31225.5
1428	133	4.7	286	7	CR640321	D26.A01.F										
1429	133	4.7	286	7	CO067491	Mdfc3014e										
1430	133	4.7	287	6	CB350053	CAB28G000										
1431	133	4.7	288	5	BU761103	sas63b02.										
1432	133	4.7	288	9	CNS02JF6	Tetraodon										
1433	133	4.7	289	5	BU764209	sas54a02.										
1434	133	4.7	289	7	CO192898	EC34741.5										
1435	133	4.7	289	9	CNS03NIR	Tetraodon										
1436	133	4.7	290	5	BM884774	BM884774										
1437	133	4.7	290	5	BX501576	DKFZp779M										
1438	133	4.7	290	6	CA802066	sau29f03.										
1439	133	4.7	290	6	CF056298	OC017e01.										
1440	133	4.7	291	7	CF927173	laf48e11.										
1441	133	4.7	291	7	CR549807	DKFZp4691										
1442	133	4.7	292	4	BG736181	rk52e11.y										
1443	133	4.7	292	6	CD422569	laa02h05.										
1444	133	4.7	292	6	CNS966002	Mdfc30031										
1445	133	4.7	292	7	BM186087	fv97g08.y										
1446	133	4.7	293	4	BM186087	fv97g08.y										
1447	133	4.7	293	6	CD640448	AGENCOURT										
1448	133	4.7	293	6	CF123306	UI-HF-CHO										
1449	133	4.7	294	4	BG361880	gb46b12.y										
1450	133	4.7	294	6	CA802699	sau40g02.										
1451	133	4.7	294	6	CA8040781	pt57h12.y										
1452	133	4.7	294	6	CB083753	hg03e02.b										
1453	133	4.7	295	1	AL349772	ta96e04.x										
1454	133	4.7	295	1	AL663392	AL663392										
1455	133	4.7	295	1	AL723228	AL723228										
1456	133	4.7	295	6	CB075676	CB075676										
1457	133	4.7	295	7	CK429478	oj37b09.y										
1458	133	4.7	295	7	CO184039	EC26979.5										
1459	133	4.7	296	4	BG155473	sab44e12.										
1460	133	4.7	296	7	CF640327	D25.A01.F										
1461	133	4.7	296	7	CK353572	AGENCOURT										
1462	133	4.7	296	7	CO488925	QQ0255.B3										
1463	133	4.7	296	7	CR559765	DKFZp459J										
1464	133	4.7	297	1	AJ797542	AJ797542										
1465	133	4.7	297	4	BM531692	fx90a12.y										
1466	133	4.7	297	5	BQ128810	1123d03.y										
1467	133	4.7	298	4	BJ295031	BJ295031										
1468	133	4.7	298	5	BJ765639	sab13d10.										
1469	133	4.7	298	5	BM532321	DKFZp781D										
1470	133	4.7	298	7	CNS65487	UNC-bend										
1471	133	4.7	299	4	BG735891	rk48e01.y										
1472	133	4.7	299	4	BM034391	kh52e08.y										
1473	133	4.7	299	7	CO416217	Mdfc3010c										
1474	133	4.7	302	4	BM493167	LIT000085										
1475	133	4.7	302	7	CO181976	EC18096.5										
1476	133	4.7	302	7	CR546452	DKFZp470A										
1477	133	4.7	303	5	BM489223	DKFZp686P										
1478	133	4.7	303	7	CO193390	EC35696.5										
1479	133	4.7	304	1	AL698019	DKFZp686O										
1480	133	4.7	304	4	BJ686940	BJ686940										
1481	133	4.7	304	7	CNS927725	000530AEP										
1482	133	4.7	305	5	BM473779	DKFZp686B										
1483	133	4.7	305	6	CD520469	AGENCOURT										
1484	133	4.7	305	7	CO168362	Mdfc3001f										

RESULTS

LOCUS HSM806734 3165 bp mRNA linear HTC 22-SEP-2004

DEFINITION Homo sapiens mRNA; cDNA DKFZp686N24154 (from clone DKFZp686N24154).

ACCESSION BX640676

VERSION BX640676.1 GI:34364725

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 3165)

AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Oeanger, A., Fobo, G., Han, M. and Wiemann, S.

CONSORTM The German cDNA Consortium

TITLE Direct Submission

JOURNAL Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMPZ (Biomedical Research Center at the Heinrich-Heine-University, Dueseldorff/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686N24154) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686N24154 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

FEATURES

Location/Qualifiers

1..3165

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="RZPD:DKFZp686N24154Q"

/db_xref="taxon:9606"

/clone="DKFZp686N24154"

/tissue_type="colon endothel, primary cell culture"

/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host DH10B; sites SfiIA + SfiIB"

/dev_stage="adult"

/note="hypothetical protein"

1..3165

/gene="DKFZp686N24154"

447..2609

/gene="DKFZp686N24154"

/codon_start=1

/product="hypothetical protein"

/protein_id="CAE45808.1"

/db_xref="GI:34364726"

/db_xref="UniProt/TREMBL:Q6N062"

/translation="MELGCVTQLGLTFLQLLLISLIPREYTVINACPGAENIMCRE CCEYDQIECVCPGKREVVGYTIPCCRNENECDCLIHPGCTIFENCSCSRNGSGGT"

LDDFYKGYCAECRAGWYGDRCGOVLRAKPGQIILLESYPLNAHCWTHAKPGF
VIOLEFVMSLEFDYMCODYVEVDFDNRDGOIIRKVCGNERPAPIOSIGSSHLVLF
HSDCKDPDFGHAIYEEITACSSSPCFHDGTCYLDKAGSYKACLACLAGTGRCENLLE
ERNCSKDPGVNGYQKITGGPELINGRHAKITGVVFFCNNSYVLSNGNEKRTQQNGE
WSGKOPICIKACREPKISDLVRRRVLPMQVSRETPHLQYSAAFSKQKLSAPTKP
ALPFDLPWGQHLHTQYECISFPYRLGSRRTCLRTGKWSGRAPSCPIPGKIE
NITAPKTQGLRWPQAAIYRRTSGVHDSLHKGAWFLVCSGALVNERVTVVAAHCVTD
LGKWTMIATDLKVLGKPYRDDREKTIOSLRISAILHPNDYDPIILLDADIALKL
LDKARISFVQPICLAASRDLSTSFQESHITVAGNVLADYRSFGFNDTLRSVSV
VDSLLCEQHEDHGILPVSVDIWNMFCASWEPAPTSDICTAEAGGIAAIVSFPGRASPEPR
WHLMLGVSWSYDKTCSHRLSTAFTKVLPLFPKOWIERNMK"

ORIGIN

Query Match		86.7%;	Score 2468;	DB 3;	Length 3165;
Best Local Similarity		99.8%;	Pred. No. 0;		
Matches 2718;		Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;
Qy	1	CGCTCGGCACACAGCGCGGCAAGATGAGCTGGGTTGCTGGACGCAAGTTGGGGCTCAC	60		
Db	422	CGCTCGGCACACAGCGCGGCAAGATGAGCTGGGTTGCTGGACGCAAGTTGGGGCTCAC	481		
Qy	61	TTTTCTTCAGCTCTCTCATCTGCTCTTGTGCAAGAGATACACAGTCATTAATGAAGC	120		
Db	482	TTTTCTTCAGCTCTCTCATCTGCTCTTGTGCAAGAGATACACAGTCATTAATGAAGC	541		
Qy	121	CTGCCCTGAGCAGAGTGAATATCATGTGTCGGAGTGTGTGAATATGATCAGATTGA	180		
Db	542	CTGCCCTGAGCAGAGTGAATATCATGTGTCGGAGTGTGTGAATATGATCAGATTGA	601		
Qy	181	CTGCGTCTGCCCCGAAAGAGAGAAAGTCTGTGGGTTATACCATCCCTTGTGCAAGAAATGA	240		
Db	602	GTGCGTCTGCCCCGAAAGAGAGAAAGTCTGTGGTTATACCATCCCTTGTGCAAGAAATGA	661		
Qy	241	GGAGAAATGAGTGTGATCTGCTGCTGATCCACCAGGTTGTACCATCTTTGAAAACTGCAA	300		
Db	662	GGAGAAATGAGTGTGATCTGCTGCTGATCCACCAGGTTGTACCATCTTTGAAAACTGCAA	721		
Qy	301	GAGCTGCCGAATGCTCATGSGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTA	360		
Db	722	GAGCTGCCGAATGCTCATGSGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTA	781		
Qy	361	CTGTGACAGATGCCGAGCAGGCTGTGACGAGGAGACTGCATGCGATGTGCGCAGGTTCT	420		
Db	782	CTGTGACAGATGCCGAGCAGGCTGTGACGAGGAGACTGCATGCGATGTGCGCAGGTTCT	841		
Qy	421	CGAGCCCCAAGGTCAGATTTGTGTGAAAGCTATCCCTAAATGCTCACTGTGAATG	480		
Db	842	CGAGCCCCAAGGTCAGATTTGTGTGAAAGCTATCCCTAAATGCTCACTGTGAATG	901		
Qy	481	GACCAATTCATGCTAAACCTGGGTTGTTCATCCAACTAAGATTGTGATGAGTCTGGA	540		
Db	902	GACCAATTCATGCTAAACCTGGGTTGTTCATCCAACTAAGATTGTGATGAGTCTGGA	961		
Qy	541	GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTCTGATGAGAGCAACCCGCGATGG	600		
Db	962	GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTCTGATGAGAGCAACCCGCGATGG	1021		
Qy	601	CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCAGCTCTATCCAGAGCATAGGATC	660		
Db	1022	CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCAGCTCTATCCAGAGCATAGGATC	1081		
Qy	661	CTCACTCCAGCGTCTCTTCCACTCCGATGGGTCCTCAAGAAATTTGACGGTTTCCATGCCAT	720		
Db	1082	CTCACTCCAGCGTCTCTTCCACTCCGATGGGTCCTCAAGAAATTTGACGGTTTCCATGCCAT	1141		
Qy	721	TTATGAGGAGATCACAGCATGCTCTCATCCCTTTGTTTCCATGACGCGCAGTGCCTCT	780		
Db	1142	TTATGAGGAGATCACAGCATGCTCTCATCCCTTTGTTTCCATGACGCGCAGTGCCTCT	1201		
Qy	781	TGACAGGCTGGATCTTCAAGTGTGCTGCTTGGCAGGCTATCTAGGCGAGCGCTGTGA	840		
Db	1202	TGACAGGCTGGATCTTCAAGTGTGCTGCTTGGCAGGCTATCTAGGCGAGCGCTGTGA	1261		

Qy	841	AAATCTCTTGAAGAAAGAAACTGCTCAGACCTCGGGGGCCAGTCAATGGGTACAGAA	900		
Db	1262	AAATCTCTTGAAGAAAGAAACTGCTCAGACCTCGGGGGCCAGTCAATGGGTACAGAA	1321		
Qy	901	AATAACAGGGGGCCCTGGGCTTATCAACGGACGCGCATCTCTAAAATTGGCACCGTGGTGC	960		
Db	1322	AATAACAGGGGGCCCTGGGCTTATCAACGGACGCGCATCTCTAAAATTGGCACCGTGGTGC	1381		
Qy	961	TTTTCTTTGTAACTACTCTATGTTCTTAGTGGCAATGAGAAAGAACTTGCACAGAA	1020		
Db	1382	TTTTCTTTGTAACTACTCTATGTTCTTAGTGGCAATGAGAAAGAACTTGCACAGAA	1441		
Qy	1021	TGGAGAGTGGTCAAGGAAACAGCCCATCTGCATAAAAGCCTGCCGAGAACCAAGATTTC	1080		
Db	1442	TGGAGAGTGGTCAAGGAAACAGCCCATCTGCATAAAAGCCTGCCGAGAACCAAGATTTC	1501		
Qy	1081	AGACTGTGTGAGAGAGGAGTCTTTCGATGCAAGGTTCACTCAAGGGAGACACCAATTACA	1140		
Db	1502	AGACTGTGTGAGAGAGGAGTCTTTCGATGCAAGGTTCACTCAAGGGAGACACCAATTACA	1561		
Qy	1141	CCAGCTATCTCAGCGGCTTTCAGCAAGCAGAACTGCAGAGTGGCCCTTACCAAGAGCC	1200		
Db	1562	CCAGCTATCTCAGCGGCTTTCAGCAAGCAGAACTGCAGAGTGGCCCTTACCAAGAGCC	1621		
Qy	1201	AGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTA	1260		
Db	1622	AGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTA	1681		
Qy	1261	TGAGTGCATCTCAACCTTCTACCGCGCTTGGGAGCAGCAGGAGGACATGTCTGAGGAC	1320		
Db	1682	TGAGTGCATCTCAACCTTCTACCGCGCTTGGGAGCAGCAGGAGGACATGTCTGAGGAC	1741		
Qy	1321	TGGAGTGGAGTGGGCGGCGACCATCTGCTGATCCCTATCTCGCGGAAATTTGAGAAAT	1380		
Db	1742	TGGAGTGGAGTGGGCGGCGACCATCTGCTGATCCCTATCTCGCGGAAATTTGAGAAAT	1801		
Qy	1381	CACCTGCTCAAGACCCAAAGGTTGCGCTGCGCTGGCAGGAGGAGCATCTACAGAGGAC	1440		
Db	1802	CACCTGCTCAAGACCCAAAGGTTGCGCTGCGCTGGCAGGAGGAGCATCTACAGAGGAC	1861		
Qy	1441	CAGCGGGTGCATGACCGCAGCCTACAAAGGAGCGTGGTTCCTAGTCTGACGGGTGC	1500		
Db	1862	CAGCGGGTGCATGACCGCAGCCTACAAAGGAGCGTGGTTCCTAGTCTGACGGGTGC	1921		
Qy	1501	CCTGTTGAATCAGCGCAGTGTGGTGGCTGCCACTGTGTTACTGACCTGGGGAAAGT	1560		
Db	1922	CCTGTTGAATCAGCGCAGTGTGGTGGCTGCCACTGTGTTACTGACCTGGGGAAAGT	1981		
Qy	1561	CACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAATTTCTACCGGGATGATGA	1620		
Db	1982	CACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAATTTCTACCGGGATGATGA	2041		
Qy	1621	CCGGGATGAGAAACCATCCAGAGCCTACAGTTCTGCTATCATCTTGCATCCCACTA	1680		
Db	2042	CCGGGATGAGAAACCATCCAGAGCCTACAGTTCTGCTATCATCTTGCATCCCACTA	2101		
Qy	1681	TGACCCCATCTGCTTGAATGCTGATCGCCATCTCTGAAGCTCTTAGACAAAGGCCCGTAT	1740		
Db	2102	TGACCCCATCTGCTTGAATGCTGATCGCCATCTCTGAAGCTCTTAGACAAAGGCCCGTAT	2161		
Qy	1741	CAGCACCGAGTCCAGGCCCATCTGCTCGCTGCCAGTCCGGATCTTCAGCACTTCTTCCA	1800		
Db	2162	CAGCACCGAGTCCAGGCCCATCTGCTCGCTGCCAGTCCGGATCTTCAGCACTTCTTCCA	2221		
Qy	1801	GGAGTCCCAATCATCTGTGGCTGGTGAATGTCTTGGCAGACGCTGAGGAGCCCTGGCTT	1860		
Db	2222	GGAGTCCCAATCATCTGTGGCTGGTGAATGTCTTGGCAGACGCTGAGGAGCCCTGGCTT	2281		
Qy	1861	CAAGAACGACACATCTGGGCTGCTGAGTGTGGTGGACTCGCTGCTGTGTGAGGA	1920		
Db	2282	CAAGAACGACACATCTGGGCTGCTGAGTGTGGTGGACTCGCTGCTGTGTGAGGA	2341		
Qy	1921	GCAGATGAGGACCATGGCATCCCGATGAGTGTCACTGATTAACATGTTCTGTGCGCAGCTG	1980		

Db 2342 GAGCATGAGGACCATGCGATCCCGAGTCAGTGTCTACTATACATGTTCTGTGCCAGTGT 2401
Qy 1981 GGAAACCCACTGCCCCCTTCTGATATCTGCACTGCGAGAGCAGGAGCATCGGGCTGTCTC 2040
Db 2402 GGAACCCACTGCCCTTCTGATATCTGCACTGCGAGAGCAGGAGCATCGGGCTGTCTC 2461
Qy 2041 CTTCCCGGAGCAGCATCTCTGAGCCACGCTGCGATCTGATGCGACTGTGTGAGCTGGAG 2100
Db 2462 CTTCCCGGAGCAGCATCTCTGAGCCACGCTGCGATCTGATGCGACTGTGTGAGCTGGAG 2521
Qy 2101 CTATGATAAACATGCGAGCCACGCTCTCCACTGCGCTTCCACAGGCTGCGCTTTTAA 2160
Db 2522 CTATGATAAACATGCGAGCCACGCTCTCCACTGCGCTTCCACAGGCTGCGCTTTTAA 2581
Qy 2161 AGACTGGATTGAAAGAAATATGAATGAACCATGCTCATGCACTCTTTCGAGAAGTGTTC 2220
Db 2582 AGACTGGATTGAAAGAAATATGAATGAACCATGCTCATGCACTCTTTCGAGAAGTGTTC 2641
Qy 2221 TGTATATCCGCTGTATCTGTGTCTATTCGCTGAAGCAGTGTGGGCTGAAAGTGTGATTG 2280
Db 2642 TGTATATCCGCTGTATCTGTGTCTATTCGCTGAAGCAGTGTGGGCTGAAAGTGTGATTG 2701
Qy 2281 GCCTGTGAACCTTGGCTGTGCCAGGGCTTCTGACTTCAGGGACAAACTCAGTGAAGGCTG 2340
Db 2702 GCCTGTGAACCTTGGCTGTGCCAGGGCTTCTGACTTCAGGGACAAACTCAGTGAAGGCTG 2761
Qy 2341 AGTAGACCTCCATGCTGCTAGGCTGATGCGCGCTCCACTACTAGGACAGCAATGGAA 2400
Db 2762 AGTAGACCTCCATGCTGCTAGGCTGATGCGCGCTCCACTACTAGGACAGCAATGGAA 2821
Qy 2401 GATGCCAGGCTTGCAGAAAGTAACTTCTTCAAAAGAGACATATACAAACCTCTCCA 2460
Db 2822 GATGCCAGGCTTGCAGAAAGTAACTTCTTCAAAAGAGACATATACAAACCTCTCCA 2881
Qy 2461 CTCCACTGACCTGGTGGCTTCTTCCCAACTTTCAGTTATACGATCCATCAGCTTGACCA 2520
Db 2882 CTCCACTGACCTGGTGGCTTCTTCCCAACTTTCAGTTATACGATCCATCAGCTTGACCA 2941
Qy 2521 GGGAAAGATCTGGGCTTCATGAGGCCCTTTTGGAGCTCTCAAGTCTTAGAGAGCTGCCTG 2580
Db 2942 GGGAAAGATCTGGGCTTCATGAGGCCCTTTTGGAGCTCTCAAGTCTTAGAGAGCTGCCTG 3001
Qy 2581 TGGGACACCCAGGCGACAGAGCTGGATGTGGTGCATGCTTGTGTATCATGGCCACA 2640
Db 3002 TGGGACACCCAGGCGACAGAGCTGGATGTGGTGCATGCTTGTGTATCATGGCCACA 3061
Qy 2641 GTACAGTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTTAAATTAAGGCTTG 2700
Db 3062 GTACAGTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTTAAATTAAGGCTTG 3121
Qy 2701 GCTTCTGAACCTACAAAAA 2723
Db 3122 GCTTCTGAACCTACAAAAA 3144

RESULT 2
AF370388
LOCUS AF370388 2650 bp mRNA linear HTC 31-DEC-2003
DEFINITION Homo sapiens FP938 mRNA, complete cds.
ACCESSION AF370388
VERSION AF370388.1 GI:33341705
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2650)
AUTHORS Huang, Y., Zhou, X.M., Zhang, P.P., Jiang, H.Q., Qin, W.X., Zhao, X.T.,
Wan, D.P. and Gu, J.R.
TITLE Novel human cDNA clones with function of inhibiting cancer cell
growth
JOURNAL Unpublished

2 (bases 1 to 2650)
Qin, W.X., Wan, D.P., Zhou, X.M., Zhang, P.P., Jiang, H.Q., Huang, Y.,
Zhao, X.T. and Gu, J.R.
Direct Submission
Submitted (16-APR-2001) National Laboratory For Oncogenes & Related
Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie-Tu Road, Shanghai
200032, P. R. China
FEATURES
source Location/Qualifiers
1. .2650
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
845..2098
/codon_start=1
/product="FP938"
/protein_id="AAQ15224.1"
/db_xref="GI:33341706"
translation="MLKLAPWCLSFVTPMFLVAMRKELASRMRSWKGKOPICIKACR
EPKISDLVRRVLPQVQSRRTCLRTGKMSGRAPSCIPICGKIENITAPKTQGLWQYH
LHTQJQECISPFYRLGSSRRITLRTGKMSGRAPSCIPICGKIENITAPKTQGLWQYH
WQAAIYRTSGVHDSGLHGWFLVCSALNERTVVAHCVHVDLGLKVIKIDALDK
VVLGKPYRDDDDDEKTIQSQISAIILHPNYDPIILDADIAIKLLDARISTRVQPI
CLAASRLSTSFQESHITVAGWNLADVRSPGKNDLTRSGVSVVDLLCEQHEHDH
GIPSVVDNMFCASWEPASDICTAETGGIAAVFPGRASPEPRWHLMLGLVLSWSDYK
TCSHRLSTAFTKVLPFKDWIERNMK"
ORIGIN
Query Match 84.1%; Score 2394; DB 3; Length 2650;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2614; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 93 CAAGAGAGTACACAGTCAATTAATGAAGCCTGCCCTGGAGCAGAGTGAATATCATGTGTC 152
Db 2 CAAGAGAGTACACAGTCAATTAATGAAGCCTGCCCTGGAGCAGAGTGAATATCATGTGTC 61
Qy 153 GGGAGTGTGATATGATCAGATTGAGTGGCTGCGCCGGAAGAGGAGGAGTGTG 212
Db 62 GGGAGTGTGATATGATCAGATTGAGTGGCTGCGCCGGAAGAGGAGGAGTGTG 121
Qy 213 GTTATACCATCCCTTGTGTCAGAGGATGAGGAGATGAGTGTGCTCTGCTGATCCACC 272
Db 122 GTTATACCATCCCTTGTGTCAGAGGATGAGGAGATGAGTGTGCTCTGCTGATCCACC 181
Qy 273 CAGGTGTGACATCTTTGAAACCTGCAAGAGCTGCGGAAATGGCTCATGGGGGGTACCT 332
Db 182 CAGGTGTGACATCTTTGAAACCTGCAAGAGCTGCGGAAATGGCTCATGGGGGGTACCT 241
Qy 333 TGGATGATCTTCTATGTAAGGGGTTCTACTGTCAGAGTGGCGAGCAGGCTGTACGGAG 392
Db 242 TGGATGATCTTCTATGTAAGGGGTTCTACTGTCAGAGTGGCGAGCAGGCTGTACGGAG 301
Qy 393 GAGACTGCATGCGATGTGGCCAGGTTCTGCGAGGCCCAAGGGTCAGATTGTTGTTGAAA 452
Db 302 GAGACTGCATGCGATGTGGCCAGGTTCTGCGAGGCCCAAGGGTCAGATTGTTGTTGAAA 361
Qy 453 GCTATCCCTAAATGCTCAGTGAATGGAACAATTCATGCTGCTAAACCTGGGTTTGTATCC 512
Db 362 GCTATCCCTAAATGCTCAGTGAATGGAACAATTCATGCTGCTAAACCTGGGTTTGTATCC 421
Qy 513 AACTAAGATTGTCATGTTGAGTCTGGAGTTTGACTACATGTCAGTATGATGATGTTG 572
Db 422 AACTAAGATTGTCATGTTGAGTCTGGAGTTTGACTACATGTCAGTATGATGATGTTG 481
Qy 573 AGTTTGTGATGGAGACAAACCGCATGCCAGATCATCAAGCGTGTCTGTGTGCAACGAGC 632
Db 482 AGTTTGTGATGGAGACAAACCGCATGCCAGATCATCAAGCGTGTCTGTGTGCAACGAGC 541
Qy 633 GGCCAGCTCTCTATCCAGAGCATAGATCCTCACTCCAGCTCCTCTTCCATCCCGATGGCT 692
Db 542 GGCCAGCTCTCTATCCAGAGCATAGATCCTCACTCCAGCTCCTCTTCCATCCCGATGGCT 601
Qy 693 CCAAGATTGTCAGGTTTCCATGTCATTTATGAGGATCATCAGCATGCTCTCTATCC 752

Db 602 CCAAGAAATTTTGAAGCTTTCCATGCCATTTATGAGGAGATCACAGCATGCTCTCATCCC 661
Qy 753 CTGTGTTTCCATGACGGCAGCTGCGTCCCTTGACAAAGCTGGAATCTTACAAAGTGTGCTGCT 812
Db 662 CTGTGTTTCCATGACGGCAGCTGCGTCCCTTGACAAAGCTGGAATCTTACAAAGTGTGCTGCT 721
Qy 813 TGGCAGGCTTATCTGGGAGCGCTGTGAAAATCTCTTTGAAGAAAGAAATCTGCTCAGACC 872
Db 722 TGGCAGGCTTATCTGGGAGCGCTGTGAAAATCTCTTTGAAGAAAGAAATCTGCTCAGACC 781
Qy 873 CTGGGGGCCAGTCAATGGGTACAGAAAATAACAGGGGGCCCTGGGCTTATCAACGGAC 932
Db 782 CTGGGGGCCAGTCAATGGGTACAGAAAATAACAGGGGGCCCTGGGCTTATCAACGGAC 841
Qy 933 GCCATGCTTAAATTTGGCACCGTGTGCTTTCTTTTGTAAACATCTTATGTTCTTAGTG 992
Db 842 GCCATGCTTAAATTTGGCACCGTGTGCTTTCTTTTGTAAACATCTTATGTTCTTAGTG 901
Qy 993 GCAATGAGAAAAGAACTTGCAGCAGAGAAATGGAGA-GTGGTCAAGGGAAAACAGCCCATCTGC 1051
Db 902 GCNATGAGAAAAGAACTTGCAGCAGAGAAATGGAGGTGGTCAAGGAAACAGCCCATCTGC 961
Qy 1052 ATAAAGCCTGCGAGAACCAAGATTTCAAGCTTGGTGGAGAGAGTCTTCCGATG 1111
Db 962 ATAAAGCCTGCGAGAACCAAGATTTCAAGCTTGGTGGAGAGAGTCTTCCGATG 1021
Qy 1112 CAGGTTCAAGTCAAGGGAGACCAATTAACAGAGTATATCAAGCGCTTATCAAGCAAGCAG 1171
Db 1022 CAGGTTCAAGTCAAGGGAGACCAATTAACAGAGTATATCAAGCGCTTATCAAGCAAGCAG 1081
Qy 1172 AAATGTCAGAGTGCCCTTACCAAGAGCAGCCCTTCCCTTTTGGAGATCTGCCATGGGA 1231
Db 1082 AAATGTCAGAGTGCCCTTACCAAGAGCAGCCCTTCCCTTTTGGAGATCTGCCATGGGA 1141
Qy 1232 TACCAATCTGCATACCCAGCTCAGATGATGATGATCACTCACTTCTTCAAGCGCGCTG 1291
Db 1142 TACCAATCTGCATACCCAGCTCAGATGATGATGATCACTCACTTCTTCAAGCGCGCTG 1201
Qy 1292 GGCAGCAGAGGAGACATGCTGAGGACTGGAGTGGAGTGGGCGGACCACTCTGC 1351
Db 1202 GGCAGCAGAGGAGACATGCTGAGGACTGGAGTGGAGTGGGCGGACCACTCTGC 1261
Qy 1352 ATCCCTATCTCGGGAAAATTTAGAAACATCACTGCTCCAAAGACCCAAAGGGTGGCGTGG 1411
Db 1262 ATCCCTATCTCGGGAAAATTTAGAAACATCACTGCTCCAAAGACCCAAAGGGTGGCGTGG 1321
Qy 1412 CCGTGGCAGGAGCCATCTACAGAGGACCAAGCGGGGTGCATGACGGCAGCCTACACAAG 1471
Db 1322 CCGTGGCAGGAGCCATCTACAGAGGACCAAGCGGGGTGCATGACGGCAGCCTACACAAG 1381
Qy 1472 GGAGCGTGGTTCCTAGTCTGACGGGTGCCCTGGTGAATGAGCGCACCTGCTGGTGGCT 1531
Db 1382 GGAGCGTGGTTCCTAGTCTGACGGGTGCCCTGGTGAATGAGCGCACCTGCTGGTGGCT 1441
Qy 1532 GCGCACTGTGTTACTGACCTGGGAAGGTCAACCATGATCAAGACAGCAGACCTGAAAGTT 1591
Db 1442 GCGCACTGTGTTACTGACCTGGGAAGGTCAACCATGATCAAGACAGCAGACCTGAAAGTT 1501
Qy 1592 GTTTTGGGAAAATTTCTACCGGGATGATGACCGGGATGAGAGACCAATCCAGAGCCTACAG 1651
Db 1502 GTTTTGGGAAAATTTCTACCGGGATGATGACCGGGATGAGAGACCAATCCAGAGCCTACAG 1561
Qy 1652 ATTTCTGCTATCTGATCTGCATCCCAACTATGACCCCACTGCTGATGCTGATGATCGCC 1711
Db 1562 ATTTCTGCTATCTGATCTGCATCCCAACTATGACCCCACTGCTGATGCTGATGATCGCC 1621
Qy 1712 ATCTCTGAAGCTCTAGACAAAGCCCGTATCAGCACCCGAGTCCAGCCCATCTGCTCGCT 1771
Db 1622 ATCTCTGAAGCTCTAGACAAAGCCCGTATCAGCACCCGAGTCCAGCCCATCTGCTCGCT 1681
Qy 1772 GCGAGTCCGGATCTCAGACATCTCTTCCAGAGTCCCAATCACTGCTGGCTGGGAAT 1831
Db 1682 GCGAGTCCGGATCTCAGACATCTCTTCCAGAGTCCCAATCACTGCTGGCTGGGAAT 1741

Qy 1832 GTCTGGCAGACGCTTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTC 1891
Db 1742 GTCTGGCAGACGCTTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTC 1801
Qy 1892 AGTGTGGTGGACTCGCTGCTGTGTAGGAGCAGCATGAGGACCAATGGCATCCCACTGAGT 1951
Db 1802 AGTGTGGTGGACTCGCTGCTGTGTAGGAGCAGCATGAGGACCAATGGCATCCCACTGAGT 1861
Qy 1952 GTCACTGATAACATGTTCTGTGCCAGCTGGGAAACCCACTGCCCCCTTCTGATATCTGCACT 2011
Db 1862 GTCACTGATAACATGTTCTGTGCCAGCTGGGAAACCCACTGCCCCCTTCTGATATCTGCACT 1921
Qy 2012 GCAGAGACAGCAGGAGCATCGCGCTGTGTCTTCCGGACGAGCATCTCTGAGCCACGC 2071
Db 1922 GCAGAGACAGCAGGAGCATCGCGCTGTGTCTTCCGGACGAGCATCTCTGAGCCACGC 1981
Qy 2072 TGGCATCTGATGGGACTGCTGCTGAGCTGATATGATAAAACATGCAGCCACAGGCTCTCC 2131
Db 1982 TGGCATCTGATGGGACTGCTGCTGAGCTGATATGATAAAACATGCAGCCACAGGCTCTCC 2041
Qy 2132 ACTGCTTCAACAGGCTGCTGCTTTTAAAGACTGGATTTGAAGAAATATGAAATGAACC 2191
Db 2042 ACTGCTTCAACAGGCTGCTGCTTTTAAAGACTGGATTTGAAGAAATATGAAATGAACC 2101
Qy 2192 ATGCTCATGCACTCTTGTGAGAAAGTGTCTGTATATCCGTCTGTACGTGTGTATGCGT 2251
Db 2102 ATGCTCATGCACTCTTGTGAGAAAGTGTCTGTATATCCGTCTGTACGTGTGTATGCGT 2161
Qy 2252 GAAGCAGTGTGGGCTGAAAGTGTGATTTGGCTGTGAACTTTGGCTGTGCCAGGGCTCTG 2311
Db 2162 GAAGCAGTGTGGGCTGAAAGTGTGATTTGGCTGTGAACTTTGGCTGTGCCAGGGCTCTG 2221
Qy 2312 ACTTCAGGGACAAACACTCAGTGAAGGTTGAGTAGACCTCCATTTCTGCTGAGGCTGATGCC 2371
Db 2222 ACTTCAGGGACAAACACTCAGTGAAGGTTGAGTAGACCTCCATTTCTGCTGAGGCTGATGCC 2281
Qy 2372 CGCTCCACTACTAGGACAGCCAAATTTGAAGAGTGCAGGGCTTGCAGAAAGTAAAGTTCTT 2431
Db 2282 AGCTCCACTACTAGGACAGCCAAATTTGAAGAGTGCAGGGCTTGCAGAAAGTAAAGTTCTT 2341
Qy 2432 CAAAGAGACATATACAAAACCTCTCCACTCCACTGACCTGGTGTCTTCCCCAACCTT 2491
Db 2342 CAAAGAGACATATACAAAACCTCTCCACTCCACTGACCTGGTGTCTTCCCCAACCTT 2401
Qy 2492 CAGTTATACGAATGCCATCAGCTTGAACAGGAGAGATCTGGGCTTCATGAGGCCCTTTT 2551
Db 2402 CAGTTATACGAATGCCATCAGCTTGAACAGGAGAGATCTGGGCTTCATGAGGCCCTTTT 2461
Qy 2552 GAGGCTCTCAAGTTCTTAGAGAGCTGCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATG 2611
Db 2462 GAGGCTCTCAAGTTCTTAGAGAGCTGCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATG 2521
Qy 2612 TGGTGCATGCTTTGTGTACATGAGCCACAGTACAGTCTGGTCTTTTCTTCCCCCATCTC 2671
Db 2522 TGGTGCATGCTTTGTGTACATGAGCCACAGTACAGTCTGGTCTTTTCTTCCCCCATCTC 2581
Qy 2672 TTGTACACATTTTAAATAAAGGTTGGCTTCTGA 2708
Db 2582 TTGTACACATTTTAAATAAAGGTTGGCTTCTGA 2618

RESULT 3
AY406074
LOCUS
DEFINITION Homo sapiens HCM2436 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY406074
VERSION
AY406074.1
GI:39762048
KEYWORDS
GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 2214)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 2214)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..2214
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>2214
/locus_tag="HCM2436"
ORIGIN
Query Match 39.7%; Score 1130; DB 9; Length 2214;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1059 C T G C C G A G A A C C A A G A T T T C A G A C C T G G T G A G A A G A G A G T T C T C G A T G C A G G T T C 1118
Db 1085 C T G C C G A G A A C C A A G A T T T C A G A C C T G G T G A G A A G A G A G T T C T C G A T G C A G G T T C 1144
Qy 1119 A G T C A A G G G A G A C A C A T T A C A C C A G T A T A C T C A G C G G C C T T C A G C A A G C A G A A A C T G C 1178
Db 1145 A G T C A A G G G A G A C A C A T T A C A C C A G T A T A C T C A G C G G C C T T C A G C A A G C A G A A A C T G C 1204
Qy 1179 A G A G T C C C T A C C A A G A A G C A G C C C T C C C T T T G G A G A T C T G C C C A T G G A T C C A A C 1238
Db 1205 A G A G T C C C C T A C C A A G A A G C A G C C C T C C C T T T G G A G A T C T G C C C A T G G A T C C A A C 1264
Qy 1239 A T C T C A T A C C C A G T C C A G T A T A G T G C A T C T C A C C C T T T A C C G C G C C T G G C A G C A 1298
Db 1265 A T C T C A T A C C C A G T C C A G T A T A G T G C A T C T C A C C C T T T A C C G C G C C T G G C A G C A 1324
Qy 1299 G C A G A G A C A T G T C T G A G G A C T G G G A A G T G G A G T G G G C G G C A C C A T C C T G C A T C C C T A 1358
Db 1325 G C A G A G A C A T G T C T G A G G A C T G G G A A G T G G A G T G G G C G G C A C C A T C C T G C A T C C C T A 1384
Qy 1359 T C T C G G G A A A T T G A G A A C A T C A T C T G T C A A A G A C C C A A G G T T G C G T G C C G T G G C 1418
Db 1385 T C T C G G G A A A T T G A G A A C A T C A T C T G T C C A A A G A C C C A A G G T T G C G T G C C G T G G C 1444
Qy 1419 A G C A G C A C A T C A C A G G A G C A C G G G T G C A T G C A G C G A C C T A C A C A A G G A G G C G T 1478
Db 1445 A G C A G C A C A T C A C A G G A G C A C G G G T G C A T G C A G C G A C C T A C A C A A G G A G G C G T 1504
Qy 1479 G G T T C C T A G T C T G C A G C G G T C C C T G G T G A A T G A G C G C A C T G T G T G T G G T G C C C A C T 1538
Db 1505 G G T T C C T A G T C T G C A G C G G T C C C T G G T G A A T G A G C G C A C T G T G T G T G G T G C C C A C T 1564
Qy 1539 G T G T T A C T G A C C T G G G A A G T C A C A T G A T C A A G A C A G A C A C C T G A A A G T T G T T T G G 1598
Db 1565 G T G T T A C T G A C C T G G G A A G T C A C A T G A T C A A G A C A G A C C C T G A A A G T T G T T T G G 1624
Qy 1599 G G A A A T T C A C C G G A T G A T G A C C G G A T G A A G A C C A C C A T C A G A G C C T A C A G A T T T C T G 1658
Db 1625 G G A A A T T C A C C G G A T G A T G A C C G G A T G A A G A C C A C C A T C A G A G C C T A C A G A T T T C T G 1684

Qy 1659 C T A T C A T T C T G C A T C C C A A C T A T A T A C C C C A T C T C T G A T G A T G C T G A C A T G C G C A T C C T G A 1718
Db 1685 C T A T C A T T C T G C A T C C C A A C T A T A T A C C C C A T C T C T G A T G A T G C T G A C A T G C G C A T C C T G A 1744
Qy 1719 A G C T C T A G A C A A G C C C G T A T C A C A C C C A G T C A G C C C A T C T G C C T G C G T G C C A G T C 1778
Db 1745 A G C T C T A G A C A A G C C C G T A T C A C A C C C A G T C A G C C C A T C T G C C T G C G T G C C A G T C 1804
Qy 1779 G G G A T C T C A G C A C T T C C T T C C A G G A G T C C C A C A T C A C T G T G G C T G G C T G G A A T G T C C T G G 1838
Db 1805 G G G A T C T C A G C A C T T C C T T C C A G G A G T C C C A C A T C A C T G T G G C T G G C T G G A A T G T C C T G G 1864
Qy 1839 C A G A C T G A G A G C C C T G C T T C A A G A A G A C A C A C A C T G G C T C T G G G T G T G T C A G T G T G G 1898
Db 1865 C A G A C T G A G A G C C C T G C T T C A A G A A C A C A C A C A C T G C G C T C T G G G T G T G T C A G T G T G G 1924
Qy 1899 T G G A C T C C C T G T G T G A G G A G C A G C A T G A G G A C C A T G G C A T C C C A G T G A G T G T C A C A T G 1958
Db 1925 T G G A C T C C C T G T G T G A G G A G C A G C A T G A G G A C C A T G G C A T C C C A G T G A G T G T C A C A T G 1984
Qy 1959 A T A C A T G T T C T G T G C C A G C T G G G A A C C C A C T G C C C C T T C T G A T A T C T G C A C T G C A G A 2018
Db 1985 A T A C A T G T T C T G T G C C A G C T G G G A A C C C A C T G C C C C T T C T G A T A T C T G C A C T G C A G A 2044
Qy 2019 C A G A G G C A T C C G G C T G T G T C C C G G A G A G A C A T C T C C T G A G C C A C C G T G G C A T C 2078
Db 2045 C A G A G G C A T C C G G C T G T G T C C C G G A G A G A C A T C T C C T G A G C C A C C G T G G C A T C 2104
Qy 2079 T G A T G G A C T G T C A G C T G G A C T A T A T A A A C A T G A A A C A T G C A G C A C A G G C T C C A C T G C C T 2138
Db 2105 T G A T G G A C T G T C A G C T G G A C T A T A T A A A C A T G C A G C C A C C A G G C T C C A C T G C C T 2164
Qy 2139 T C A C C A A G G T G T G C C T T T T A A A G A C T G G A T T G A A A G A A A T A T A A A T G A 2188
Db 2165 T C A C C A A G G T G T G C C T T T T A A A G A C T G G A T T G A A A G A A A T A T A A A T G A 2214
RESULT 4
BX337780/c
LOCUS BX337780 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1051YA20 3-PRIME, mRNA sequence.
ACCESSION BX337780
VERSION BX337780.2 GI:46266544
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 1, 2003 this sequence version replaced gi:30312629.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5757.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0D1051BALONP1&c=5757.r.
Location/Qualifiers
1..1100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1051YA20"
/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN	Query Match Best Local Similarity 31.2%; Score 889; DB 5; Length 1100; Matches 939; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1722 TCCTAGACAGGCCCGTATCAGCACCCGAGTCACGCCCATCTGCTCGCTGCCAGTCGGG 1781
Db	962 TCCTAGACAGGCCCGTATCAGCACCCGAGTCACGCCCATCTGCTCGCTGCCAGTCGGG 903
QY	1782 ATCTCAGACATCTCTTCCAGGAGTCCACATCATCTGCTGGCTGGGAATGTCCTGGCAG 1841
Db	902 ATCTCAGACATCTCTTCCAGGAGTCCACATCATCTGCTGGCTGGGAATGTCCTGGCAG 843
QY	1842 ACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGCTGCTCAGTGTGGTG 1901
Db	842 ACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGCTGCTCAGTGTGGTG 783
QY	1902 ACTGCTCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGGTGTCTCACTGATA 1961
Db	782 ACTGCTCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGGTGTCTCACTGATA 723
QY	1962 ACATGTTCTGTGCGAGCTGGGAACCCACTGCCCCCTTCTGATATCTGCACTGCAGAGAC 2021
Db	722 ACATGTTCTGTGCGAGCTGGGAACCCACTGCCCCCTTCTGATATCTGCACTGCAGAGAC 663
QY	2022 GAGGCATCGCGCTGTGCTTCCCGGACGAGCATCTCCTGAGCCACGCTGGCATCTGA 2081
Db	662 GAGGCATCGCGCTGTGCTTCCCGGACGAGCATCTCCTGAGCCACGCTGGCATCTGA 603
QY	2082 TGGGACTGGTCTGAGTGTGATGATAAAACATGACGACACAGGCTCTCCACTGCTTCA 2141
Db	602 TGGGACTGGTCTGAGTGTGATGATAAAACATGACGACACAGGCTCTCCACTGCTTCA 543
QY	2142 CCAAGTCTGCTTTTAAAGACTGGATTGAAAGAAATATGAATGAACCATGCTCATGC 2201
Db	542 CCAAGTCTGCTTTTAAAGACTGGATTGAAAGAAATATGAATGAACCATGCTCATGC 483
QY	2202 ACTCCTTCAGAAAGTGTCTGTATATCGTCTGTACGTGTGTCATTTGGTGAAGCAGTGT 2261
Db	482 ACTCCTTCAGAAAGTGTCTGTATATCGTCTGTACGTGTGTCATTTGGTGAAGCAGTGT 423
QY	2262 GGGCTGAAGTGTGATTTGGCTGTGAACTTGGCTGTGCCAGGGCTTCTGACTTCAGGGA 2321
Db	422 GGGCTGAAGTGTGATTTGGCTGTGAACTTGGCTGTGCCAGGGCTTCTGACTTCAGGGA 363
QY	2322 CAAGACTCAGTGAAGGGTGAAGTACCTCCATTGCTGTAGCTGATGCCGGTCCACTA 2381
Db	362 CAAGACTCAGTGAAGGGTGAAGTACCTCCATTGCTGTAGCTGATGCCGGTCCACTA 303
QY	2382 CTAGGACAGCAATTTGGAAGATGCGAGGGCTTGCAAGAAAGTAAAGTTCTTCAAGAAAGAC 2441
Db	302 CTAGGACAGCAATTTGGAAGATGCGAGGGCTTGCAAGAAAGTAAAGTTCTTCAAGAAAGAC 243
QY	2442 CATATACAAAACCTTCCACTCCACTGACCTGGTGTCTTCCCAACTTTTCAAGTTATACG 2501
Db	242 CATATACAAAACCTTCCACTCCACTGACCTGGTGTCTTCCCAACTTTTCAAGTTATACG 183
QY	2502 AATGCCATCAGCTTGACGAGGAGATCTGGGCTTCATGAGGCCCTTTTGAAGCTTCA 2561
Db	182 AATGCCATCAGCTTGACGAGGAGATCTGGGCTTCATGAGGCCCTTTTGAAGCTTCA 123
QY	2562 AGTTCTAGAGAGTGCCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGC 2621
Db	122 AGTTCTAGAGAGTGCCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGC 63
QY	2622 CTTTGTGTACATGCCACAGTACAGTCTGGTCTTTTCTT 2661

Db	62 CTTTGTGTACATGCCACAGTACAGTCTGTGCTTTTCTCT 23
RESULT 5	
LOCUS	BX434191/c
DEFINITION	BX434191 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DB009YD01
ACCESSION	BX434191
VERSION	BX434191.2
KEYWORDS	3-PRIME, mRNA sequence.
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	1 (bases 1 to 897)
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	On May 15, 2003 this sequence version replaced gi:30775248. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5757.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0BAK025BH09NM1&c=5757.r.
FEATURES	Location/Qualifiers
source	1. .897 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DB009YD01" /tissue_type="PLACENTA" /clone_lib="Homo sapiens PLACENTA" /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
ORIGIN	
Query Match	27.6%; Score 786; DB 5; Length 897;
Best Local Similarity	99.9%; Pred. No. 0;
Matches	836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1861 CAAGAACGACACACTGGGCTCTGGGCTGCTCAGTGTGGTGGACTGCTGCTGTGAGGA 1920
Db	845 CAAGAACGACACACTGGGCTCTGGGCTGCTCAGTGTGGTGGACTGCTGCTGTGAGGA 786
QY	1921 GCAGCATGAGGACCATGGCATCCAGTGGTGTCTGATTAACATGTTCTGTGCCAGCTG 1980
Db	785 GCAGCATGAGGACCATGGCATCCAGTGGTGTCTGATTAACATGTTCTGTGCCAGCTG 726
QY	1981 GGAACCCACTGCCCTTCTGATATCTGCATCTGCAGAGACAGAGGCATCGCGGCTGTGTC 2040
Db	725 GGAACCCACTGCCCTTCTGATATCTGCATCTGCAGAGACAGAGGCATCGCGGCTGTGTC 666
QY	2041 CTTCCGGGAGAGCATCTCTGAGCCACGCTGGCATCTGATGGAGCTGGTCAAGCTGGAG 2100
Db	665 CTTCCGGGAGAGCATCTCTGAGCCACGCTGGCATCTGATGGAGCTGGTCAAGCTGGAG 606
QY	2101 CTATGATAAACAATGACAGCCACAGGCTCTCCACTGCTTACCAAGGTCGCTGCTTTTAA 2160
Db	605 CTATGATAAACAATGACAGCCACAGGCTCTCCACTGCTTACCAAGGTCGCTGCTTTTAA 546
QY	2161 AGACTGGATTGAAAGAAATATGAATGAACCATGCTCATGCACTCTTGTGAGAGTGTTC 2220

Db 492 GGAGACACATTACACAGCTATATCTCAGCGCCTTCAGCAAGCAGAGAACTGCAGAGTGC 551
Qy 1186 CCCTACCAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGATACCAACATCTGCA 1245
Db 552 CCCTACCAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGATACCAACATCTGCA 611
Qy 1246 TACCAGCTCCAGTATGAGTGCATCTCACCCCTTCTACCGCGCCCTGGGCGAGCAGCAGGAG 1305
Db 612 TACCAGCTCCAGTATGAGTGCATCTCACCCCTTCTACCGCGCCCTGGGCGAGCAGCAGGAG 671
Qy 1306 GACATGCTGAGGACTCGGAAGTGAAGTGGGGCGGACCACTCTGCACTCCCTATCTGCGG 1365
Db 672 GACATGCTGAGGACTCGGAAGTGAAGTGGGGCGGACCACTCTGCACTCCCTATCTGCGG 731
Qy 1366 GAAA 1369
Db 732 GAAA 735

RESULT 7
BX399905
LOCUS BX399905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1086Y021 5-PRIME, mRNA sequence.
ACCESSION BX399905
VERSION BX399905.2 GI:46876619
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1049)
Li W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30622029.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5757.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1086AH1QPI&c=5757.r.

FEATURES
source
1. 1049
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1086Y021"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 24.8%; Score 706; DB 5; Length 1049;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 756; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 GCCCGGCAAGGATGAGCTGGTTCGCGAGCGAGTGGGGCTCACATTTTCTTCAGCTC 73
Db 1 GCCCGGCAAGGATGAGCTGGTTCGCGAGCGAGTGGGGCTCACATTTTCTTCAGCTC 60
Qy 74 CTTCTCATCTCGTCTGCCAAGAGATACACAGTCATTATGAAGCTGCCCTGGAGCA 133

Db 61 CTTCTCATCTCGTCTGCCAAGAGATACACAGTCATTATGAAGCTGCCCTGGAGCA 120
Qy 134 GAGTGGAAATATCATGTGTCGGGAGTGTCTGCAATATGATCATGATTGAGTGGCTCTGCCCC 193
Db 121 GAGTGGAAATATCATGTGTCGGGAGTGTCTGCAATATGATCATGATTGAGTGGCTCTGCCCC 180
Qy 194 GGAAAGAGGGGAAGTCGTGGGTATACCATCCCTTCTGTCAGGAAATGAGGAGAATGAGTGT 253
Db 181 GGAAAGAGGGGAAGTCGTGGGTATACCATCCCTTCTGTCAGGAAATGAGGAGAATGAGTGT 240
Qy 254 GACTCTCGCTGATTCACCCAGGTTGTACCACTTTTGAATACTGCAAGAGCTGCCGAAT 313
Db 241 GACTCTCGCTGATTCACCCAGGTTGTACCACTTTTGAATACTGCAAGAGCTGCCGAAT 300
Qy 314 GGCTCATGGGGGGGTACCTTCGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGC 373
Db 301 GGCTCATGGGGGGGTACCTTCGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGC 360
Qy 374 CGAGCAGGCTGGTACGGAGGAGACTGCAATGCGATGTGGCCAGGTTCTCGAGGCCCAAG 433
Db 361 CGAGCAGGCTGGTACGGAGGAGACTGCAATGCGATGTGGCCAGGTTCTCGAGGCCCAAG 420
Qy 434 GGTGAGATTTTGTGGAAAGCTATCCCTAAATGCTACTGTGATGAGCAATTCATGCT 493
Db 421 GGTGAGATTTTGTGGAAAGCTATCCCTAAATGCTACTGTGATGAGCAATTCATGCT 480
Qy 494 AAACCTGGTTTGTCAATCCAACTAAGATTTCTGATGTTGAGTCTGGAGTTTGACTACATG 553
Db 481 AAACCTGGTTTGTCAATCCAACTAAGATTTCTGATGTTGAGTCTGGAGTTTGACTACATG 540
Qy 554 TGCCAGTATGACTATGTTGAGTTCGTGATGGAGACAACCCGATGGCCAGATCATCAAG 613
Db 541 TGCCAGTATGACTATGTTGAGTTCGTGATGGAGACAACCCGATGGCCAGATCATCAAG 600
Qy 614 CGTGTCTGTCGCAAGAGCGGCCAGCTCTTATCCAGAGCATAGGATCTCACTCCAGCTC 673
Db 601 CGTGTCTGTCGCAAGAGCGGCCAGCTCTTATCCAGAGCATAGGATCTCACTCCAGCTC 660
Qy 674 CTCCTTCCACTCCGATGGCTCCAAAGATTTTCCAGCGTTTCCATGCCATTTATGAGGAGATC 733
Db 661 CTCCTTCCACTCCGATGGCTCCAAAGATTTTCCAGCGTTTCCATGCCATTTATGAGGAGATC 720
Qy 734 ACAGCATGCTCTCATCCCTTGTTCATGACCGCA 770
Db 721 ACAGCATGCTCTCATCCCTTGTTCATGACCGCA 757

RESULT 8
BX399904/c

LOCUS BX399904 1008 bp mRNA linear EST 29-APR-2004
DEFINITION BX399904 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1086Y021 3-PRIME, mRNA sequence.
ACCESSION BX399904
VERSION BX399904.2 GI:46874780
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1008)
Li W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30622027.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster

5757.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?sa=CS0DI086AH11NP1&c=5757.r.

FEATURES
Location/Qualifiers
1..1008
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI086Y021"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 24.3%; Score 691; DB 5; Length 1008;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 791; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1869 ACACACTGCGCTCTGGGTGGTCACTGTGGTCACTCGCTGCTGTGTGAGGAGCAGCATG 1928
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 815 ACACACTGCGCTCTGGGTGGTCACTGTGGTCACTCGCTGCTGTGTGAGGAGCAGCATG 756
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1929 AGGACCATGGCATCCAGTGAAGTGTCACTGATPAACATGTTCTGTGCCAGCTGGGAACCCA 1988
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 755 AGGACCATGGCATCCAGTGAAGTGTCACTGATPAACATGTTCTGTGCCAGCTGGGAACCCA 696
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1989 CTGCCCCCTTCGATATCTGCACTGAGAGACAGGAGGAGGATCGCGCTGTCTTCCCGG 2048
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 695 CTGCCCCCTTCGATATCTGCACTGAGAGACAGGAGGAGGATCGCGCTGTCTTCCCGG 636
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2049 GACGAGCATCTCTGAGCAGCAGCTGGCATCTGATGGACTGTGAGTGGAGCTATGATA 2108
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 635 GACGAGCATCTCTGAGCAGCAGCTGGCATCTGATGGACTGTGAGTGGAGCTATGATA 576
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2109 AAACATGAGCCACAGGCTCTCCACTGCTTCCACCAAGGTGCTGCTTTTAAAGACTGGA 2168
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 575 AAACATGAGCCACAGGCTCTCCACTGCTTCCACCAAGGTGCTGCTTTTAAAGACTGGA 516
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2169 TTGAAGAAATATGAATGAACCATCTGCTGCTTCCACCAAGGTGCTGCTTTTAAAGACTGGA 2228
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 515 TTGAAGAAATATGAATGAACCATCTGCTGCTTCCACCAAGGTGCTGCTTTTAAAGACTGGA 456
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2229 CGTCTGACGTGTGTCATTGGTGAAGCAGTGTGGCTGGAAGTGTGATTTGGCCCTGTGA 2288
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 455 CGTCTGACGTGTGTCATTGGTGAAGCAGTGTGGCTGGAAGTGTGATTTGGCCCTGTGR 396
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2289 ACTTGGCTGTGTCAGGGCTTCTGACTTCAGGGACAAACTCAGTGAAGGGTGAAGTAC 2348
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 395 ACTTGGCTGTGTCAGGGCTTCTGACTTCAGGGACAAACTCAGTGAAGGGTGAAGTAC 336
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2349 TCCATGTGTGATGCTGATGCGCGTCTCACTACTAGAGAGCCAAATGGAGATGCCAG 2408
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 335 TCCATGTGTGATGCTGATGCGCGTCTCACTACTAGAGAGCCAAATGGAGATGCCAG 276
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2409 GGTCTGCAAGAGTAAAGTCTTCAAGAGAGACCATATACAAACCTCTCCACTCCACTG 2468
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 275 GGTCTGCAAGAGTAAAGTCTTCAAGAGAGACCATATACAAACCTCTCCACTCCACTG 216
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2469 ACCTGGTGTCTTCCCAACTTTCAGTTATAGAAATGCGCATCAGCTTGACAGGGAAGAT 2528
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 215 ACCTGGTGTCTTCCCAACTTTCAGTTATAGAAATGCGCATCAGCTTGACAGGGAAGAT 156
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2529 CTGGGCTTCATGAGGCGCCCTTTTGAAGCTCTCAAGTCTTAGAGAGCTGCTGTGGGACAG 2588
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 155 CTGGGCTTCATGAGGCGCCCTTTTGAAGCTCTCAAGTCTTAGAGAGCTGCTGTGGGACAG 96
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2589 CCCAGGCGAGAGCTGGAGTGTGCTGATGCTCTTTGTGTACATGGCCACAGATACATC 2648
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 95 CCCAGGCGAGAGCTGGAGTGTGCTGATGCTCTTTGTGTACATGGCCACAGATACATC 36
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 2649 TGGTCCCTTTTCCT 2661
Db |||||||||||||||||||
35 TGGTCCCTTTTCCT 23

RESULT 9
CD514783 879 bp mRNA linear EST 06-JUN-2003
LOCUS
DEFINITION
AGNCOURT 14376424 NIH MGC 181 Homo sapiens cDNA clone
IMAGE:30396311 5', mRNA sequence.
CD514783
ACCESSION
CD514783.1 GI:31446501
VERSION
EST.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 879)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgsbbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: NDAM477 row: m column: 24
High quality sequence stop: 613.
Location/Qualifiers
1..879
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30396311"
/tissue_type="White Matter"
/dev_stage="Unknown"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/note="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV
(destroyed); Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.42 kb. Library was constructed by
(Invitrogen). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 24.1%; Score 685; DB 6; Length 879;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 785; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 952 CGTGTGTCTTTCTTTTGTAACTCTATGTTCTTAGTGGCAATGAGAAAGAACTTG 1011
Db |||||||GTCCTTTTGTAACTCTCTATGTTCTTAGTGGCAATGAGAAAGAACTTG 60
1 CGTGTGTCTTTCTTTTGTAACTCTCTATGTTCTTAGTGGCAATGAGAAAGAACTTG 60
Qy 1012 CCAGCAGATGGAGTGGTCAGGGAACAGCCCATCTGCATATAAGCTGCCGAGAAC 1071
Db |||||||GAGTGGTCAGGGAACAGCCCATCTGCATATAAGCTGCCGAGAAC 120
61 CCAGCAGATGGAGTGGTCAGGGAACAGCCCATCTGCATATAAGCTGCCGAGAAC 120
Qy 1072 AAAGATTTACACCTGGTGAAGAGAGTCTTCCGATGCAAGTTCAGTCAAGGAGAC 1131
Db |||||||TACACCTGGTGAAGAGAGTCTTCCGATGCAAGTTCAGTCAAGGAGAC 1131
121 AAAGATTTACACCTGGTGAAGAGAGTCTTCCGATGCAAGTTCAGTCAAGGAGAC 180
Qy 1132 ACCATTACACAGCTATATCTCAGCGGCTTCAGCAAGCAGAACTGCAGAGTGCCTTAC 1191
Db |||||||TACACAGCTATATCTCAGCGGCTTCAGCAAGCAGAACTGCAGAGTGCCTTAC 240
181 ACCATTACACAGCTATATCTCAGCGGCTTCAGCAAGCAGAACTGCAGAGTGCCTTAC 240
Qy 1192 CAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCA 1251
Db |||||||AAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCA

ACCESSION B0014545
VERSION B0014545.1 GI:19739446
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE 1 (bases 1 to 723)
JOURNAL NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

1..723 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5833419"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP ED1"
/note="Organ: Left Pubic Bone; Vector: p7T73-Pac
(Pharmacia) with a modified polylinker; Site 1: Ecor I;
Site 2: Not I; NCI CGAP ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C55. The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an Ecor I adaptor, digested with Not
I, and cloned directionally into p7T73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG TISSUE=chondrosarcoma
TAG_L1IB=UI-H-ED1
TAG_SEQ=CGTCAAGGCT"

ORIGIN

Query Match 23.6%; Score 672; DB 5; Length 723;
Best Local Similarity 99.9%; Pred. No. 1.8e-313;
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2007 GCATGCGAGACAGAGGACATCGCGGTGTGCTCTCCCGGAGCAGACATCTCTGTAGC 2066
Db 723 GCATGCGAGACAGAGGACATCGCGGTGTGCTCTCCCGGAGCAGACATCTCTGTAGC 664
Qy 2067 CACGCTGCATCTGATGGAGCTGCTCAGCTGGAGCTATGATTAACATGCGAGCCACAGGC 2126
Db 663 CACGCTGCATCTGATGGAGCTGCTCAGCTGGAGCTATGATTAACATGCGAGCCACAGGC 604
Qy 2127 TCTCCACTGCCTTACCAAGGTGCTGCTTTTAAAGACTGGATTGAAAGAAATATGAAT 2186
Db 603 TCTCCACTGCCTTACCAAGGTGCTGCTTTTAAAGACTGGATTGAAAGAAATATGAAT 544
Qy 2187 GAACCATGCTCATGCACTCTTGTGAGAGTGTTCGTATATCCGCTGTACGTGTGTCAT 2246
Db 543 GAACCATGCTCATGCACTCTTGTGAGAGTGTTCGTATATCCGCTGTACGTGTGTCAT 484
Qy 2247 TCGTGAAGCAGTGTGGCCCTGAAGTGTGATTTGGCCCTGTGAATTCGCTGTGCCAGGC 2306

Db 483 TCGTGAAGCAGTGTGGCCCTGAAGTGTGATTTGGCCCTGTGAATTCGCTGTGCCAGGC 424
Qy 2307 TTCTGACTTCAGGAGCAAAACTCAGTGAAGGTTGAGTAGACCTCCATTCGCTGTGAGGCTG 2366
Db 423 TTCTGACTTCAGGAGCAAAACTCAGTGAAGGTTGAGTAGACCTCCATTCGCTGTGAGGCTG 364
Qy 2367 ATGCGCGCTCCACTACTAGGACAGCAATTTGAAGATGCCAGGCTTCGAGAAGTAAGT 2426
Db 363 ATGCCACGTCCTCACTACTAGGACAGCAATTTGAAGATGCCAGGCTTCGAGAAGTAAGT 304
Qy 2427 TTCTTCAAGAGAACCATATACAAACCTCTCCACTCCACTGACCTGGTGTCTTCCCCA 2486
Db 303 TTCTTCAAGAGAACCATATACAAACCTCTCCACTCCACTGACCTGGTGTCTTCCCCA 244
Qy 2487 ACTTTCAGTTATACGAATGCCATCAGCTTGACAGGGAAGATCTGGGCTTCATGAGGCC 2546
Db 243 ACTTTCAGTTATACGAATGCCATCAGCTTGACAGGGAAGATCTGGGCTTCATGAGGCC 184
Qy 2547 CTTTGTAGGCTCTCAAGTCTTAGAGAGCTGCTGTGGACAGCCAGGCGGACAGAGCTG 2606
Db 183 CTTTGTAGGCTCTCAAGTCTTAGAGAGCTGCTGTGGACAGCCAGGCGGACAGAGCTG 124
Qy 2607 GGATGTGTGTCATGCTCTTTGTGTATCATGGCCACAGTACAGTCTGCTCTTTCTTCCCC 2666
Db 123 GGATGTGTGTCATGCTCTTTGTGTATCATGGCCACAGTACAGTCTGCTCTTTCTTCCCC 64
Qy 2667 ATCTCTTGTACACATTTTAAATAAATAGGCTTGGCTTCTGAACCTACAAAAA 2726
Db 63 ATCTCTTGTACACATTTTAAATAAATAGGCTTGGCTTCTGAACCTACAAAAA 4
Qy 2727 AAA 2729
Db 3 AAA 1
RESULT 12
BX337781 886 bp mRNA linear EST 07-APR-2004
LOCUS BX337781 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSODI051YA20 5-PRIME, mRNA sequence.
ACCESSION BX337781.2 GI:46268407
VERSION BX337781.2
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT On May 2, 2003 this sequence version replaced gi:30333640.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segret@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5757.r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CSODI051BA10QPI&c=5757.r>.
FEATURES
source
1..886
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI051YA20"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN									
Query Match 22.7%; Score 647; DB 5; Length 886; Best Local Similarity 99.8%; Pred. No. 1.9e-301; Matches 817; Conservative 0; Mismatches 1; Indels 1; Gaps 1									
Qy	1	CGCTCGGGCACCAGCGCGGCAAGGATGGAGCTGGGTGCTGGACGCGAGTTGGGGCTCAC	60						
Db	38	CGCTCGGGCACCAGCGCGGCAAGGATGGAGCTGGGTGCTGGACGCGAGTTGGGGCTCAC	97						
Qy	61	TTTTCTTCAGCTCCTTCATCTCGTCCCTGCCAAGAGAGTACACAGTCATTAAATGAAGC	120						
Db	98	TTTTCTTCAGCTCCTTCATCTCGTCCCTGCCAAGAGAGTACACAGTCATTAAATGAAGC	157						
Qy	121	CTGCCCTGGAGCAGAGTGGAAATATCATGTGTGGGAGTGTGTGAATATGATCAGATTGA	180						
Db	158	CTGCCCTGGAGCAGAGTGGAAATATCATGTGTGGGAGTGTGTGAATATGATCAGATTGA	217						
Qy	181	GTGGCTCTGCCCGGAAAGAGGGAAAGTCGTGGGTTATACCAATCCCTTGCTCGAGGAATGA	240						
Db	218	GTGGCTCTGCCCGGAAAGAGGGAAAGTCGTGGGTTATACCAATCCCTTGCTCGAGGAATGA	277						
Qy	241	GGAAATGAGTGTGACTCCTCGCTGATCCACCCAGGTGTACCACTCTTTGAAAACCTGCAA	300						
Db	278	GGAAATGAGTGTGACTCCTCGCTGATCCACCCAGGTGTACCACTCTTTGAAAACCTGCAA	337						
Qy	301	GAGCTGCCGAAATGGCTCATCGGGGGGTACCTTGATGACTTCTATGTGAAGGGGTTCTTA	360						
Db	338	GAGCTGCCGAAATGGCTCATCGGGGGGTACCTTGATGACTTCTATGTGAAGGGGTTCTTA	397						
Qy	361	CTGTGCAGAGTCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTGSCCAGGTTCT	420						
Db	398	CTGTGCAGAGTCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTGSCCAGGTTCT	457						
Qy	421	GCGAGCCCCAAAGGGTCAGATTTTGTGGAAAGCTATCCCCCTAAATGCTCACTGTGATG	480						
Db	458	GCGAGCCCCAAAGGGTCAGATTTTGTGGAAAGCTATCCCCCTAAATGCTCACTGTGATG	517						
Qy	481	GACCAATCATGCTAAACCT--GGGTTTGTCACTCAACCTAAAGATTTGTCAATGTTGAGTCTGG	539						
Db	518	GACCAATCATGCTAAACCTGGGGTTTGTCACTCAACCTAAAGATTTGTCAATGTTGAGCTTGG	577						
Qy	540	AGTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTTCGTGATGGAGACAAACCGCGATG	599						
Db	578	AGTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTTCGTGATGGAGACAAACCGCGATG	637						
Qy	600	GCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATTCAGAGCATAGAT	659						
Db	638	GCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATTCAGAGCATAGAT	697						
Qy	660	CCTCACCTCCAGTCTCTTCCACATCCGATGCTCCAGAAATTTTGAAGGTTTCCATGCCA	719						
Db	698	CCTCACCTCCAGTCTCTTCCACATCCGATGCTCCAGAAATTTTGAAGGTTTCCATGCCA	757						
Qy	720	TTTTATGAGGAGATCACAGCATGCTCCTCATCCCCCTTGTTTCCATGACGCGACGTGCGTCC	779						
Db	758	TTTTATGAGGAGATCACAGCATGCTCCTCATCCCCCTTGTTTCCATGACGCGACGTGCGTCC	817						
Qy	780	TTGACAAGGCTGGATCTTTACAAGTGTGCTGCTGGCAG	818						
Db	818	TTGACAAGGCTGGATCTTTACAAGTGTGCTGCTGGCAG	856						

KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 645)	
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.	
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery	
JOURNAL	Genome Res. 6 (9), 791-806 (1996)	
MEDLINE	97044477	
PUBMED	8889548	
COMMENT	Contact: Soares, MB Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: bento-soares@uiowa.edu Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa cDNA sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com/). Seq primer: M13 Reverse. Location/Qualifiers 1. .645	
FEATURES		
SOURCE		

ORIGIN

[illegible]

QY 2274 TGATTTGGCTGTGAACCTTGGCTGTGGCCAGGGCTTCTGACTTCAGGGACAAACCTCAGTG 2333
Db |||||
QY 181 TGATTTGGCTGTGAACCTTGGCTGTGGCCAGGGCTTCTGACTTCAGGGACAAACCTCAGTG 240
Db |||||
QY 2334 AAGGGTGAAGTACAGCTCCATTCGTGTAGGCTGTGGCCGCTCCTACTAGGACAGCCA 2393
Db |||||
QY 241 AAGGGTGAAGTACAGCTCCATTCGTGTAGGCTGTGGCCGCTCCTACTAGGACAGCCA 300
Db |||||
QY 2394 ATTGAAGATGTCAGGGCTTGCAGGAAGTAAGTTCTTCAAGAAGACCATATACAAAC 2453
Db |||||
QY 301 ATTGAAGATGTCAGGGCTTGCAGGAAGTAAGTTCTTCAAGAAGACCATATACAAAC 360
Db |||||
QY 2454 CTCTCCACTCCAGTACAGCTGTGGCTTCCCAACTTCAGTTATACGAATCCATCAGC 2513
Db |||||
QY 361 CTCTCCACTCCAGTACAGCTGTGGCTTCCCAACTTCAGTTATACGAATCCATCAGC 420
Db |||||
QY 2514 TTGACCGGAGATCTGGCTTCATGAGGCCCTTTGAGGCTCTCAAGTTCTAGAGAG 2573
Db |||||
QY 421 TTGACCGGAGATCTGGCTTCATGAGGCCCTTTGAGGCTCTCAAGTTCTAGAGAG 480
Db |||||
QY 2574 CTGCTGTGGACAGCCAGGCGCAGAGCTGGGATGTGTGCATGCTTTGTGTACAT 2633
Db |||||
QY 481 CTGCTGTGGACAGCCAGGCGCAGAGCTGGGATGTGTGCATGCTTTGTGTACAT 540
Db |||||
QY 2634 GGCCACAGTACAGTCTGGCTCTTTTCCCTCCCATCTCTGTGACACATTTAATAAATA 2693
Db |||||
QY 541 GGCCACAGTACAGTCTGGCTCTTTTCCCTCCCATCTCTGTGACACATTTAATAAATA 600
Db |||||
QY 2694 AGGGTTGGCTTCTGAACTACAAAAAATAAATAAATAAATAAATAAATAAATA 2733
Db |||||
QY 601 AGGGTTGGCTTCTGAACTACAAAAAATAAATAAATAAATAAATAAATAAATA 640
Db |||||

RESULT 14
BM930545
LOCUS
DEFINITION
UI-E-EJ1-ajm-e-22-0-UI-r1 UI-E-EJ1 Homo sapiens cDNA clone
UI-E-EJ1-ajm-e-22-0-UI 5', mRNA sequence.
ACCESSION
BM930545
VERSION
BM930545.1 GI:19389718
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 645)
AUTHORS
Bonaldo, M.P., Lennon, G. and Soares, M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
PUBMED
8889548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 REVERSE.
Location/Qualifiers
1. .645
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ1-ajm-e-22-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,"

ORIGIN

Query Match 22.5%; Score 640; DB 5; Length 645;
Best Local Similarity 100.0%; Pred. No. 4.8e-298;
Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2094 GCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCACTGCTTCCACGAGGTGCTGC 2153
Db ||||| 1 GCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCACTGCTTCCACGAGGTGCTGC 60
QY 2154 CTTTAAAGACTGGATTGAAAAGAAATATGAATGAACCATGCTCATGCACCTCTTTGAGAA 2213
Db ||||| 61 CTTTAAAGACTGGATTGAAAAGAAATATGAATGAACCATGCTCATGCACCTCTTTGAGAA 120
QY 2214 GTGTTTCTGTATATCCGCTGTAGCTGTGTCTATTCGCTGAAGAGCATGTGGGCTGAAGTG 2273
Db ||||| 121 GTGTTTCTGTATATCCGCTGTAGCTGTGTCTATTCGCTGAAGAGCATGTGGGCTGAAGTG 180
QY 2274 TGATTTGGCTGTGAACCTTGGCTGTGGCCAGGGCTTCTGACTTCAGGGACAAACCTCAGTG 2333
Db ||||| 181 TGATTTGGCTGTGAACCTTGGCTGTGGCCAGGGCTTCTGACTTCAGGGACAAACCTCAGTG 240
QY 2334 AAGGGTGAAGTACAGCTCCATTCGTGTAGGCTGTAGTCCGCTCCACTACTAGGACAGCCA 2393
Db ||||| 241 AAGGGTGAAGTACAGCTCCATTCGTGTAGGCTGTAGTCCGCTCCACTACTAGGACAGCCA 300
QY 2394 ATTGAAGATGCCAGGGCTTGCAGGAAGTAAGTTCTTCAAGAAGACCATATACAAAC 2453
Db ||||| 301 ATTGAAGATGCCAGGGCTTGCAGGAAGTAAGTTCTTCAAGAAGACCATATACAAAC 360
QY 2454 CTCTCCACTCCAGTACAGCTGTGGCTTCCCAACTTCAGTTATACGAATCCATCAGC 2513
Db ||||| 361 CTCTCCACTCCAGTACAGCTGTGGCTTCCCAACTTCAGTTATACGAATCCATCAGC 420
QY 2514 TTGACCGGAGATCTGGCTTCATGAGGCCCTTTGAGGCTCTCAAGTTCTAGAGAG 2573
Db ||||| 421 TTGACCGGAGATCTGGCTTCATGAGGCCCTTTGAGGCTCTCAAGTTCTAGAGAG 480
QY 2574 CTGCTGTGGACAGCCAGGCGCAGAGCTGGGATGTGTGCATGCTTTGTGTACAT 2633
Db ||||| 481 CTGCTGTGGACAGCCAGGCGCAGAGCTGGGATGTGTGCATGCTTTGTGTACAT 540
QY 2634 GGCCACAGTACAGTCTGGCTCTTTTCCCTCCCATCTCTGTGACACATTTAATAAATA 2693
Db ||||| 541 GGCCACAGTACAGTCTGGCTCTTTTCCCTCCCATCTCTGTGACACATTTAATAAATA 600
QY 2694 AGGGTTGGCTTCTGAACTACAAAAAATAAATAAATAAATAAATAAATAAATA 2733
Db ||||| 601 AGGGTTGGCTTCTGAACTACAAAAAATAAATAAATAAATAAATAAATAAATA 640

optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev stage="fetal and adult"
/lab host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="UI-E-EJ1"
/note="Organ: eye; Vector: p7773-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EJ1 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p7773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGATTCAGAG; lens, CGATTAGCGA; eye anterior segment,
AATGCCGCAI; optic nerve, CCATTAGTG; retina, CCGGG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."

RESULT 15
 BU742056/c
 LOCUS
 DEFINITION BU742056 722 bp mRNA linear EST 10-OCT-2002
 UI-E-E01-aiy-g-09-0-UI.s1 UI-E-E01 Homo sapiens cDNA clone
 UI-E-E01-aiy-g-09-0-UI 3', mRNA sequence.
 ACCESSION
 VERSION BU742056
 KEYWORDS
 SOURCE EST.
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS 1 (bases 1 to 722)
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL
 MEDLINE Genome Res. 6 (9), 791-806 (1996)
 PUBMED 97044477
 COMMENT 8889548

Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565

Email: bento-soares@uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

Seq primer: M13 FORWARD

POLYA=yes.

FEATURES

Location/Qualifiers
 1..722
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-E-E01-aiy-g-09-0-UI"
 /tissue_type="fetal eye"
 /dev_stage="fetal"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-E01"
 /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-E01 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
 TAG_TISSUE=human fetal eye
 TAG_LIB=UI-E-E01
 TAG_SEQ=CGGTATACC"

ORIGIN

Query Match 22.5%; Score 640; DB 5; Length 722;
 Best Local Similarity 99.9%; Pred. No. 4.7e-298;
 Matches 690; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2039 TCCTTCCCGGACGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGG 2098
 DB 691 TCCTTCCCGGACGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGG 632

QY 2099 AGCTATGATAAAACATGACGAGCCACAGGCTCTCCACTGCTTCCACCAAGGTGCTGCTTTT 2158
 |||||||
 DB 631 AGCTATGATAAAACATGACGAGCCACAGGCTCTCCACTGCTTCCACCAAGGTGCTGCTTTT 572
 |||||||
 QY 2159 AAAGACTCGATTGAAAGAAATATGAAATGAAACCATGCTCATGCTCTTGTAGAAAGTGT 2218
 |||||||
 DB 571 AAAGACTCGATTGAAAGAAATATGAAATGAAACCATGCTCATGCTCTTGTAGAAAGTGT 512
 |||||||
 QY 2219 TCTGTATATCCGTCTGTACGTGTGTCATTTGGTGAAGCAGTGTGGGCTGAAGTGTGATT 2278
 |||||||
 DB 511 TCTGTATATCCGTCTGTACGTGTGTCATTTGGTGAAGCAGTGTGGGCTGAAGTGTGATT 452
 |||||||
 QY 2279 TGGCTGTGAACCTTGGGCTGTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGG 2338
 |||||||
 DB 451 TGGCTGTGAACCTTGGGCTGTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGG 392
 |||||||
 QY 2339 TGAGTAGACCTCCATTTGCTGTGTAGCTGATGCCGGCTCCACTATAGGACAGGCCAATTGG 2398
 |||||||
 DB 391 TGAGTAGACCTCCATTTGCTGTGTAGCTGATGCCGGCTCCACTATAGGACAGGCCAATTGG 332
 |||||||
 QY 2399 AAGATGCCAGGGCTTGCAGGAAGTAAAGTTCTTCAAGAAGACCATATACAAAACCTCTC 2458
 |||||||
 DB 331 AAGATGCCAGGGCTTGCAGGAAGTAAAGTTCTTCAAGAAGACCATATACAAAACCTCTC 272
 |||||||
 QY 2459 CACTCCACTGACCTGGTGTCTTCCCAAACTTTTCAGTTATACGAATGCCATCAGCTTGAC 2518
 |||||||
 DB 271 CACTCCACTGACCTGGTGTCTTCCCAAACTTTTCAGTTATACGAATGCCATCAGCTTGAC 212
 |||||||
 QY 2519 CAGGAAAGATCTGGGCTTTCATGAGGCCCTTTTGGGGCTCTCAAGTTCTTAGAGAGCTGCC 2578
 |||||||
 DB 211 CAGGAAAGATCTGGGCTTTCATGAGGCCCTTTTGGGGCTCTCAAGTTCTTAGAGAGCTGCC 152
 |||||||
 QY 2579 TGTGGGACAGCCCGAGGGCAGCAGAGCTGGGATGTGGTCATGCCCTTTGTGTACATGGCCA 2638
 |||||||
 DB 151 TGTGGGACAGCCCGAGGGCAGCAGAGCTGGGATGTGGTCATGCCCTTTGTGTACATGGCCA 92
 |||||||
 QY 2639 CAGTACAGTCTGGTCTCTTTTCTTCCCATCTCTTTGTACACATTTTAATAAATAAGGGT 2698
 |||||||
 DB 91 CAGTACAGTCTGGTCTCTTTTCTTCCCATCTCTTTGTACACATTTTAATAAATAAGGGT 32
 |||||||
 QY 2699 TGGCTTCTGAACCTACAAAAAATAAAAAA 2729
 |||||||
 DB 31 TGGCTTCTGAACCTACAAAAAATAAAAAA 1
 |||||||

Search completed: May 8, 2005, 13:11:45
 Job time : 6103 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2005, 11:21:33 ; Search time 1081 Seconds
(without alignments)
16098.112 Million cell updates/sec

Perfect score: 2846

Sequence: 1 cgtcgggaccgcccggg.....aaaaaaaaaaaaaaaaaaaaa 2846

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 5654200 seqs, 3057283753 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11308400

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : Published Applications NA: *

```
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
27	2846	100.0	2846	10	US-09-997-428-230	Sequence 230, App
560	2846	100.0	2846	16	US-10-174-587-169	Sequence 169, App
624	2846	100.0	2846	16	US-10-063-742-37	Sequence 37, Appl
739	2846	100.0	2846	15	US-10-972-317-37	Sequence 37, Appl
740	2556	89.8	2845	15	US-10-101-510-644	Sequence 644, App
741	2043	71.8	2306	14	US-10-004-551-3	Sequence 3, Appl
742	2043	71.8	2306	16	US-10-098-871-25	Sequence 25, Appl
743	1880	66.1	2144	15	US-10-037-270-969	Sequence 969, App
744	1880	66.1	2144	17	US-10-117-722-969	Sequence 969, App
745	1827	64.2	2142	15	US-10-037-270-1006	Sequence 1006, App
746	1827	64.2	2142	17	US-10-117-722-1006	Sequence 1006, App
747	1787	62.8	2259	13	US-10-067-422-2	Sequence 2, Appl

748	1672	58.7	2632	17	US-10-274-639-38	Sequence 38, Appl
749	1672	58.7	2632	17	US-10-333-574-38	Sequence 38, Appl
750	1633	57.4	1867	14	US-10-004-551-1	Sequence 1, Appl
c 751	337	11.8	337	9	US-09-954-531-789	Sequence 789, App
c 752	337	11.8	337	9	US-09-954-531-1223	Sequence 1223, App
c 753	337	11.8	337	19	US-10-843-641A-1856	Sequence 1856, App
c 754	337	11.8	337	19	US-10-843-641A-2290	Sequence 2290, App
c 755	314	11.0	548	15	US-10-101-510-29	Sequence 29, Appl
756	232	8.2	403	18	US-09-918-995-6744	Sequence 6744, App
757	202	7.1	286	18	US-10-723-860-4638	Sequence 4638, App
c 758	202	7.1	554	13	US-10-027-632-275184	Sequence 275184, Sequence 275184,
c 759	202	7.1	554	17	US-10-027-632-275184	Sequence 1714, App
760	136	4.8	2226	17	US-10-374-780A-1714	Sequence 1354, App
761	136	4.8	2226	17	US-10-412-699B-1354	Sequence 96, Appl
c 762	136	4.8	11394	15	US-10-240-453-96	Sequence 344, App
c 763	135	4.7	165	9	US-09-764-846-34	Sequence 709, App
764	135	4.7	165	10	US-09-764-872-709	Sequence 7491, App
765	135	4.7	165	10	US-09-764-891-7491	Sequence 9815, App
766	135	4.7	165	14	US-09-764-891-9815	Sequence 344, App
c 767	135	4.7	165	14	US-10-091-483-344	Sequence 956, App
768	135	4.7	165	15	US-10-205-428-956	Sequence 4616, App
c 769	135	4.7	450	18	US-10-021-323-4616	Sequence 7487, App
c 770	135	4.7	528	18	US-10-425-115-7487	Sequence 7972, App
771	135	4.7	564	18	US-10-021-323-7972	Sequence 33678, App
772	135	4.7	584	18	US-10-425-115-33678	Sequence 54715, A
773	135	4.7	606	18	US-10-437-963-54715	Sequence 131283, Sequence 115631,
774	135	4.7	685	18	US-10-425-115-131293	Sequence 422, App
775	135	4.7	677	17	US-10-424-599-115631	Sequence 165957, A
776	135	4.7	716	19	US-10-764-420-422	Sequence 59302, A
777	135	4.7	1235	18	US-10-425-115-165957	Sequence 4367, App
778	135	4.7	1272	18	US-10-425-115-58302	Sequence 18496, A
779	135	4.7	2028	18	US-10-739-930-4367	Sequence 19557, A
780	135	4.7	2197	18	US-10-425-115-18496	Sequence 15, Appl
781	135	4.7	2323	18	US-10-425-115-19557	Sequence 15, Appl
782	135	4.7	2753	9	US-09-789-561-15	Sequence 15, Appl
783	135	4.7	2753	9	US-10-883-936-15	Sequence 15, Appl
784	135	4.7	3415	9	US-09-823-245A-438	Sequence 5012, App
785	135	4.7	3931	18	US-10-723-860-5012	Sequence 894, App
c 786	135	4.7	5195	15	US-10-311-455-894	Sequence 484, App
c 787	135	4.7	5306	17	US-10-311-455-484	Sequence 408, App
c 788	135	4.7	6192	17	US-10-221-714A-408	Sequence 112, App
c 789	135	4.7	6944	15	US-10-172-086-112	Sequence 114, App
c 790	135	4.7	6944	18	US-10-311-507-114	Sequence 112, App
c 791	135	4.7	6944	18	US-10-480-846-112	Sequence 2147, Appl
c 792	135	4.7	113515	15	US-10-311-455-2147	Sequence 1, Appl
c 793	135	4.7	3673778	16	US-10-312-841-1	Sequence 2, Appl
c 794	135	4.7	3673778	16	US-10-312-841-2	Sequence 1301, App
c 795	134	4.7	181	9	US-09-960-352-1301	Sequence 134227, Sequence 120644,
796	134	4.7	315	18	US-10-425-115-134227	Sequence 165946, Sequence 8650, App
797	134	4.7	334	17	US-10-424-599-120644	Sequence 76171, A
798	134	4.7	344	18	US-10-425-115-165946	Sequence 138566, A
799	134	4.7	355	18	US-10-021-323-8650	Sequence 10489, A
800	134	4.7	359	18	US-10-437-963-76171	Sequence 8873, App
801	134	4.7	368	18	US-10-425-115-138566	Sequence 57615, A
802	134	4.7	381	18	US-10-021-323-10489	Sequence 37, Appl
803	134	4.7	381	18	US-10-357-930-58681	Sequence 92366, A
804	134	4.7	389	18	US-10-437-963-8873	Sequence 71220, A
805	134	4.7	396	18	US-10-357-930-57615	Sequence 9484, App
806	134	4.7	409	9	US-09-822-849A-37	Sequence 15260, A
807	134	4.7	411	17	US-10-425-115-92366	Sequence 87401, A
808	134	4.7	416	17	US-10-424-599-71220	Sequence 95616, A
809	134	4.7	426	18	US-10-021-323-9484	Sequence 11004, A
810	134	4.7	431	18	US-10-021-323-15260	Sequence 158896, A
811	134	4.7	437	17	US-10-424-599-87401	Sequence 14917, A
812	134	4.7	457	18	US-10-425-115-95616	Sequence 16622, A
813	134	4.7	458	18	US-10-021-323-11004	Sequence 57078, A
814	134	4.7	479	18	US-10-425-115-158896	Sequence 4109, App
815	134	4.7	481	18	US-10-021-323-14917	Sequence 170711, A
816	134	4.7	483	18	US-10-021-323-16622	Sequence 46262, A
c 817	134	4.7	490	18	US-10-357-930-57078	
818	134	4.7	496	18	US-10-021-323-4109	
819	134	4.7	500	18	US-10-425-115-170711	
820	134	4.7	508	17	US-10-424-599-46262	

C 821	134	4.7	508	18	US-10-021-323-5403	Sequence 5403, Ap	C 894	134	4.7	1803	17	US-10-412-699B-1438	Sequence 1438, Ap
C 822	134	4.7	509	18	US-10-021-323-6707	Sequence 6707, Ap	895	134	4.7	1929	18	US-10-425-115-161709	Sequence 161709, A
C 823	134	4.7	510	18	US-10-437-963-1928	Sequence 1928, Ap	896	134	4.7	1958	17	US-10-424-599-60709	Sequence 60709, A
C 824	134	4.7	518	18	US-10-021-323-4634	Sequence 4634, Ap	897	134	4.7	1999	18	US-10-723-860-7767	Sequence 7767, Ap
C 825	134	4.7	524	18	US-10-425-115-109499	Sequence 109499, c	898	134	4.7	2094	18	US-10-425-115-51614	Sequence 51614, A
C 826	134	4.7	526	18	US-10-425-115-130137	Sequence 130137, c	899	134	4.7	2096	18	US-10-425-115-27838	Sequence 27838, A
C 827	134	4.7	528	18	US-10-425-115-137716	Sequence 137716, c	900	134	4.7	2235	19	US-10-887-553A-987	Sequence 987, App
C 828	134	4.7	536	18	US-10-021-323-14752	Sequence 14752, A	901	134	4.7	2270	17	US-10-424-599-44604	Sequence 44604, A
C 829	134	4.7	540	18	US-10-021-323-10245	Sequence 10245, A	902	134	4.7	2288	17	US-10-424-599-67031	Sequence 67031, A
C 830	134	4.7	544	18	US-10-425-115-162816	Sequence 162816, A	903	134	4.7	2322	17	US-10-424-599-1231	Sequence 1231, Ap
C 831	134	4.7	545	18	US-10-021-323-6099	Sequence 6099, Ap	904	134	4.7	2333	17	US-10-424-599-127867	Sequence 127867, A
C 832	134	4.7	547	18	US-10-437-963-20806	Sequence 20806, A	905	134	4.7	2499	18	US-10-723-860-5438	Sequence 5438, Ap
C 833	134	4.7	553	18	US-10-021-323-7987	Sequence 7987, Ap	906	134	4.7	2520	17	US-10-389-566-205	Sequence 205, App
C 834	134	4.7	554	18	US-10-425-115-882	Sequence 882, App	907	134	4.7	2617	18	US-10-425-115-151022	Sequence 151022, A
C 835	134	4.7	554	18	US-10-425-115-23306	Sequence 23306, A	908	134	4.7	2809	17	US-10-172-118-340	Sequence 340, App
C 836	134	4.7	557	18	US-10-425-115-148098	Sequence 148098, A	909	134	4.7	2809	17	US-10-342-887-340	Sequence 340, App
C 837	134	4.7	560	18	US-10-021-323-3016	Sequence 3016, Ap	910	134	4.7	2971	18	US-10-425-115-103107	Sequence 103107, A
C 838	134	4.7	568	17	US-10-424-599-117111	Sequence 117111, c	911	134	4.7	3275	9	US-09-738-973-151	Sequence 151, App
C 839	134	4.7	570	18	US-10-021-323-143	Sequence 143, App	912	134	4.7	3275	9	US-09-854-133-151	Sequence 151, App
C 840	134	4.7	578	18	US-10-021-323-7450	Sequence 7450, Ap	913	134	4.7	3275	15	US-10-144-649A-151	Sequence 81706, A
C 841	134	4.7	583	18	US-10-767-795-134	Sequence 134, App	914	134	4.7	3758	18	US-10-437-963-81706	Sequence 81706, A
C 842	134	4.7	595	18	US-10-425-115-175716	Sequence 175716, A	915	134	4.7	4824	18	US-10-723-860-5191	Sequence 5191, Ap
C 843	134	4.7	596	17	US-10-424-599-18370	Sequence 18370, A	916	134	4.7	6171	15	US-10-311-455-761	Sequence 761, App
C 844	134	4.7	597	18	US-10-021-323-138	Sequence 138, App	917	134	4.7	6486	18	US-10-433-793-80	Sequence 80, Appl
C 845	134	4.7	598	18	US-10-021-323-11423	Sequence 11423, A	918	134	4.7	7115	18	US-10-723-860-7372	Sequence 7372, Ap
C 846	134	4.7	606	17	US-10-424-599-54586	Sequence 54586, A	919	134	4.7	7369	18	US-10-473-126-277	Sequence 277, App
C 847	134	4.7	606	17	US-10-424-599-93300	Sequence 93300, A	920	134	4.7	7369	19	US-10-486-319A-56	Sequence 56, Appl
C 848	134	4.7	608	18	US-10-021-323-636	Sequence 636, App	921	134	4.7	8899	15	US-10-311-455-810	Sequence 810, App
C 849	134	4.7	616	18	US-10-021-323-5390	Sequence 5390, Ap	922	134	4.7	8899	17	US-10-257-166-156	Sequence 156, App
C 850	134	4.7	647	18	US-10-425-115-18397	Sequence 18397, A	923	134	4.7	8946	15	US-10-311-455-884	Sequence 884, App
C 851	134	4.7	684	18	US-10-425-115-168572	Sequence 168572, A	924	134	4.7	15832	14	US-10-239-676-106	Sequence 106, App
C 852	134	4.7	704	18	US-10-425-115-21405	Sequence 21405, A	925	134	4.7	15832	15	US-10-311-455-1316	Sequence 1316, Ap
C 853	134	4.7	718	18	US-10-425-115-154975	Sequence 154975, c	926	134	4.7	15832	15	US-10-240-453-118	Sequence 118, App
C 854	134	4.7	831	9	US-09-723-674-67	Sequence 67, Appl	927	134	4.7	40324	18	US-10-433-793-179	Sequence 179, App
C 855	134	4.7	831	18	US-10-913-553-67	Sequence 67, Appl	928	133	4.7	148	9	US-09-764-869-1437	Sequence 1437, Ap
C 856	134	4.7	899	18	US-10-437-963-27088	Sequence 27088, A	929	133	4.7	148	9	US-09-764-846-272	Sequence 272, App
C 857	134	4.7	924	18	US-10-425-115-173094	Sequence 173094, A	930	133	4.7	148	9	US-09-764-846-285	Sequence 285, App
C 858	134	4.7	936	17	US-10-424-599-69990	Sequence 69990, A	931	133	4.7	148	9	US-09-764-846-295	Sequence 295, Appl
C 859	134	4.7	936	17	US-10-424-599-112681	Sequence 112681, A	932	133	4.7	148	9	US-09-764-846-337	Sequence 337, App
C 860	134	4.7	980	18	US-10-723-860-4894	Sequence 4894, Ap	933	133	4.7	148	10	US-09-764-891-7489	Sequence 7489, Ap
C 861	134	4.7	987	17	US-10-424-599-114407	Sequence 114407, A	934	133	4.7	148	10	US-09-764-891-7703	Sequence 7703, Ap
C 862	134	4.7	1068	18	US-10-437-963-86611	Sequence 86611, A	935	133	4.7	148	10	US-09-764-891-9406	Sequence 9406, Ap
C 863	134	4.7	1091	18	US-10-723-860-6015	Sequence 6015, Ap	936	133	4.7	148	10	US-09-764-891-9809	Sequence 9809, Ap
C 864	134	4.7	1103	18	US-10-425-115-68317	Sequence 68317, A	937	133	4.7	148	11	US-09-973-278-836	Sequence 836, App
C 865	134	4.7	1129	18	US-10-425-115-88252	Sequence 88252, A	938	133	4.7	148	14	US-10-091-483-272	Sequence 272, App
C 866	134	4.7	1130	18	US-10-425-115-131870	Sequence 131870, A	939	133	4.7	148	14	US-10-091-483-285	Sequence 285, App
C 867	134	4.7	1133	18	US-10-425-115-59679	Sequence 59679, A	940	133	4.7	148	14	US-10-091-483-295	Sequence 295, App
C 868	134	4.7	1140	18	US-10-437-963-26438	Sequence 26438, A	941	133	4.7	148	14	US-10-091-483-337	Sequence 337, App
C 869	134	4.7	1233	17	US-10-424-599-44264	Sequence 44264, A	942	133	4.7	148	14	US-10-091-504-1437	Sequence 1437, Ap
C 870	134	4.7	1301	18	US-10-425-115-179473	Sequence 179473, A	943	133	4.7	148	15	US-10-205-428-950	Sequence 950, App
C 871	134	4.7	1306	18	US-10-425-115-83709	Sequence 83709, A	944	133	4.7	148	17	US-10-091-414-274	Sequence 274, App
C 872	134	4.7	1398	18	US-10-425-115-169951	Sequence 169951, A	945	133	4.7	148	17	US-10-227-577-1437	Sequence 1437, Ap
C 873	134	4.7	1459	17	US-10-818-609-3	Sequence 3, Appl	946	133	4.7	195	17	US-10-282-122A-13382	Sequence 13382, A
C 874	134	4.7	1463	17	US-10-424-599-88284	Sequence 88284, A	947	133	4.7	196	18	US-10-668-749A-5	Sequence 5, Appl
C 875	134	4.7	1482	18	US-10-425-115-24588	Sequence 24588, A	948	133	4.7	212	17	US-10-242-535A-22243	Sequence 22243, A
C 876	134	4.7	1494	18	US-10-425-115-103271	Sequence 103271, A	949	133	4.7	212	17	US-10-085-783A-22243	Sequence 22243, A
C 877	134	4.7	1504	18	US-10-425-115-63627	Sequence 63627, A	950	133	4.7	220	9	US-09-960-352-14522	Sequence 14522, A
C 878	134	4.7	1512	18	US-10-425-115-131408	Sequence 131408, A	951	133	4.7	225	9	US-09-925-299-744	Sequence 744, App
C 879	134	4.7	1519	18	US-10-425-115-17631	Sequence 17631, A	952	133	4.7	225	10	US-09-925-299-744	Sequence 744, App
C 880	134	4.7	1521	17	US-10-172-118-1450	Sequence 1450, Ap	953	133	4.7	231	17	US-10-242-535A-30412	Sequence 30412, A
C 881	134	4.7	1521	17	US-10-342-887-1450	Sequence 1450, Ap	954	133	4.7	231	17	US-10-085-783A-30412	Sequence 30412, A
C 882	134	4.7	1576	18	US-10-723-860-5808	Sequence 5808, Ap	955	133	4.7	242	9	US-09-960-352-3873	Sequence 3873, Ap
C 883	134	4.7	1603	18	US-10-357-930-22091	Sequence 22091, A	956	133	4.7	260	17	US-10-242-535A-40371	Sequence 40371, A
C 884	134	4.7	1603	18	US-10-357-930-23103	Sequence 23103, A	957	133	4.7	260	17	US-10-085-783A-40371	Sequence 40371, A
C 885	134	4.7	1603	18	US-10-357-930-27953	Sequence 27953, A	958	133	4.7	286	9	US-09-960-352-13342	Sequence 13342, A
C 886	134	4.7	1603	18	US-10-357-930-28971	Sequence 28971, A	959	133	4.7	305	17	US-10-231-956A-85	Sequence 85, Appl
C 887	134	4.7	1617	17	US-10-425-115-164014	Sequence 164014, A	960	133	4.7	309	18	US-10-357-930-45013	Sequence 45013, A
C 888	134	4.7	1638	17	US-10-425-115-96402	Sequence 96402, A	961	133	4.7	313	18	US-10-021-323-13390	Sequence 13390, A
C 889	134	4.7	1667	18	US-10-425-115-39856	Sequence 39856, A	962	133	4.7	318	18	US-10-021-323-6340	Sequence 6340, Ap
C 890	134	4.7	1678	18	US-10-437-963-95688	Sequence 95688, A	963	133	4.7	325	17	US-10-424-599-59828	Sequence 59828, A
C 891	134	4.7	1678	18	US-10-425-115-71345	Sequence 71345, A	964	133	4.7	325	18	US-10-021-323-8658	Sequence 8658, Ap
C 892	134	4.7	1708	17	US-10-310-154-71	Sequence 71, Appl	965	133	4.7	327	9	US-09-960-352-4630	Sequence 4630, Ap
C 893	134	4.7	1803	17	US-10-374-780A-1279	Sequence 1279, Ap	966	133	4.7	338	18	US-10-425-115-65485	Sequence 65485, A

c 967	133	4.7	341	18	US-10-021-323-451	Sequence 451, App	c1040	133	4.7	527	18	US-10-021-323-16206	Sequence 16206, A
c 968	133	4.7	351	10	US-09-814-353-17579	Sequence 17579, A	1041	133	4.7	528	17	US-10-424-599-37260	Sequence 37260, A
c 969	133	4.7	359	18	US-10-425-115-99058	Sequence 99058, A	c1042	133	4.7	528	18	US-10-021-323-1809	Sequence 1809, A
c 970	133	4.7	361	17	US-10-424-599-25589	Sequence 25589, A	c1043	133	4.7	528	18	US-10-021-323-8131	Sequence 8131, A
c 971	133	4.7	365	9	US-09-960-352-8271	Sequence 8271, App	1044	133	4.7	531	17	US-10-424-599-54674	Sequence 54674, A
c 972	133	4.7	372	18	US-10-425-115-24788	Sequence 24788, A	1045	133	4.7	532	17	US-10-424-599-43810	Sequence 43810, A
c 973	133	4.7	375	18	US-10-357-930-44930	Sequence 44930, A	1046	133	4.7	532	18	US-10-021-323-870	Sequence 870, App
c 974	133	4.7	378	18	US-10-425-115-80509	Sequence 80509, A	1047	133	4.7	538	18	US-10-424-599-76890	Sequence 76890, A
c 975	133	4.7	391	18	US-10-425-115-13025	Sequence 13025, A	1048	133	4.7	539	17	US-10-425-115-152949	Sequence 152949, A
c 976	133	4.7	394	18	US-10-357-930-13555	Sequence 13555, A	1049	133	4.7	540	18	US-10-425-115-81745	Sequence 81745, A
c 977	133	4.7	396	9	US-09-825-294-53	Sequence 53, App1	c1050	133	4.7	541	18	US-10-021-323-11946	Sequence 11946, A
c 978	133	4.7	396	9	US-09-970-966-53	Sequence 53, App1	c1051	133	4.7	542	18	US-10-021-323-6883	Sequence 6883, A
c 979	133	4.7	396	15	US-10-212-677-53	Sequence 53, App1	c1052	133	4.7	542	18	US-10-425-115-7873	Sequence 7873, A
c 980	133	4.7	396	17	US-10-361-811-53	Sequence 53, App1	1053	133	4.7	543	18	US-10-437-963-40831	Sequence 40831, A
c 981	133	4.7	396	17	US-10-369-186-53	Sequence 53, App1	1054	133	4.7	544	18	US-10-425-115-26104	Sequence 26104, A
c 982	133	4.7	398	18	US-10-021-323-7863	Sequence 7863, App	1055	133	4.7	545	17	US-10-424-599-4829	Sequence 4829, App
c 983	133	4.7	403	18	US-10-425-115-155989	Sequence 155989, A	1056	133	4.7	545	18	US-10-021-323-6889	Sequence 6889, App
c 984	133	4.7	404	18	US-10-425-115-131668	Sequence 131668, A	1057	133	4.7	545	18	US-10-425-115-38204	Sequence 38204, A
c 985	133	4.7	406	10	US-09-814-353-4900	Sequence 4900, App	1058	133	4.7	547	18	US-10-021-323-6195	Sequence 6195, App
c 986	133	4.7	406	10	US-09-814-353-11195	Sequence 11195, A	1059	133	4.7	547	18	US-10-021-323-8671	Sequence 8671, App
c 987	133	4.7	406	18	US-10-357-930-34697	Sequence 34697, A	c1060	133	4.7	547	18	US-10-021-323-16890	Sequence 16890, A
c 988	133	4.7	408	18	US-10-357-930-43554	Sequence 43554, A	c1061	133	4.7	549	18	US-10-021-323-7101	Sequence 7101, App
c 989	133	4.7	411	18	US-10-021-323-7694	Sequence 7694, App	1062	133	4.7	549	18	US-10-437-963-43799	Sequence 43799, A
c 990	133	4.7	419	17	US-10-424-599-58948	Sequence 58948, A	c1063	133	4.7	552	18	US-10-021-323-17351	Sequence 17351, A
c 991	133	4.7	421	18	US-10-021-323-7658	Sequence 7658, App	1064	133	4.7	552	18	US-10-425-115-42027	Sequence 42027, A
c 992	133	4.7	421	18	US-10-425-115-167836	Sequence 167836, A	1065	133	4.7	554	17	US-10-424-599-17501	Sequence 17501, A
c 993	133	4.7	422	18	US-10-425-115-108647	Sequence 108647, A	c1066	133	4.7	554	18	US-10-021-323-4489	Sequence 4489, App
c 994	133	4.7	424	18	US-10-437-963-34803	Sequence 34803, A	c1067	133	4.7	557	18	US-10-021-323-2566	Sequence 2566, App
c 995	133	4.7	430	18	US-10-425-115-170993	Sequence 170993, A	c1068	133	4.7	560	18	US-10-021-323-2253	Sequence 2253, App
c 996	133	4.7	432	18	US-10-425-115-94211	Sequence 94211, A	1069	133	4.7	560	18	US-10-425-115-21207	Sequence 21207, A
c 997	133	4.7	433	18	US-10-425-115-12621	Sequence 12621, A	1070	133	4.7	561	18	US-10-425-115-169551	Sequence 169551, A
c 998	133	4.7	435	18	US-10-021-323-11676	Sequence 11676, A	1071	133	4.7	564	17	US-10-424-599-39558	Sequence 39558, A
c 999	133	4.7	436	18	US-10-425-115-172404	Sequence 172404, A	c1072	133	4.7	565	18	US-10-021-323-11125	Sequence 11125, A
1000	133	4.7	443	18	US-10-021-323-6814	Sequence 6814, App	1073	133	4.7	565	18	US-10-357-930-57918	Sequence 57918, A
c1001	133	4.7	446	9	US-09-960-352-3400	Sequence 3400, App	1074	133	4.7	566	18	US-10-767-701-17472	Sequence 17472, A
1002	133	4.7	447	18	US-10-425-115-122788	Sequence 122788, A	1075	133	4.7	567	17	US-10-424-599-68710	Sequence 68710, A
1003	133	4.7	452	18	US-10-021-323-4768	Sequence 4768, App	1076	133	4.7	567	18	US-10-021-323-8240	Sequence 8240, App
1004	133	4.7	456	9	US-09-960-352-9659	Sequence 9659, App	1077	133	4.7	568	18	US-10-425-115-4891	Sequence 4891, A
1005	133	4.7	463	17	US-10-424-599-101158	Sequence 101158, A	1078	133	4.7	568	18	US-10-425-115-22899	Sequence 22899, A
1006	133	4.7	466	17	US-10-424-599-17164	Sequence 17164, A	1079	133	4.7	569	18	US-10-437-963-88900	Sequence 88900, A
1007	133	4.7	467	18	US-10-437-963-94117	Sequence 94117, A	1080	133	4.7	570	18	US-10-357-930-59133	Sequence 59133, A
c1008	133	4.7	469	18	US-10-021-323-16830	Sequence 16830, A	c1081	133	4.7	571	18	US-10-021-323-6871	Sequence 6871, App
1009	133	4.7	476	18	US-10-021-323-13303	Sequence 13303, A	1082	133	4.7	573	17	US-10-424-599-19634	Sequence 19634, A
1010	133	4.7	478	18	US-10-021-323-6774	Sequence 6774, App	1083	133	4.7	573	18	US-10-425-115-31452	Sequence 31452, A
c1011	133	4.7	481	18	US-10-357-930-56267	Sequence 56267, A	c1084	133	4.7	574	18	US-10-021-323-7391	Sequence 7391, App
c1012	133	4.7	485	18	US-10-021-323-6802	Sequence 6802, App	1085	133	4.7	575	17	US-10-424-599-71318	Sequence 71318, A
1013	133	4.7	485	18	US-10-021-323-8174	Sequence 8174, App	1086	133	4.7	576	17	US-10-424-599-126135	Sequence 126135, A
1014	133	4.7	486	18	US-10-021-323-8387	Sequence 8387, App	1087	133	4.7	577	18	US-10-425-115-89366	Sequence 89366, A
c1015	133	4.7	487	18	US-10-021-323-2841	Sequence 2841, App	1088	133	4.7	578	17	US-10-424-599-124726	Sequence 124726, A
c1016	133	4.7	489	18	US-10-021-323-4517	Sequence 4517, App	1089	133	4.7	578	17	US-10-424-599-133291	Sequence 133291, A
1017	133	4.7	489	18	US-10-021-323-9165	Sequence 9165, App	c1090	133	4.7	583	18	US-10-021-323-6081	Sequence 6081, App
c1018	133	4.7	490	18	US-10-021-323-16197	Sequence 16197, A	1091	133	4.7	583	18	US-10-425-115-147942	Sequence 147942, A
c1019	133	4.7	495	18	US-10-021-323-2679	Sequence 2679, App	1092	133	4.7	584	18	US-10-425-115-74017	Sequence 74017, A
c1020	133	4.7	496	18	US-10-021-323-17062	Sequence 17062, A	1093	133	4.7	584	18	US-10-425-115-179304	Sequence 179304, A
c1021	133	4.7	498	18	US-10-425-115-12386	Sequence 12386, A	1094	133	4.7	586	18	US-10-437-963-45637	Sequence 45637, A
c1022	133	4.7	499	18	US-10-021-323-1716	Sequence 1716, App	1095	133	4.7	587	18	US-10-425-115-139419	Sequence 139419, A
1023	133	4.7	501	18	US-10-425-115-155716	Sequence 155716, A	1096	133	4.7	587	18	US-10-425-115-172648	Sequence 172648, A
1024	133	4.7	501	18	US-10-357-930-59111	Sequence 59111, A	1097	133	4.7	590	17	US-10-424-599-118116	Sequence 118116, A
c1025	133	4.7	502	18	US-10-021-323-11431	Sequence 11431, A	1098	133	4.7	591	18	US-10-021-323-13007	Sequence 13007, A
1026	133	4.7	504	18	US-10-425-115-51618	Sequence 51618, A	1099	133	4.7	591	18	US-10-425-115-118074	Sequence 118074, A
1027	133	4.7	506	18	US-10-021-323-23311	Sequence 23311, App	c1100	133	4.7	592	14	US-10-198-846-8340	Sequence 8340, App
1028	133	4.7	510	18	US-10-767-795-5097	Sequence 5097, App	1101	133	4.7	592	18	US-10-425-115-105613	Sequence 105613, A
1029	133	4.7	512	18	US-10-425-115-1891	Sequence 1891, App	1102	133	4.7	593	18	US-10-021-323-4285	Sequence 4285, App
1030	133	4.7	514	18	US-10-425-115-74503	Sequence 74503, A	1103	133	4.7	594	17	US-10-424-599-116262	Sequence 116262, A
1031	133	4.7	515	17	US-10-424-599-106126	Sequence 106126, A	c1105	133	4.7	597	14	US-10-198-846-8885	Sequence 8885, App
1032	133	4.7	516	18	US-10-021-323-10534	Sequence 10534, A	1106	133	4.7	599	18	US-10-425-115-717	Sequence 717, App
1033	133	4.7	516	18	US-10-437-963-99239	Sequence 99239, A	1107	133	4.7	599	18	US-10-425-115-167556	Sequence 167556, A
1034	133	4.7	517	17	US-10-424-599-129396	Sequence 129396, A	1108	133	4.7	600	18	US-10-425-115-76887	Sequence 76887, A
1035	133	4.7	517	18	US-10-021-323-10114	Sequence 10114, A	1109	133	4.7	601	18	US-10-425-115-70972	Sequence 70972, A
1036	133	4.7	520	18	US-10-425-115-132906	Sequence 132906, A	c1110	133	4.7	602	18	US-10-425-115-61525	Sequence 61525, A
1037	133	4.7	522	18	US-10-021-323-869	Sequence 869, App	1111	133	4.7	603	18	US-10-425-115-62402	Sequence 62402, A
1038	133	4.7	524	17	US-10-424-599-11691	Sequence 11691, A	1112	133	4.7	608	17	US-10-424-599-90628	Sequence 90628, A
1039	133	4.7	524	18	US-10-425-115-56601	Sequence 56601, A							

1113	133	4.7	608	18	US-10-437-963-19184	Sequence 19184, A	1186	133	4.7	1138	18	US-10-425-115-108606	Sequence 108606,
1114	133	4.7	608	18	US-10-425-115-157602	Sequence 157602, A	1187	133	4.7	1159	18	US-10-425-115-6815	Sequence 6815, Ap
1115	133	4.7	609	17	US-10-424-599-97699	Sequence 97699, A	1188	133	4.7	1182	18	US-10-425-115-129960	Sequence 129960,
1116	133	4.7	609	18	US-10-437-963-23843	Sequence 23843, A	1189	133	4.7	1198	9	US-09-789-561-55	Sequence 55, Appl
1117	133	4.7	611	18	US-10-425-115-178893	Sequence 178893, A	1190	133	4.7	1198	19	US-10-883-936-55	Sequence 55, Appl
1118	133	4.7	612	17	US-10-424-599-90936	Sequence 90936, A	1191	133	4.7	1211	18	US-10-739-930-4124	Sequence 4124, Ap
1119	133	4.7	617	17	US-10-424-599-71934	Sequence 71934, A	1193	133	4.7	1215	18	US-10-723-860-5254	Sequence 5254, Ap
1120	133	4.7	619	18	US-10-425-115-102831	Sequence 102831, A	1193	133	4.7	1226	17	US-10-424-599-43121	Sequence 43121, A
1121	133	4.7	624	18	US-10-425-115-52818	Sequence 52818, A	c1194	133	4.7	1233	18	US-10-425-115-82555	Sequence 82555, A
1122	133	4.7	626	18	US-10-437-963-2840	Sequence 2840, Ap	1195	133	4.7	1245	18	US-10-425-115-15266	Sequence 15266, A
1123	133	4.7	626	18	US-10-425-115-6250	Sequence 6250, Ap	1196	133	4.7	1255	18	US-10-437-963-87628	Sequence 87628, A
1124	133	4.7	627	17	US-10-424-599-50144	Sequence 50144, A	1197	133	4.7	1300	18	US-10-668-749A-1	Sequence 1, Appl
1125	133	4.7	627	18	US-10-021-323-73	Sequence 73, Appl	1198	133	4.7	1316	18	US-10-425-115-109626	Sequence 109626,
1126	133	4.7	627	18	US-10-425-115-75673	Sequence 75673, A	1199	133	4.7	1323	18	US-10-425-115-54043	Sequence 54043, A
1127	133	4.7	630	18	US-10-425-115-95100	Sequence 95100, A	1200	133	4.7	1367	18	US-10-425-115-85766	Sequence 85766, A
1128	133	4.7	631	18	US-10-425-115-140103	Sequence 140103, A	1201	133	4.7	1383	17	US-10-310-154-230	Sequence 230, App
1129	133	4.7	634	18	US-10-425-115-8940	Sequence 8940, Ap	1202	133	4.7	1400	17	US-10-424-599-125443	Sequence 125443, A
1130	133	4.7	634	18	US-10-425-115-122963	Sequence 122963, A	1203	133	4.7	1405	18	US-10-425-115-42749	Sequence 42749, A
1131	133	4.7	640	17	US-10-424-599-122753	Sequence 122753, A	1204	133	4.7	1416	17	US-10-395-027-688	Sequence 688, App
1132	133	4.7	640	18	US-10-021-323-8853	Sequence 8853, Ap	1205	133	4.7	1432	18	US-10-767-795-3350	Sequence 3350, Ap
1133	133	4.7	641	17	US-10-424-599-106274	Sequence 106274, A	1206	133	4.7	1460	17	US-10-424-599-142655	Sequence 142655,
1134	133	4.7	641	17	US-10-424-599-117136	Sequence 117136, A	1207	133	4.7	1466	18	US-10-425-115-176985	Sequence 176985,
1135	133	4.7	642	17	US-10-424-599-125436	Sequence 125436, A	1208	133	4.7	1495	17	US-10-424-599-36589	Sequence 36589, A
1136	133	4.7	643	17	US-10-424-599-97217	Sequence 97217, A	1209	133	4.7	1583	18	US-10-425-115-57459	Sequence 57459, A
1137	133	4.7	645	18	US-10-425-115-116277	Sequence 116277, A	1210	133	4.7	1642	17	US-10-424-599-42140	Sequence 42140, A
1138	133	4.7	647	17	US-10-424-599-8609	Sequence 8609, Ap	1211	133	4.7	1696	14	US-10-274-971-1	Sequence 1, Appl
1139	133	4.7	647	18	US-10-425-115-170206	Sequence 170206, Ap	1212	133	4.7	1808	9	US-09-989-920-46	Sequence 46, Appl
1140	133	4.7	649	18	US-10-425-115-72863	Sequence 72863, A	1213	133	4.7	1811	17	US-10-424-599-59218	Sequence 59218, A
1141	133	4.7	654	17	US-10-424-599-129198	Sequence 129198, A	1214	133	4.7	1868	18	US-10-425-115-165307	Sequence 165307,
1142	133	4.7	655	17	US-10-424-599-107600	Sequence 107600, A	1215	133	4.7	1875	17	US-10-374-780A-1941	Sequence 1941, Ap
1143	133	4.7	657	18	US-10-425-115-60368	Sequence 60368, A	1216	133	4.7	1975	18	US-10-425-115-80851	Sequence 80851, A
1144	133	4.7	658	18	US-10-425-115-51887	Sequence 51887, A	1217	133	4.7	1985	17	US-10-424-599-67834	Sequence 67834, A
1145	133	4.7	677	18	US-10-425-115-131288	Sequence 131288, A	1218	133	4.7	2057	17	US-10-366-829-15	Sequence 15, Appl
c1146	133	4.7	681	9	US-09-822-830A-26	Sequence 26, Appl	1219	133	4.7	2060	17	US-10-424-599-89326	Sequence 89326, Ap
c1147	133	4.7	683	18	US-10-425-115-92182	Sequence 92182, A	1220	133	4.7	2091	18	US-10-425-115-93227	Sequence 93227, A
1148	133	4.7	684	18	US-10-425-115-62433	Sequence 62433, A	1221	133	4.7	2134	18	US-10-425-115-176649	Sequence 176649, A
c1149	133	4.7	684	18	US-10-425-115-110165	Sequence 110165, A	1222	133	4.7	2138	18	US-10-437-963-66396	Sequence 66396, A
1150	133	4.7	697	18	US-10-425-115-20836	Sequence 20836, A	1223	133	4.7	2148	18	US-10-739-930-2257	Sequence 2257, Ap
1151	133	4.7	698	9	US-09-764-846-131	Sequence 131, App	1224	133	4.7	2177	18	US-10-425-115-115991	Sequence 115991,
1152	133	4.7	698	14	US-10-091-483-131	Sequence 131, App	1225	133	4.7	2190	17	US-10-424-599-9903	Sequence 9903, Ap
c1153	133	4.7	711	17	US-10-424-599-42333	Sequence 42333, A	1226	133	4.7	2291	18	US-10-425-115-140658	Sequence 140658,
1154	133	4.7	736	17	US-10-424-599-60906	Sequence 60906, A	1227	133	4.7	2297	18	US-10-425-115-154441	Sequence 154441,
1155	133	4.7	737	17	US-10-424-599-95307	Sequence 95307, A	1228	133	4.7	2248	18	US-10-425-115-65796	Sequence 65796, A
1156	133	4.7	738	18	US-10-425-115-178509	Sequence 178509, A	1229	133	4.7	2265	18	US-10-425-115-28893	Sequence 28893, A
1157	133	4.7	751	18	US-10-425-115-71448	Sequence 71448, A	1230	133	4.7	2289	18	US-10-425-115-48241	Sequence 48241, A
1158	133	4.7	760	18	US-10-357-930-29439	Sequence 29439, A	1231	133	4.7	2366	18	US-10-425-115-86057	Sequence 86057, A
1159	133	4.7	761	18	US-10-425-115-17031	Sequence 17031, A	1232	133	4.7	2372	18	US-10-425-115-58985	Sequence 58985, A
1160	133	4.7	767	17	US-10-424-599-45104	Sequence 45104, A	1233	133	4.7	2481	18	US-10-473-126-218	Sequence 440, App
1161	133	4.7	768	18	US-10-425-115-98337	Sequence 98337, A	c1234	133	4.7	2501	18	US-10-425-115-440	Sequence 218, App
1162	133	4.7	774	19	US-10-487-901-4626	Sequence 4626, Ap	1235	133	4.7	2525	17	US-10-473-126-364	Sequence 364, App
1163	133	4.7	879	18	US-10-425-115-106266	Sequence 106266, A	1236	133	4.7	2566	18	US-10-424-599-101605	Sequence 101605,
1164	133	4.7	895	18	US-10-425-115-135838	Sequence 135838, A	1237	133	4.7	2566	18	US-10-734-564-47	Sequence 47, Appl
1165	133	4.7	904	18	US-10-425-115-51691	Sequence 51691, A	1238	133	4.7	2575	18	US-10-723-860-7683	Sequence 7683, Ap
1166	133	4.7	935	18	US-10-425-115-51691	Sequence 112572, A	c1239	133	4.7	2700	18	US-10-723-860-5126	Sequence 5126, Ap
1167	133	4.7	936	9	US-09-739-907-47	Sequence 47, Appl	1240	133	4.7	2921	9	US-09-925-301-223	Sequence 223, App
1168	133	4.7	936	11	US-09-938-671-47	Sequence 47, Appl	1241	133	4.7	2922	18	US-10-357-930-23149	Sequence 23149, A
1169	133	4.7	936	19	US-10-935-098-47	Sequence 47, Appl	1242	133	4.7	3055	18	US-10-425-115-128140	Sequence 128140,
1170	133	4.7	937	17	US-10-424-599-69518	Sequence 69518, A	c1243	133	4.7	3343	18	US-10-425-115-4626	Sequence 4626, Ap
1171	133	4.7	945	18	US-10-425-115-13415	Sequence 13415, A	1244	133	4.7	3454	18	US-10-723-860-6412	Sequence 6412, Ap
c1172	133	4.7	947	17	US-10-425-115-97521	Sequence 97521, A	1245	133	4.7	3505	17	US-10-389-566-204	Sequence 204, App
1173	133	4.7	973	17	US-10-424-599-58879	Sequence 58879, A	1246	133	4.7	3908	18	US-10-425-115-70814	Sequence 70814, A
1174	133	4.7	1012	18	US-10-425-115-25975	Sequence 25975, A	c1247	133	4.7	3973	15	US-10-311-455-144	Sequence 144, App
c1175	133	4.7	1016	17	US-10-424-599-133400	Sequence 133400, A	1248	133	4.7	4001	15	US-10-172-086-96	Sequence 96, Appl
1176	133	4.7	1047	17	US-10-366-288-47	Sequence 47, Appl	c1249	133	4.7	4001	18	US-10-311-507-10	Sequence 10, Appl
1177	133	4.7	1070	18	US-10-425-115-61473	Sequence 61473, A	c1250	133	4.7	4001	18	US-10-480-846-96	Sequence 20, Appl
1178	133	4.7	1071	17	US-10-170-385-338	Sequence 338, App	1251	133	4.7	4237	9	US-09-745-763-20	Sequence 20, Appl
1179	133	4.7	1078	18	US-10-425-115-13215	Sequence 13215, A	c1252	133	4.7	5586	17	US-10-257-166-86	Sequence 86, Appl
c1180	133	4.7	1086	18	US-10-425-115-168545	Sequence 168545, A	c1253	133	4.7	6134	18	US-10-433-793-170	Sequence 170, App
1181	133	4.7	1093	18	US-10-425-115-44079	Sequence 44079, A	c1254	133	4.7	6161	15	US-10-311-455-384	Sequence 384, App
1182	133	4.7	1123	18	US-10-425-115-3770	Sequence 3770, Ap	c1255	133	4.7	7369	18	US-10-473-126-131	Sequence 131, App
1183	133	4.7	1125	18	US-10-425-115-599739	Sequence 99739, A	c1256	133	4.7	7369	19	US-10-486-319A-34	Sequence 34, Appl
1184	133	4.7	1134	18	US-10-425-115-164438	Sequence 164438, A	c1257	133	4.7	8079	17	US-10-240-589C-122	Sequence 122, App
1185	133	4.7	1137	18	US-10-739-930-635	Sequence 635, App	c1258	133	4.7	10369	15	US-10-311-455-365	Sequence 365, App

c1259	133	4.7	10369	17	US-10-221-714A-25	Sequence 25, Appl	1332	130	4.6	491	18	US-10-425-115-88030	Sequence 88030, A
c1260	133	4.7	11416	15	US-10-311-455-91	Sequence 91, Appl	1333	130	4.6	501	17	US-10-424-599-50100	Sequence 50100, A
c1261	133	4.7	11416	17	US-10-221-613-19	Sequence 19, Appl	1334	130	4.6	508	17	US-10-424-599-142552	Sequence 142552, A
c1262	133	4.7	11729	15	US-10-311-455-868	Sequence 868, App	c1335	130	4.6	517	18	US-10-021-323-11054	Sequence 11054, A
c1263	133	4.7	12007	15	US-10-311-455-690	Sequence 690, App	1336	130	4.6	576	18	US-10-425-115-129331	Sequence 129331, A
c1264	133	4.7	14798	15	US-10-311-455-1005	Sequence 1005, App	1337	130	4.6	586	17	US-10-424-599-137481	Sequence 137481, A
c1265	133	4.7	16033	15	US-10-311-455-1377	Sequence 1377, App	1338	130	4.6	597	18	US-10-425-115-157303	Sequence 157303, A
c1266	133	4.7	21354	17	US-10-221-714A-512	Sequence 512, App	c1339	130	4.6	603	18	US-10-021-323-59666	Sequence 59666, App
c1267	133	4.7	35962	18	US-10-473-126-98	Sequence 98, Appl	1340	130	4.6	629	18	US-10-425-115-95192	Sequence 95192, A
c1268	133	4.7	35962	18	US-10-473-126-244	Sequence 244, App	1341	130	4.6	642	18	US-10-425-115-181737	Sequence 181737, A
c1269	133	4.7	1223197	13	US-10-027-633-179264	Sequence 179264, A	1342	130	4.6	1447	17	US-10-224-880C-27	Sequence 27, Appl
c1270	133	4.7	1223197	17	US-10-027-633-179264	Sequence 179264, A	1343	130	4.6	1509	17	US-10-424-599-53298	Sequence 53298, A
c1271	133	4.7	2140405	13	US-10-027-633-76212	Sequence 76212, A	1344	130	4.6	1615	18	US-10-425-115-149513	Sequence 149513, A
c1272	133	4.7	2140405	17	US-10-027-633-76212	Sequence 76212, A	1345	130	4.6	1738	9	US-09-918-909-27	Sequence 27, Appl
c1273	132	4.6	437	18	US-10-425-115-32234	Sequence 32234, A	1346	130	4.6	1738	18	US-10-641-991-27	Sequence 27, Appl
c1274	132	4.6	489	18	US-10-437-963-44760	Sequence 44760, A	1347	130	4.6	1782	17	US-10-424-599-22752	Sequence 22752, A
c1275	132	4.6	492	18	US-10-437-963-22765	Sequence 22765, A	1348	130	4.6	1885	17	US-10-424-599-41943	Sequence 41943, A
c1276	132	4.6	494	18	US-10-437-963-47523	Sequence 47523, A	1349	130	4.6	2444	18	US-10-425-115-122151	Sequence 122151, A
c1277	132	4.6	501	17	US-10-424-599-137556	Sequence 137556, A	1350	130	4.6	3436	9	US-09-789-561-12	Sequence 12, Appl
c1278	132	4.6	524	17	US-10-424-599-50104	Sequence 50104, A	1351	130	4.6	3436	9	US-09-790-622-3	Sequence 3, Appl
c1279	132	4.6	526	18	US-10-437-963-40887	Sequence 40887, A	1352	130	4.6	3436	15	US-10-141-953-3	Sequence 3, Appl
c1280	132	4.6	531	18	US-10-021-323-14639	Sequence 14639, A	1353	130	4.6	3436	15	US-10-083-936-12	Sequence 12, Appl
c1281	132	4.6	549	18	US-10-357-930-56681	Sequence 56681, A	c1354	129	4.5	160	9	US-09-960-352-11058	Sequence 11058, A
c1282	132	4.6	558	18	US-10-437-963-8817	Sequence 8817, App	c1355	129	4.5	242	9	US-09-960-352-3217	Sequence 3217, App
c1283	132	4.6	565	18	US-10-425-115-110392	Sequence 110392, A	c1356	129	4.5	249	18	US-10-021-323-3385	Sequence 3385, App
c1284	132	4.6	577	18	US-10-425-115-118615	Sequence 118615, A	1357	129	4.5	315	18	US-10-425-115-33701	Sequence 33701, A
c1285	132	4.6	578	18	US-10-021-323-8035	Sequence 8035, App	1358	129	4.5	368	18	US-10-021-323-5024	Sequence 5024, App
c1286	132	4.6	584	18	US-10-425-115-66870	Sequence 66870, A	1359	129	4.5	376	18	US-10-425-115-53779	Sequence 53779, A
c1287	132	4.6	608	18	US-10-425-115-179191	Sequence 179191, A	1360	129	4.5	376	18	US-10-425-115-80307	Sequence 80307, A
c1288	132	4.6	701	17	US-10-424-599-66331	Sequence 66331, A	1361	129	4.5	383	9	US-09-960-352-4720	Sequence 4720, App
c1289	132	4.6	789	18	US-10-425-115-39743	Sequence 39743, A	1362	129	4.5	395	9	US-09-960-352-8519	Sequence 8519, App
c1290	132	4.6	970	17	US-10-264-049-91	Sequence 91, Appl	1363	129	4.5	421	9	US-09-960-352-9222	Sequence 9222, App
c1291	132	4.6	1389	18	US-10-723-860-5322	Sequence 5322, App	1364	129	4.5	422	18	US-10-425-115-54417	Sequence 54417, A
c1292	132	4.6	1468	18	US-10-425-115-155843	Sequence 155843, A	1365	129	4.5	432	17	US-10-424-599-83231	Sequence 83231, A
c1293	132	4.6	2110	18	US-10-425-115-181585	Sequence 181585, A	1366	129	4.5	460	9	US-09-960-352-4953	Sequence 4953, App
c1294	132	4.6	2394	9	US-09-800-729-33	Sequence 33, Appl	1367	129	4.5	497	17	US-10-424-599-47120	Sequence 47120, A
c1295	132	4.6	2585	18	US-10-425-115-54177	Sequence 54177, A	1368	129	4.5	502	18	US-10-357-930-57784	Sequence 57784, A
c1296	132	4.6	2721	18	US-10-425-115-26594	Sequence 26594, A	1369	129	4.5	513	18	US-10-425-115-90741	Sequence 90741, A
c1297	132	4.6	6775	18	US-10-433-793-189	Sequence 189, App	1370	129	4.5	513	17	US-10-424-599-141420	Sequence 141420, A
c1298	131	4.6	131	9	US-09-770-696-616	Sequence 616, App	1371	129	4.5	538	17	US-10-424-599-8435	Sequence 8435, App
c1299	131	4.6	358	17	US-10-242-535A-16192	Sequence 16192, A	c1372	129	4.5	548	18	US-10-021-323-16019	Sequence 16019, A
c1300	131	4.6	358	17	US-10-085-783A-16192	Sequence 16192, A	1373	129	4.5	560	18	US-10-021-323-12802	Sequence 12802, A
c1301	131	4.6	362	18	US-10-425-115-36607	Sequence 36607, A	1374	129	4.5	569	17	US-10-424-599-50759	Sequence 50759, A
c1302	131	4.6	459	18	US-10-437-963-6545	Sequence 6545, App	c1375	129	4.5	578	18	US-10-021-323-7928	Sequence 7928, App
c1303	131	4.6	505	18	US-10-425-115-43909	Sequence 43909, A	1376	129	4.5	588	18	US-10-437-963-55397	Sequence 55397, A
c1304	131	4.6	526	17	US-10-424-599-89355	Sequence 89355, A	1377	129	4.5	595	17	US-10-424-599-128362	Sequence 128362, A
c1305	131	4.6	527	18	US-10-425-115-133198	Sequence 133198, A	1378	129	4.5	639	18	US-10-767-795-230	Sequence 230, App
c1306	131	4.6	539	17	US-10-424-599-61810	Sequence 61810, A	1379	129	4.5	650	17	US-10-424-599-8610	Sequence 8610, App
c1307	131	4.6	559	18	US-10-425-115-130331	Sequence 130331, A	1380	129	4.5	662	18	US-10-424-599-8610	Sequence 104281, A
c1308	131	4.6	576	18	US-10-425-115-86318	Sequence 86318, A	1381	129	4.5	679	18	US-10-425-115-54897	Sequence 54897, A
c1309	131	4.6	589	18	US-10-437-963-16840	Sequence 16840, A	1382	129	4.5	703	18	US-10-425-115-165037	Sequence 165037, A
c1310	131	4.6	597	18	US-10-425-115-176033	Sequence 176033, A	1383	129	4.5	710	17	US-10-424-599-30592	Sequence 30592, A
c1311	131	4.6	603	18	US-10-425-115-152926	Sequence 152926, A	1384	129	4.5	972	18	US-10-425-115-51692	Sequence 51692, A
c1312	131	4.6	612	18	US-10-425-115-56968	Sequence 56968, A	1385	129	4.5	1045	17	US-10-424-599-60872	Sequence 60872, A
c1313	131	4.6	840	17	US-10-424-599-49578	Sequence 49578, A	1386	129	4.5	1051	9	US-09-893-238-10	Sequence 10, Appl
c1314	131	4.6	1015	17	US-10-424-599-96139	Sequence 96139, A	1387	129	4.5	1163	18	US-10-425-115-173100	Sequence 173100, A
c1315	131	4.6	1088	18	US-10-425-115-95565	Sequence 95565, A	1388	129	4.5	1311	17	US-10-411-120-36	Sequence 36, Appl
c1316	131	4.6	1302	18	US-10-425-115-56162	Sequence 56162, A	1389	129	4.5	1880	18	US-10-425-115-44753	Sequence 44753, A
c1317	131	4.6	1372	19	US-10-887-553A-1050	Sequence 1050, App	1390	129	4.5	2034	18	US-10-739-930-3948	Sequence 3948, App
c1318	131	4.6	1635	18	US-10-425-115-85095	Sequence 85095, A	1391	129	4.5	2634	18	US-10-425-115-148096	Sequence 148096, A
c1319	131	4.6	1806	18	US-10-775-920-225	Sequence 225, App	c1392	129	4.5	6577	15	US-10-311-455-1329	Sequence 1329, App
c1320	131	4.6	1812	18	US-10-425-115-53485	Sequence 53485, A	c1393	128	4.5	6577	17	US-10-221-613-181	Sequence 181, App
c1321	131	4.6	2827	18	US-10-357-930-22992	Sequence 22992, A	c1394	128	4.5	152	9	US-09-960-352-6995	Sequence 6995, App
c1322	131	4.6	2827	18	US-10-357-930-28857	Sequence 28857, A	1395	128	4.5	365	9	US-09-960-352-5456	Sequence 5456, App
c1323	131	4.6	3101	17	US-10-424-599-95087	Sequence 95087, A	1396	128	4.5	375	17	US-10-424-599-20347	Sequence 20347, A
c1324	131	4.6	4670	18	US-10-723-860-2449	Sequence 2449, App	1397	128	4.5	391	18	US-10-425-115-12313	Sequence 12313, A
c1325	131	4.6	4672	18	US-10-723-860-6624	Sequence 6624, App	c1398	128	4.5	429	9	US-09-960-352-11097	Sequence 11097, A
c1326	130	4.6	320	18	US-10-425-115-138457	Sequence 138457, A	c1399	128	4.5	444	18	US-10-425-115-666130	Sequence 666130, A
c1327	130	4.6	399	18	US-10-425-115-150156	Sequence 150156, A	1400	128	4.5	489	18	US-10-425-115-14467	Sequence 14467, A
c1328	130	4.6	449	18	US-10-425-115-47881	Sequence 47881, A	1401	128	4.5	510	17	US-10-424-599-34481	Sequence 34481, A
c1329	130	4.6	467	18	US-10-425-115-148915	Sequence 148915, A	1402	128	4.5	511	18	US-10-425-115-63146	Sequence 63146, A
c1330	130	4.6	468	18	US-10-021-323-8271	Sequence 8271, App	1403	128	4.5	549	18	US-10-425-115-114423	Sequence 114423, A
c1331	130	4.6	474	18	US-10-021-323-10842	Sequence 10842, A	1404	128	4.5	555	18	US-10-425-115-90821	Sequence 90821, A

1405	128	4.5	556	18	US-10-021-323-14847	Sequence 14847, A
c1406	128	4.5	563	18	US-10-425-115-10912	Sequence 10912, A
1407	128	4.5	567	18	US-10-425-115-143483	Sequence 143483,
c1408	128	4.5	571	18	US-10-425-115-861	Sequence 861, App
c1409	128	4.5	577	18	US-10-021-323-162	Sequence 162, App
1410	128	4.5	579	18	US-10-357-930-58709	Sequence 58709, A
1411	128	4.5	581	18	US-10-425-115-36960	Sequence 36960, A
1412	128	4.5	582	18	US-10-425-115-83069	Sequence 83069, A
c1413	128	4.5	584	18	US-10-021-323-6395	Sequence 6395, Ap
1414	128	4.5	600	18	US-10-425-115-81134	Sequence 81134, A
1415	128	4.5	603	18	US-10-425-115-40308	Sequence 40308, A
c1416	128	4.5	606	18	US-10-425-115-147131	Sequence 147131,
1417	128	4.5	637	18	US-10-425-115-48251	Sequence 48251, A
1418	128	4.5	663	18	US-10-425-115-114479	Sequence 114479,
1419	128	4.5	1093	17	US-10-424-599-95648	Sequence 95648, A
1420	128	4.5	1099	18	US-10-425-115-36774	Sequence 36774, A
1421	128	4.5	1269	18	US-10-425-115-119668	Sequence 119668,
c1422	128	4.5	1629	18	US-10-425-115-72646	Sequence 72646, A
1423	128	4.5	1881	17	US-10-424-599-12512	Sequence 12512, A
1426	128	4.5	1985	9	US-09-905-291A-212	Sequence 212, App

Search completed: May 8, 2005, 16:05:52

Job time : 1113 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 8, 2005, 15:25:38 ; Search time 23 Seconds
(without alignments)
3012.003 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 3945

Sequence: 1 MELGCWTQLGLTFLQLLLIS.....LSTAFKVLPPKDWIERNMK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : PIR 79:*

1: Piri:*

2: Piri2:*

3: Piri3:*

4: Piri4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	949	24.1	181	2 T08805	hypothetical prote
2	672	17.0	2	A38738	coagulation factor
3	482	12.2	699	1 I54763	Ra-reactive factor
4	403.5	10.2	705	1 C1HURB	complement subcomp
5	400.5	10.2	686	1 A59271	Ra-reactive factor
6	378.5	9.6	695	1 S05008	complement subcomp
7	354	9.0	1524	2 T30337	polyprotein - Afri
8	340.5	8.6	694	2 JC6554	complement subcomp
9	334	8.5	688	1 C1HUS	complement subcomp
10	331.5	8.4	1019	1 A56318	enteropeptidase (E
11	330.5	8.4	1034	1 A53663	enteropeptidase (E
12	320	8.1	461	1 JX0210	protein C (activat
13	317.5	8.0	1035	1 A43090	enteropeptidase (E
14	314.5	8.0	475	1 EXCH	coagulation factor
15	313	7.9	855	2 JC7731	membrane-bound arg
16	310.5	7.9	461	1 KXHU	protein C (activat
17	299.5	7.6	443	2 I46932	coagulation factor
18	293.5	7.4	407	1 KFR07	coagulation factor
19	292	7.4	461	1 S18994	protein C (activat
20	285.5	7.2	452	1 A30351	coagulation factor
21	283.5	7.2	482	1 EXRT	coagulation factor
22	282	7.1	456	1 KXBO	protein C (activat
23	281.5	7.1	558	2 JC5878	plasma hyaluronan-
24	281	7.1	492	1 EXBO	coagulation factor
25	280.5	7.1	264	2 I38136	chymotrypsin-like
26	280	7.1	562	1 UKHUT	t-plasminogen acti
27	278.5	7.1	466	1 KFHU7	coagulation factor
28	278	7.0	488	1 EXHU	coagulation factor
29	278	7.0	1113	2 JE0315	low-density lipopr

30	277	7.0	559	1 A29941	t-plasminogen acti
31	277	7.0	559	1 A35029	hepatocyte growth
32	276.5	7.0	655	1 A46688	thrombin (EC 3.4.2
33	274.5	7.0	625	1 TBBO	plasma hyaluronan-
34	273	6.9	560	1 JC4795	t-plasminogen acti
35	270	6.8	477	2 JS0597	t-plasminogen acti
36	264.5	6.7	431	2 JS0599	thrombin (EC 3.4.2
37	264.5	6.7	618	2 A35827	coagulation factor
38	262.5	6.7	461	1 KFHU	t-plasminogen acti
39	262	6.6	477	2 JS0598	u-plasminogen acti
40	261.5	6.6	442	1 UKPG	u-plasminogen acti
41	261	6.6	431	1 UKHU	u-plasminogen acti
42	261	6.6	433	1 JN0560	u-plasminogen acti
43	260	6.6	477	1 A34369	chymotrypsin B - A
44	259	6.6	244	2 S72219	coagulation factor
45	259	6.6	416	1 KFO	serine proteinase
46	258.5	6.6	786	1 A47547	29K serine protein
47	258	6.5	251	2 PC1235	u-plasminogen acti
48	258	6.5	433	1 UKBAY	complement factor
49	257.5	6.5	1004	2 T30338	thrombin (EC 3.4.2
50	255.5	6.5	763	2 I50807	thrombin (EC 3.4.2
51	254	6.4	617	2 S10511	thrombin (EC 3.4.2
52	253	6.4	1070	2 T31069	thrombin (EC 3.4.2
53	249.5	6.3	400	1 A48050	coagulation factor
54	249.5	6.3	986	1 B58788	procollagen C-endo
55	248.5	6.3	459	2 JQ0419	coagulation factor
56	248	6.3	263	2 A31299	chymotrypsin (EC 3
57	248	6.3	638	1 KQHUP	plasma kallikrein
58	247.5	6.3	991	2 I49540	procollagen C-endo
59	247	6.3	275	2 A32410	trypsin (EC 3.4.2
60	247	6.3	764	1 BBHU	complement factor
61	246.5	6.2	347	2 G00006	haptoglobin - blac
62	246.5	6.2	622	1 TBHU	thrombin (EC 3.4.2
63	246	6.2	236	2 C42696	thrombin (EC 3.4.2
64	246	6.2	812	1 PLBO	plasmin (EC 3.4.21
65	245	6.2	234	2 F42696	thrombin (EC 3.4.2
66	244	6.2	638	1 KQMSPL	plasma kallikrein
67	242.5	6.1	730	1 BMHU1	procollagen C-endo
68	241.5	6.1	823	1 A58788	procollagen C-endo
69	240	6.1	242	2 S49489	trypsin (EC 3.4.21
70	239.5	6.1	406	2 HPHU2	haptoglobin precu
71	239	6.1	245	1 KYBOA	chymotrypsin (EC 3
72	238	6.0	237	1 TRCY1	trypsin (EC 3.4.21
73	238	6.0	263	2 A21195	chymotrypsin (EC 3
74	238	6.0	347	1 HPHU1	haptoglobin precu
75	238	6.0	375	1 A23689	limulus clotting e
76	237.5	6.0	810	2 I46260	plasmin (EC 3.4.21
77	237	6.0	263	1 KRTTB	chymotrypsin (EC 3
78	236.5	6.0	274	2 JC4171	trypsin (EC 3.4.2
79	236.5	6.0	707	2 JC2218	procollagen C-endo
80	235	6.0	270	2 S56160	mast cell tryptase
81	235	6.0	345	2 I36941	haptoglobin - chlm
82	235	6.0	1420	2 A32869	apolipoprotein(a)
83	233.5	5.9	263	2 S47537	chymotrypsin (EC 3
84	232	5.9	416	1 S33777	hepsin (EC 3.4.21.
85	232	5.9	638	1 KQRTPL	plasma kallikrein
86	229.5	5.8	329	1 HPDG	haptoglobin precu
87	228.5	5.8	235	2 E42696	thrombin (EC 3.4.2
88	228.5	5.8	347	1 HPMS	haptoglobin precu
89	228.5	5.8	861	2 A48825	Notch homolog Motc
90	228.5	5.8	2531	2 A46019	notch-1 protein -
91	228	5.8	812	1 PLMS	plasmin (EC 3.4.21
92	227.5	5.8	242	2 S31775	trypsin (EC 3.4.21
93	227.5	5.8	349	2 I36944	haptoglobin - chlm
94	227	5.8	242	2 S31776	trypsin (EC 3.4.21
95	227	5.8	1464	2 S58984	development protei
96	226.5	5.7	238	2 S31779	trypsin (EC 3.4.21
97	226.5	5.7	761	2 JC5759	brain-specific ser
98	226	5.7	394	2 JS0600	t-plasminogen acti
99	226	5.7	625	1 KFHU1	coagulation factor
100	225	5.7	615	1 KFHU12	coagulation factor
101	224.5	5.7	271	1 ELRT2	pancreatic elastas
102	224	5.7	245	1 KYBOB	chymotrypsin (EC 3

103	223.5	5.7	274	2	S35339	trypsin (EC 3.4.21	176	199.5	5.1	2555	2	A40043	notch protein homo
104	223.5	5.7	348	1	HPHUR	haptoglobin-relate	177	198.5	5.0	229	1	TRBOTR	trypsin (EC 3.4.21
105	222.5	5.6	417	1	S00845	hepsin (EC 3.4.21.	178	198.5	5.0	232	1	KQPG	tissue kallikrein
106	222.5	5.6	434	1	A35005	u-plasminogen acti	179	198.5	5.0	237	2	S55378	serine proteinase
107	222.5	5.6	790	1	PLPG	plasmin (EC 3.4.21	180	198	5.0	259	2	S68424	allergen Der f III
108	222	5.6	269	2	A26823	pancreatic elastas	181	198	5.0	270	2	B29934	pancreatic elastas
109	222	5.6	275	2	B35863	trypsin (EC 3.4.2	182	198	5.0	760	1	C2MS	classical-comple
110	221.5	5.6	231	2	S18188	notch protein homo	183	197.5	5.0	250	2	T01779	trypsin (EC 3.4.21
111	221	5.6	231	2	S31778	trypsin (EC 3.4.21	184	197.5	5.0	258	2	I36947	haptoglobin Hpp -
112	220.5	5.6	274	2	A45754	trypsin (EC 3.4.2	185	196.5	5.0	269	2	C26823	pancreatic elastas
113	220.5	5.6	1057	1	A32888	dorsal-ventral pat	186	196.5	5.0	570	2	A48836	fibroblastin C prec
114	220	5.6	235	2	A35863	trypsin (EC 3.4.2	187	196.5	5.0	767	2	T30018	hypothetical prote
115	219.5	5.6	235	2	H42696	thrombin (EC 3.4.2	188	196.5	5.0	2524	2	A35844	xotch protein - Af
116	219.5	5.6	271	2	A25528	pancreatic elastas	189	196	5.0	3623	2	T08618	intrinsic factor-B
117	219.5	5.6	761	1	BBMS	complement factor	190	195.5	5.0	271	2	I46580	factor IX - pig (f
118	218	5.5	343	1	A57014	proctasin (EC 3.4.	191	195	5.0	432	1	S18932	u-plasminogen acti
119	218	5.5	271	2	S41308	serine proteinase (192	194.5	4.9	246	1	TRRT1	trypsin (EC 3.4.21
120	217.5	5.5	243	2	A56338	venom proteinase	193	194	4.9	261	2	A25606	tissue kallikrein
121	217	5.5	239	2	A27207	tissue kallikrein	194	194	4.9	267	2	A40006	trypsin (EC 3.4.21
122	217	5.5	268	2	S68825	pancreatic elastas	195	193.5	4.9	249	2	A55634	granzyme M (EC 3.4
123	217	5.5	273	2	A47246	trypsin (EC 3.4.2	196	193.5	4.9	347	1	HPRT	haptoglobin precu
124	217	5.5	603	2	S28941	coagulation factor	197	193.5	4.9	2471	2	A49128	cell-fate determin
125	217	5.5	2703	1	A24420	notch protein - fr	198	193	4.9	240	1	CPBOA3	procarboxypeptidas
126	216.5	5.5	236	2	I42696	thrombin (EC 3.4.2	199	193	4.9	246	1	DBHU	complement factor
127	216.5	5.5	346	2	I36942	haptoglobin - chim	200	191.5	4.9	247	1	A25852	trypsin (EC 3.4.21
128	216.5	5.5	216	2	A57096	nudel protein prec	201	191.5	4.9	281	2	T13596	trypsin homolog -
129	216	5.5	810	1	PLHU	plasmin (EC 3.4.21	202	191.5	4.9	830	2	A30359	P-selectin precurs
130	215.5	5.5	247	1	TRDG	trypsin (EC 3.4.21	203	190.5	4.8	579	2	JC7629	membrane-type friz
131	215.5	5.5	248	2	S55066	trypsin (EC 3.4.21	204	190.5	4.8	768	2	A42755	P-selectin precurs
132	215	5.4	241	2	S39048	trypsin (EC 3.4.21	205	190.5	4.8	1064	2	A40136	fibroblastin Ia - s
133	215	5.4	268	2	S68826	pancreatic elastas	206	189.5	4.8	266	2	S54146	trypsin (EC 3.4.21
134	214.5	5.4	247	2	S18133	trypsin (EC 3.4.21	207	189.5	4.8	1737	2	T00209	MEGF8 protein - hu
135	214.5	5.4	366	2	JE0105	testicular serine	208	189	4.8	246	2	JQ1472	trypsin (EC 3.4.21
136	214.5	5.4	593	2	S45281	coagulation factor	209	189	4.8	247	2	S05494	serine proteinase
137	214	5.4	275	2	C35863	trypsin (EC 3.4.2	210	189	4.8	253	2	A53968	pancreatic elastas
138	213.5	5.4	235	2	D42696	thrombin (EC 3.4.2	211	189	4.8	258	4	S70439	probable pancreati
139	213.5	5.4	232	2	T30201	Notch homolog prot	212	189	4.8	267	4	A56615	P-selectin precurs
140	212	5.4	260	2	I58559	neutropsin - mouse	213	189	4.8	646	2	UN0473	coagulation factor
141	212	5.4	455	2	A61545	plasmin (EC 3.4.21	214	188.5	4.8	282	2	I84621	tissue kallikrein
142	211	5.3	237	2	S68702	trypsin (EC 3.4.2	215	188	4.8	263	2	S15686	serine proteinase
143	211	5.3	276	2	A36154	mast cell protein	216	187.5	4.8	250	2	S55493	trypsin (EC 3.4.21
144	210.5	5.3	1220	2	A56136	jagged protein pre	217	187.5	4.8	259	2	I38363	trypsin (EC 3.4.21
145	210	5.3	2437	1	UKMS	transmembrane prot	218	187.5	4.8	304	2	S33496	trypsin (EC 3.4.21
146	209	5.3	433	1	UKMS	u-plasminogen acti	219	187	4.7	246	2	JQ1471	tissue kallikrein
147	208.5	5.3	258	2	I36945	haptoglobin Hp - C	220	187	4.7	261	2	S45303	chymotrypsin (EC 3
148	207.5	5.3	239	2	G42696	thrombin (EC 3.4.2	221	187	4.7	1594	2	T30549	hensin - rabbit
149	207.5	5.3	269	2	B26823	pancreatic elastas	222	186	4.7	927	1	JQ0948	macrophage-stimula
150	207	5.2	238	1	TRWVSY	trypsin-like prote	223	185.5	4.7	711	1	A47136	A5 antigen precurs
151	206.5	5.2	246	2	TRRT2	trypsin (EC 3.4.21	224	185.5	4.7	927	1	JQ0948	7S nerve growth fa
152	206.5	5.2	256	2	T10109	trypsin (EC 3.4.21	225	185	4.7	256	1	NGMSA	hypothetical prote
153	206	5.2	430	1	A24702	serine proteinase	226	183.5	4.7	1372	2	T25933	tissue kallikrein
154	206	5.2	4548	1	S00657	apoprotein(a) (EC	227	183	4.6	265	1	KQRTP	serine proteinase
155	205.5	5.2	269	2	B32410	mastocytoma protei	228	183	4.6	392	2	A30100	E-selectin - pig
156	205.5	5.2	460	2	B61545	plasmin (EC 3.4.21	229	182.5	4.6	482	2	JCS092	DELTA-like 1 - mou
157	204.5	5.2	367	2	JE0104	testicular serine	230	182.5	4.6	722	2	I48324	notch homolog - se
158	204.5	5.2	752	1	C2HU	complement C2 prec	231	182.5	4.6	2531	2	T31070	tissue kallikrein
159	204.5	5.2	1203	2	A49175	Notch B protein -	232	182	4.6	261	1	TRMSM5	trypsin (EC 3.4.21
160	203.5	5.2	247	1	B25852	trypsin (EC 3.4.21	233	181.5	4.6	247	2	PRMSCL	granzyme B (EC 3.4
161	203.5	5.2	263	1	I55608	complement factor	234	181.5	4.6	247	2	S12764	trypsin (EC 3.4.21
162	203.5	5.2	285	2	I48144	coagulation factor	235	181.5	4.6	258	2	A45161	serine proteinase
163	203.5	5.2	309	2	B49878	coagulation factor	236	181.5	4.6	437	2	S18407	acrosin (EC 3.4.21
164	203.5	5.2	3623	2	T09456	intrinsic factor-B	237	181	4.6	261	1	NGMSG	7S nerve growth fa
165	203	5.1	403	2	C82228	probable trypsin V	238	181	4.6	418	2	A37344	hypothetical prote
166	202	5.1	240	2	S39047	trypsin (EC 3.4.21	239	181	4.6	1291	2	T21694	trypsin (EC 3.4.21
167	202	5.1	2321	2	S78549	notch3 protein - h	240	180.5	4.6	248	2	S55067	factor IX - rabbit
168	201.5	5.1	246	2	B25528	trypsin (EC 3.4.21	241	180.5	4.6	275	2	I46712	acrosin (EC 3.4.21
169	200.5	5.1	226	1	KCUF	bradykinin (EC 3.4	242	180.5	4.6	436	2	JX0172	trypsin-like prote
170	200.5	5.1	231	1	TRPGTR	trypsin (EC 3.4.21	243	180	4.6	254	2	S49329	tissue kallikrein
171	200.5	5.1	810	2	B30848	plasmin (EC 3.4.21	244	180	4.6	261	2	S01971	trypsin (EC 3.4.21
172	199.5	5.1	247	2	A23547	trypsin (EC 3.4.21	245	180	4.6	275	2	S40005	complement factor
173	199.5	5.1	257	2	S33772	tissue kallikrein	246	179.5	4.6	243	2	A35871	trypsin (EC 3.4.21
174	199.5	5.1	258	2	G02959	haptoglobin - rhes	247	179.5	4.6	259	1	WNMS28	coagulation factor
175	199.5	5.1	275	2	S40007	trypsin (EC 3.4.21	248	179.5	4.6	274	2	I47078	coagulation factor

249	179.5	4.6	728	2	I50719	C-Delta-1 - chicke	322	161.5	4.1	250	2	S31384	trypsin (EC 3.4.21
250	179.5	4.6	1047	1	AS5617	masquerade precurs	323	161.5	4.1	261	2	S40162	cathepsin G (EC 3.
251	179	4.5	266	1	ELPG	pancreatic elastas	324	161.5	4.1	265	2	T15451	hypothetical prote
252	179	4.5	612	2	B42755	E-selectin precurs	325	161.5	4.1	832	2	A31246	neurogenic protein
253	178.5	4.5	402	2	JH0403	procollagen I C-pr	326	161.5	4.1	880	2	S00670	neurogenic repetit
254	177.5	4.5	248	2	A43520	natural killer cel	327	161.5	4.1	1025	1	A43526	complement C3d/Eps
255	177.5	4.5	420	2	A55283	acrosin (EC 3.4.21	328	161	4.1	1827	2	T34288	hypothetical prote
256	177.5	4.5	1964	2	T09059	notch4 - mouse	329	160.5	4.1	661	1	KFHU13	coagulation factor
257	177	4.5	268	2	JQ1473	pancreatic elastas	330	160	4.1	262	1	A31372	granzyme A (EC 3.4
258	177	4.5	473	2	A56175	adhesive plaque pr	331	160	4.1	3002	2	A47221	fibrillin-1 precu
259	177	4.5	747	2	I51579	complement factor	332	159.5	4.0	1722	2	E89753	protein FltC7.4 [i
260	176.5	4.5	1091	1	PL0009	complement C3d/Eps	333	159	4.0	244	2	A44284	tissue kallikrein
261	176	4.5	261	2	A29745	tissue kallikrein	334	159	4.0	261	2	A28062	gamma-renin (EC 3.
262	176	4.5	261	2	A31136	tissue kallikrein	335	159	4.0	2907	2	A57278	fibrillin-2 precu
263	176	4.5	264	2	S32794	tissue kallikrein	336	158.5	4.0	247	2	S59135	mast cell proteina
264	176	4.5	2318	2	S45306	notch 3 protein -	337	158.5	4.0	835	2	S53718	homotetic protein d
265	175.5	4.4	274	2	S40004	trypsin-related pr	338	158.5	4.0	833	2	S19087	gene Delta protein
266	175	4.4	270	2	A29834	pancreatic elastas	339	158	4.0	610	2	T16761	hypothetical prote
267	175	4.4	421	1	S11674	acrosin (EC 3.4.21	340	158	4.0	2918	2	A54105	fibrillin-2 precu
268	174.5	4.4	232	2	S32398	serine proteinase	341	157.5	4.0	579	2	A56740	spem-egg recognit
269	174.5	4.4	246	1	TRDC	trypsin (EC 3.4.21	342	157.5	4.0	907	2	T27317	hypothetical prote
270	174	4.4	259	2	A29746	tissue kallikrein	343	157	4.0	261	2	JE0236	tissue kallikrein
271	174	4.4	261	1	KQWS1	tissue kallikrein	344	157	4.0	610	2	A35046	E-selectin precurs
272	174	4.4	1295	2	A32901	glpl protein precu	345	156.5	4.0	252	2	A36172	procytotoxic T-lym
273	173.5	4.4	548	2	D82175	probable trypsin v	346	156.5	4.0	275	2	JC6506	tumor necrosis fac
274	173	4.4	229	1	TRDFS	trypsin (EC 3.4.21	347	156.5	4.0	1429	2	S06434	homotetic protein 1
275	173	4.4	768	2	I53821	P-selectin - rat	348	156.5	4.0	3635	2	T10053	laminin alpha 5 ch
276	172.5	4.4	248	1	PRMSC2	granzyme C (EC 3.4	349	156	4.0	259	1	KQRTTN	tonin (EC 3.4.21.-
277	172.5	4.4	277	2	S35340	trypsin (EC 3.4.21	350	156	4.0	261	2	A29586	tissue kallikrein
278	172.5	4.4	431	2	S47538	acrosin (EC 3.4.21	351	156	4.0	702	2	T16832	hypothetical prote
279	172.5	4.4	449	2	A55362	procollagen I C-pr	352	155.5	3.9	213	2	S17537	fibrinolytic prote
280	172	4.4	254	2	S65462	trypsin-like prote	353	155.5	3.9	485	2	S36772	E-selectin - bovin
281	172	4.4	261	2	A24378	tissue kallikrein	354	155.5	3.9	533	2	JC7985	brain-specific CUB
282	172	4.4	415	1	A34170	acrosin (EC 3.4.21	355	155	3.9	250	2	S15685	kallikrein, glandu
283	171.5	4.3	230	2	A27802	hypodermin C (EC 3	356	155	3.9	2489	2	I73012	complement C3b/C4b
284	171.5	4.3	262	1	KQHU	tissue kallikrein	357	154.5	3.9	252	2	A34877	C4b-binding protei
285	171.5	4.3	2403	2	A59386	sanko - human	358	154	3.9	669	2	S65551	factor H - bovine
286	171	4.3	257	2	B45061	granzyme A (EC 3.4	359	153.5	3.9	251	2	JC2125	chymase (EC 3.4.21
287	171	4.3	260	2	A45061	granzyme A (EC 3.4	360	153.5	3.9	387	2	B49175	Motch A protein -
288	171	4.3	266	1	ELRT1	pancreatic elastas	361	153.5	3.9	551	1	I46709	endothelial leukoc
289	171	4.3	273	2	S40003	trypsin-related pr	362	153.5	3.9	1786	1	MMMSB1	laminin beta-1 cha
290	171	4.3	2139	2	A35672	crumbs protein - f	363	153	3.9	152	2	A53274	complement factor
291	170	4.3	248	2	S33756	granzyme-like prot	364	153	3.9	254	1	TRWV3Y	trypsin-like prote
292	170	4.3	266	2	JC4850	trypsin-like prote	365	153	3.9	2871	2	A55567	fibrillin I - bovi
293	169.5	4.3	251	2	T10262	mast cell serine p	366	152.5	3.9	248	1	S01007	granzyme F (EC 3.4
294	169.5	4.3	261	1	S35711	semenogelase (EC 3	367	152.5	3.9	264	2	S65663	granzyme F (EC 3.4
295	169.5	4.3	421	2	S29599	acrosin (EC 3.4.21	368	152.5	3.9	385	2	A54785	preadipocyte facto
296	169.5	4.3	560	2	T16833	hypothetical prote	369	152.5	3.9	422	1	KXHUZ	plasma protein 2 p
297	169	4.3	214	2	S17680	fibrinolytic prote	370	152	3.9	281	1	A61021	granzyme B (EC 3.4
298	169	4.3	246	2	S64707	chymase (EC 3.4.21	371	152	3.9	686	2	JC7569	Delta-4 protein -
299	169	4.3	259	2	B31136	tissue kallikrein	372	151.5	3.8	261	2	A34079	tissue kallikrein
300	169	4.3	504	2	S56745	mucin (clone pGM31	373	151.5	3.8	716	1	A40332	macrophage-stimula
301	168.5	4.3	273	2	S31755	granzyme-like prot	374	151.5	3.8	977	2	I52657	seizure-related pr
302	168	4.3	597	2	S71352	metalloproteinase	375	151	3.8	249	1	A35842	chymase (EC 3.4.21
303	168	4.3	2014	2	I36936	complement recept	376	151	3.8	261	2	A41020	tissue kallikrein
304	167.5	4.2	261	1	A32297	semenogelase (EC 3	377	151	3.8	1620	2	T27283	hypothetical prote
305	167.5	4.2	383	2	S53716	delta-like homeoti	378	150.5	3.8	248	2	S43259	granzyme-like prot
306	167	4.2	247	2	A45113	granzyme-like prot	379	150.5	3.8	277	2	A41735	hyaluronate-bindin
307	167	4.2	260	2	A37938	tissue kallikrein	380	150.5	3.8	285	2	T35195	probable serine pr
308	166	4.2	265	2	T10495	chymotrypsin (EC 3	381	150.5	3.8	685	2	JC7570	Delta-4 protein -
309	165	4.2	2043	2	T18524	scavenger receptor	382	150.5	3.8	1053	2	S46199	probable complemen
310	164.5	4.2	449	1	NBHUHS	complement factor	383	150	3.8	263	1	WMVZSP	apolipoprotein H h
311	164.5	4.2	1231	1	NBHUH	complement factor	384	150	3.8	267	1	ELHUL	leukocyte elastase
312	164	4.2	230	2	I48685	mast cell proteina	385	150	3.8	601	2	B36346	fibulin 1 precurs
313	164	4.2	613	2	S15468	complement C3b/C4b	386	150	3.8	770	2	T00203	LDL receptor-relat
314	164	4.2	2871	2	A55624	fibrillin-1 precu	387	150	3.8	3712	2	S18253	laminin alpha-1 ch
315	163	4.1	868	2	T20239	hypothetical prote	388	149.5	3.8	236	1	A32121	snake venom factor
316	162.5	4.1	276	2	A47290	TSG-6 homolog PS4	389	149.5	3.8	259	1	TRSMG	trypsin (EC 3.4.21
317	162.5	4.1	1290	2	A57190	ebnerin precursor	390	149.5	3.8	13288	2	T03099	mucin, submaxillar
318	162.5	4.1	2083	2	T42721	CRP-ductin-alpha p	391	149	3.8	216	1	KVH20	chymotrypsin (EC 3
319	162	4.1	261	1	EGMSB	tissue kallikrein	392	149	3.8	683	2	C36346	fibulin 1 precurs
320	161.5	4.1	226	2	S69370	duodenase - bovine	393	149	3.8	770	2	T02004	LDL receptor relat
321	161.5	4.1	248	2	S01006	cytotoxic T-lympho	394	149	3.8	1408	2	S16148	gene serrate prote

395	148	3.8	218	1	KYVH2C	chymotrypsin (EC 3	468	134	3.4	3034	2	T14119	seven-pass transme
396	148	3.8	668	2	A46013	coagulation factor	469	133.5	3.4	154	2	S35207	proteinase 7 - buf
397	148	3.8	1469	2	B36665	slit protein 2 pre	470	133.5	3.4	1687	2	T30176	EGF repeat transme
398	148	3.8	1480	2	A36665	slit protein 1 pre	471	133.5	3.4	3507	2	T34513	hypothetical prote
399	147.5	3.7	244	2	A46721	chymase (EC 3.4.21	472	133	3.4	810	2	T10756	Nel-homolog protei
400	147.5	3.7	244	2	A34910	mast cell protein a	473	132.5	3.4	331	2	T27906	hypothetical prote
401	147.5	3.7	597	1	S53711	C4BP alpha chain p	474	132	3.3	246	2	A38678	mast cell proteina
402	147.5	3.7	1786	1	MMHSA	laminin beta-1 cha	475	132	3.3	372	2	JC5377	L-selectin precurs
403	147.5	3.7	4391	2	A38096	perlecan precursor	476	132	3.3	558	2	S57953	C4BP protein alpha
404	147	3.7	236	2	A28566	T-cell suppressor	477	132	3.3	3109	1	I50421	aggreccan precursor
405	147	3.7	259	2	D23863	tissue kallikrein	478	132	3.3	3871	2	T28112	hypothetical prote
406	147	3.7	262	1	JC4803	macrombin A (EC 3.4	479	131.5	3.3	302	1	WMBE1E	secretory compleme
407	147	3.7	716	1	JC5061	hypothetical prote	480	131.5	3.3	1268	2	S52781	neurocan - mouse
408	147	3.7	1557	2	T28811	hypothetical prote	481	130.5	3.3	1257	2	S28764	hypothetical prote
409	147	3.7	3084	1	MMHSA	laminin alpha-1 ch	482	130.5	3.3	3672	2	T23433	probable laminin a
410	146.5	3.7	236	1	B32121	snake venom factor	483	130.5	3.3	3704	2	T37316	venombin A (EC 3.4
411	146.5	3.7	3707	2	S18252	heparan sulfate pr	484	129.5	3.3	233	1	JG0169	L-selectin precurs
412	146	3.7	263	2	T28450	hypothetical prote	485	129.5	3.3	376	2	JC4892	decay-accelerating
413	145	3.7	256	1	TRPF	trypsin-like prote	486	129.5	3.3	381	1	A26359	decay-accelerating
414	145	3.7	263	1	C36838	complement control	487	129.5	3.3	440	2	A26359	venombin AB (EC 3
415	145	3.7	372	1	A32375	L-selectin precurs	488	129	3.3	235	1	S65621	cathepsin G (EC 3
416	145	3.7	782	2	A61625	tenascin-like prote	489	128.5	3.3	255	2	A27122	hypothetical prote
417	144.5	3.7	246	2	B36678	mast cell proteina	490	128.5	3.3	321	2	T33161	azurocidin - pig
418	144.5	3.7	303	2	T13598	trypsin homolog -	491	128	3.2	219	1	TRFGAZ	cadherin-related t
419	144.5	3.7	360	2	T42921	complement control	492	128	3.2	5147	1	IJPFMT	slit-1 protein hom
420	144	3.7	263	2	B72152	B18L protein - var	493	127.5	3.2	1531	2	T42218	trypsinase 2 - rat
421	144	3.7	685	2	S78040	fibulin, splice fo	494	127	3.2	258	2	I56220	laminin gamma-1 ch
422	143.5	3.6	247	2	S23504	chymase (EC 3.4.21	495	127	3.2	1609	1	MMHUB2	laminin alpha-2 ch
423	143	3.6	3075	2	S14458	laminin alpha-1 ch	496	127	3.2	1751	1	MMHUMH	laminin alpha-2 ch
424	142.5	3.6	260	2	S26043	chymase (EC 3.4.21	497	127	3.2	3106	1	S53868	secreted leucine-r
425	142	3.6	272	2	JC4170	trypsin-like prote	498	126.5	3.2	1025	2	T42626	serine proteinase
426	141.5	3.6	310	2	S41055	metalloproteinase	499	126	3.2	265	2	A38894	serine proteinase
427	141.5	3.6	385	1	A34015	L-selectin precurs	500	126	3.2	265	2	J80260	complement factor
428	141	3.6	225	2	S43566	probable serine pr	501	126	3.2	330	2	I56100	plasma protein S p
429	141	3.6	246	2	A32692	cytotoxic T-lympho	502	126	3.2	642	2	S53433	chymotrypsin-like
430	140.5	3.6	234	1	A46504	chymase (EC 3.4.21	503	125.5	3.2	254	2	S35585	neutrophil elastas
431	140.5	3.6	1234	1	NBMWSH	complement factor	504	125.5	3.2	265	2	I48679	C4b-binding protei
432	140.5	3.6	2406	2	A54148	odx protein - frui	505	125.5	3.2	597	1	NBHUC4	serine proteinase
433	140.5	3.6	2515	2	S47008	tenascin-like prot	506	125	3.2	152	2	S35209	serine proteinase
434	140	3.5	396	1	KXBOZ	plasma protein Z -	507	125	3.2	323	1	S09702	L-selectin precurs
435	139.5	3.5	258	1	S44184	chymotrypsin (EC 3	508	125	3.2	1790	2	MMFFB1	laminin beta-1 cha
436	139.5	3.5	288	2	T33224	hypothetical prote	509	124.5	3.2	248	2	A33412	cytotoxic T-lympho
437	139.5	3.5	319	2	I51569	UVS 2 protein - Af	510	124.5	3.2	548	2	T16642	hypothetical prote
438	139	3.5	1820	2	A55494	latent transformin	511	124	3.1	330	2	T46256	brevican - human (
439	138.5	3.5	244	2	S26042	chymase (EC 3.4.21	512	124	3.1	710	1	I51283	hepatocyte growth
440	138.5	3.5	247	1	KYHUCM	chymase (EC 3.4.21	513	124	3.1	883	2	A53126	brevican precursor
441	138.5	3.5	705	2	S34968	fibulin, splice fo	514	124	3.1	1221	2	A49457	fibulin-2 precursor
442	138.5	3.5	1111	2	T26972	hypothetical prote	515	124	3.1	1523	2	T13953	MEGF5 protein - ra
443	137.5	3.5	191	2	S54115	complement factor	516	124	3.1	1584	2	T22674	hypothetical prote
444	137.5	3.5	808	2	D35069	complement factor	517	124	3.1	2180	2	T29764	hypothetical prote
445	137	3.5	258	2	S57960	C4BP protein beta	518	123.5	3.1	151	2	S35205	proteinase 5 - buf
446	137	3.5	372	2	S23936	L-selectin precurs	519	123.5	3.1	259	1	S43129	chymotrypsin (EC 3
447	137	3.5	2823	2	F87908	protein T2A3.8 (i	520	123.5	3.1	370	2	S22124	L-selectin precurs
448	137	3.5	2823	2	T23064	hypothetical prote	521	123.5	3.1	699	2	T33375	hypothetical prote
449	137	3.5	3102	2	T43291	laminin alpha chai	522	123.5	3.1	1184	2	A55184	fibulin-2 precursor
450	136.5	3.5	247	1	PRRTG	mast cell proteina	523	123	3.1	248	2	S49323	chymotrypsin (EC 3
451	136.5	3.5	1274	2	T42017	cysteine rich prot	524	123	3.1	308	2	JC7125	epidermal growth f
452	136	3.4	360	1	WMBE2E	membrane-bound com	525	123	3.1	340	2	I56234	decay-accelerating
453	136	3.4	676	2	A45900	complement C3b rec	526	123	3.1	798	2	T22793	hypothetical prote
454	136	3.4	1574	2	T13954	MEGF6 protein - ra	527	123	3.1	2844	2	S28291	hypothetical prote
455	136	3.4	1607	1	MMMSB2	laminin gamma-1 ch	528	122.5	3.1	1081	2	T31329	receptor tyrosine
456	135.5	3.4	226	2	JE0151	myonase (EC 3.4.-	529	122	3.1	152	2	S35206	serine proteinase
457	135.5	3.4	372	2	T29359	hypothetical prote	530	122	3.1	198	2	I46002	C4BP beta chain -
458	135.5	3.4	452	2	A35068	complement factor	531	122	3.1	676	1	KXHUS	plasma protein S p
459	135.5	3.4	469	1	NBMSC4	C4b-binding protei	532	122	3.1	1810	1	A32230	tenascin precursor
460	135	3.4	159	2	I84615	coagulation factor	533	122	3.1	1955	1	AGCH	agrin precursor -
461	135	3.4	343	2	G35070	apolipoprotein H-r	534	121.5	3.1	245	2	A48598	kallikrein-like se
462	135	3.4	345	1	NBUH	apolipoprotein H p	535	121.5	3.1	416	2	T20448	hypothetical prote
463	135	3.4	3051	2	S42373	hypothetical prote	536	121.5	3.1	610	2	I46001	C4b-binding protei
464	134.5	3.4	601	2	T22025	hypothetical prote	537	121.5	3.1	576	2	T42215	zonadhesin - mouse
465	134.5	3.4	601	2	D89711	protein F40E10.4 [538	121	3.1	647	2	A43902	tenascin - eastern
466	134	3.4	232	1	A54361	venombin A (EC 3.4	539	121	3.1	1627	2	S65464	pregnancy-associat
467	134	3.4	2824	2	T22759	hypothetical prote	540	121	3.1	2409	1	A60979	versican precursor

541	120.5	3.1	247	2	S64708	chymase (EC 3.4.21	614	112	2.8	228	1	S35689	venombin A (EC 3.4
542	120.5	3.1	252	2	T46247	hypothetical prote	615	112	2.8	228	2	JC4361	scavenger receptor
543	120.5	3.1	345	1	JN0465	apolipoprotein H p	616	112	2.8	1125	1	S57846	protein-tyrosine k
544	120.5	3.1	497	2	JC2054	complement regulat	617	112	2.8	1353	1	JH0675	restrictin precurs
545	120.5	3.1	646	2	S38819	plasma protein S -	618	112	2.8	1639	1	MMPEB2	laminin gamma-1 ch
546	120.5	3.1	689	2	T42760	fibulin, splice fo	619	112	2.8	3562	2	A47171	chondroitin sulfat
547	120.5	3.1	712	2	T42990	fibulin 1, splice	620	112	2.8	4307	2	T20721	hypothetical prote
548	120.5	3.1	728	1	A60185	hepatocyte growth	621	111.5	2.8	159	2	S35202	proteinasase 2 - buf
549	120.5	3.1	1394	2	A56626	transforming growt	622	111.5	2.8	370	2	JC7592	spinal cord-derive
550	120.5	3.1	1801	1	MMRTS	laminin beta-2 cha	623	111.5	2.8	651	2	T19477	hypothetical prote
551	120	3.0	257	1	JC2479	venombin B (EC 3.4	624	111.5	2.8	1328	2	T43060	agrin - electric r
552	120	3.0	363	2	B45900	complement C3d/Bps	625	111.5	2.8	1797	2	A55677	laminin beta-2 cha
553	120	3.0	493	2	JC5621	epidermal growth f	626	111.5	2.8	2019	1	JQ1322	tenascin precursor
554	120	3.0	589	2	T43210	fibulin-ID precurs	627	111.5	2.8	2531	2	T16743	hypothetical prote
555	120	3.0	912	2	A54423	brevicin precursor	628	111.5	2.8	4351	2	T00252	MEGF1 protein - ra
556	120	3.0	1548	2	S34583	serine proteinase	629	111	2.8	231	2	A60468	venombin A (EC 3.4
557	120	3.0	1643	2	T14274	versican precursor	630	111	2.8	915	2	T21773	hypothetical prote
558	120	3.0	2397	1	A55535	versican precursor	631	110.5	2.8	234	1	S20407	venombin A (EC 3.4
559	120	3.0	3381	2	T43389	versican precursor	632	110.5	2.8	297	1	NBRT	apolipoprotein H p
560	119.5	3.0	161	2	I48158	coagulation factor	633	110.5	2.8	408	2	T22801	hypothetical prote
561	119.5	3.0	482	2	A34924	complement C3b/C4b	634	110.5	2.8	583	2	A29154	complement factor
562	119.5	3.0	675	1	KXBOS	plasma protein S p	635	110.5	2.8	678	2	B48089	growth arrest-spec
563	119.5	3.0	835	2	JP0076	nel protein - chic	636	110.5	2.8	692	2	T32980	hypothetical prote
564	119.5	3.0	1247	1	MMHUND	nidogen precursor	637	110.5	2.8	961	1	TSHP4	thrombospondin 4 p
565	119.5	3.0	1506	2	T30886	integumentary muc	638	110.5	2.8	1217	1	EGMSMG	epidermal growth f
566	119	3.0	258	2	A57290	venom plasminogen	639	110.5	2.8	1894	2	JC4980	plexin 1 precursor
567	119	3.0	513	2	D88991	protein apx-1 [imp	640	110	2.8	266	2	T19292	hypothetical prote
568	118.5	3.0	674	2	I55476	growth potentiatio	641	110	2.8	1124	1	I58388	protein-tyrosine k
569	118.5	3.0	728	1	A35644	hepatocyte growth	642	110	2.8	1905	2	I51553	Plexin - African c
570	118.5	3.0	728	1	JH0579	hepatocyte growth	643	109.5	2.8	198	2	S06176	cytotoxic T-lympho
571	118	3.0	133	2	S21114	spermadhesin AWN -	644	109.5	2.8	2215	2	T00348	lukil protein - mou
572	118	3.0	196	2	T08800	hypothetical prote	645	109	2.8	661	2	T42754	hypothetical prote
573	118	3.0	293	2	B26637	neurogenic repetit	646	109	2.8	1808	2	T15099	hypothetical prote
574	118	3.0	838	2	T20125	hypothetical prote	647	109	2.8	2610	2	T20968	hypothetical prote
575	118	3.0	883	2	S57653	brevican precursor	648	108.5	2.8	236	1	A41456	venombin A (EC 3.4
576	117.5	3.0	188	2	B32340	tissue kallikrein	649	108.5	2.8	2825	2	T14271	Doc4 protein, stre
577	117.5	3.0	259	2	T21011	hypothetical prote	650	108	2.7	251	1	TRH04Z	azurocidin precurs
578	117.5	3.0	642	2	S53434	plasma protein S p	651	108	2.7	1450	2	T30273	hypothetical prote
579	117.5	3.0	996	2	JB0237	apolipoprotein E r	652	108	2.7	1700	2	S08167	hypothetical prote
580	117.5	3.0	1160	2	F88369	protein unc-52 [im	653	108	2.7	2476	2	T34022	zonadhesin - pig
581	117.5	3.0	2295	2	C88369	protein unc-52 [im	654	107.5	2.7	640	2	T19346	hypothetical prote
582	117.5	3.0	3375	1	T19821	hypothetical prote	655	107.5	2.7	670	2	I65967	disintegrin-like m
583	116.5	3.0	256	1	PRH03	proteinasase 3 (EC 3	656	107.5	2.7	3566	1	A40701	tenascin-X precurs
584	116.5	3.0	377	2	I54479	membrane cofactor	657	107.5	2.7	4544	1	S02392	alpha-2-macroglobu
585	116.5	3.0	378	2	B59180	Wnt inhibitory fac	658	107	2.7	280	2	G02741	skeletal muscle LI
586	116.5	3.0	384	2	S01896	membrane cofactor	659	107	2.7	497	2	T27827	hypothetical prote
587	116.5	3.0	1170	2	A53612	laminin Bk chain	660	106.5	2.7	192	2	E70414	hypothetical prote
588	116	2.9	1376	2	G00043	osteonidogen - hum	661	106.5	2.7	362	2	JC5194	membrane cofactor
589	115.5	2.9	440	2	A43519	complement recepto	662	106.5	2.7	369	2	JC5138	hypothetical prote
590	115.5	2.9	1474	2	D88550	protein ZC84.6 [im	663	106.5	2.7	616	2	T29234	cartilage oligomer
591	115.5	2.9	1680	2	A43434	furin (EC 3.4.21.7	664	106.5	2.7	755	2	A44315	hypothetical prote
592	115	2.9	279	2	JG0164	LIM protein, FHL4	665	106	2.7	417	2	T33376	hypothetical prote
593	115	2.9	1207	1	EGHU	epidermal growth f	666	106	2.7	657	2	T00859	hypothetical prote
594	114.5	2.9	270	2	I37278	complement factor	667	106	2.7	927	2	T21772	hypothetical prote
595	114.5	2.9	349	2	G02913	sperm CD46 - human	668	106	2.7	1133	1	EGRT	epidermal growth f
596	114.5	2.9	369	2	I57998	membrane cofactor	669	106	2.7	1142	2	T30272	hypothetical prote
597	114.5	2.9	1798	2	S53869	laminin beta-2 cha	670	106	2.7	1522	2	H88380	protein T22F7.3 [i
598	114	2.9	255	1	A28169	venombin A (EC 3.4	671	106	2.7	1805	2	T21888	hypothetical prote
599	114	2.9	741	2	T46488	hypothetical prote	672	106	2.7	2195	2	T34264	hypothetical prote
600	114	2.9	846	2	A30889	integrin beta chai	673	105.5	2.7	346	2	T46914	hypothetical prote
601	114	2.9	1069	2	T42681	hypothetical prote	674	105.5	2.7	596	2	A45664	variant-specific s
602	113.5	2.9	293	2	T22919	hypothetical prote	675	105.5	2.7	673	2	A48089	growth arrest-spec
603	113.5	2.9	502	2	T20130	hypothetical prote	676	105	2.7	860	1	QRHULD	LDL receptor precu
604	113.5	2.9	558	2	T17324	hypothetical prote	677	105	2.7	1107	2	T15884	hypothetical prote
605	113.5	2.9	574	2	B88465	protein B0244.8 [i	678	105	2.7	1746	1	S15694	tenascin precursor
606	113.5	2.9	879	1	QRRLD	LDL receptor precu	679	105	2.7	2201	2	A32160	tenascin-C - human
607	113.5	2.9	1712	2	A38261	masking protein pr	680	104.5	2.7	345	1	NEMS	apolipoprotein H p
608	112.5	2.9	161	2	I62744	coagulation factor	681	104.5	2.6	1360	2	T33922	hypothetical prote
609	112.5	2.9	264	2	A28942	pancreatic elastase	682	104	2.6	345	1	NBBO	apolipoprotein H p
610	112.5	2.9	370	2	JC7591	spinal cord-derive	683	104	2.6	360	1	A55198	transcription fact
611	112.5	2.9	677	2	A42125	trophozoite cystei	684	104	2.6	379	2	A59180	Wnt inhibitory fac
612	112.5	2.9	1228	2	A57384	multimerin, endoth	685	104	2.6	473	2	T23226	hypothetical prote
613	112.5	2.9	1797	2	T21889	hypothetical prote	686	104	2.6	2101	2	S57245	insulin receptor (

687	104	2.6	4135	2	T42629	tenascin-X - bovin	760	98	2.5	102	2	B55885	chondroitin sulfat
688	103.5	2.6	383	2	T21946	hypothetical prote	761	98	2.5	357	2	S23403	sperm surface prot
689	103	2.6	331	2	A45222	complement factor	762	98	2.5	909	1	QRXLL1	LDL receptor 1 pre
690	103	2.6	412	2	S72579	hypothetical prote	763	98	2.5	937	2	I53282	gene PAC3A protein
691	103	2.6	1296	2	T16859	hypothetical prote	764	98	2.5	1087	2	T31100	probable potassium
692	103	2.6	2148	1	A56081	insulin receptor -	765	98	2.5	1748	1	JN0786	integrin beta-4 ch
693	102.5	2.6	153	2	S35204	proteinase 4 - buf	766	98	2.5	2588	2	T14342	NSD1 protein - mou
694	102.5	2.6	473	2	T43283	ADAM 4 protein pre	767	98	2.5	4660	2	T42737	gp330 protein prec
695	102.5	2.6	565	2	T16408	hypothetical prote	768	97.5	2.5	577	2	A60501	thrombomodulin pre
696	102.5	2.6	873	1	QR8VDD	VLDL receptor prec	769	97.5	2.5	837	1	A29512	LDL receptor precu
697	102	2.6	149	2	S35208	serine proteinase	770	97.5	2.5	878	2	B71460	probable outer mem
698	102	2.6	280	2	G01884	LIM protein FHL-1,	771	97.5	2.5	884	2	T18649	hypothetical prote
699	102	2.6	380	2	G01639	transmembrane prot	772	97.5	2.5	1162	2	T21557	hypothetical prote
700	102	2.6	411	2	D88087	protein B0454.7 li	773	97.5	2.5	2946	2	T15840	hypothetical prote
701	102	2.6	718	2	T29448	hypothetical prote	774	97	2.5	126	2	A23473	chymotrypsin-like
702	102	2.6	863	1	S51789	VLDL receptor prec	775	97	2.5	379	2	T27350	hypothetical prote
703	102	2.6	1168	2	I56985	kallinin B1 - mouse	776	97	2.5	429	2	T21113	hypothetical prote
704	102	2.6	1713	2	A55347	adhesive ligand ep	777	97	2.5	626	2	T27319	hypothetical prote
705	102	2.6	4006	2	T09070	probable tenascin	778	97	2.5	799	1	IUMSPB	fibronectin recept
706	101.5	2.6	379	2	T16213	APX-1 protein homo	779	97	2.5	808	2	T23129	hypothetical prote
707	101.5	2.6	1106	2	T18739	hypothetical prote	780	97	2.5	862	2	S43922	versican - pig-tai
708	101.5	2.6	1959	1	AGRT	agrin - rat	781	97	2.5	915	1	A48225	subtilisin-like pr
709	101.5	2.6	2415	1	A39086	aggreccan precursor	782	97	2.5	1138	1	S24066	protein-tyrosine k
710	101	2.6	377	2	C88710	protein C43G2.5 li	783	97	2.5	1193	2	A44018	laminin B2t chain
711	101	2.6	463	2	T26655	hypothetical prote	784	97	2.5	1292	2	T09229	galactose binding
712	101	2.6	557	2	A48434	variant-specific s	785	96.5	2.4	149	1	KQMSM	tissue kallikrein
713	101	2.6	1371	2	A33837	insulin-like growt	786	96.5	2.4	317	2	D42526	B5R protein - vacc
714	101	2.6	1378	1	I48751	protein-tyrosine k	787	96.5	2.4	613	2	A69535	aldehyde ferredoxi
715	101	2.6	1875	2	A36429	integrin beta-4 ch	788	96.5	2.4	956	2	A57121	thrombospondin 3 p
716	100.5	2.5	417	2	T20199	hypothetical prote	789	96.5	2.4	1149	2	I38006	M130 antigen precu
717	100.5	2.5	670	2	S77463	transketolase (EC	790	96.5	2.4	1193	2	T21133	hypothetical prote
718	100.5	2.5	802	2	T24293	hypothetical prote	791	96.5	2.4	1297	2	T30274	proteolialisin - se
719	100.5	2.5	949	2	T24294	hypothetical prote	792	96.5	2.4	3133	2	S52093	hemocytin - silkw
720	100.5	2.5	956	1	A46016	thrombospondin 3 -	793	96	2.4	116	2	S17567	AQN-3 protein - pl
721	100.5	2.5	1252	2	S36016	cocyst wall protei	794	96	2.4	116	2	S39434	spermadhesin AQN-3
722	100.5	2.5	1356	2	A45445	janusin precursor,	795	96	2.4	256	2	A56593	trypsin-related pr
723	100	2.5	152	2	S35203	serine proteinase,	796	96	2.4	392	2	T25213	hypothetical prote
724	100	2.5	421	2	T23383	hypothetical prote	797	96	2.4	798	2	A28193	integrin beta-1 ch
725	100	2.5	667	2	A48579	trophozoite surfac	798	96	2.4	886	2	A57172	probable hormone r
726	100	2.5	873	1	A49729	VLDL receptor prec	799	96	2.4	4753	1	A47437	LDL-receptor-relat
727	100	2.5	1122	2	I54237	protein-tyrosine k	800	96	2.4	177	2	S23505	chymase (EC 3.4.21
728	100	2.5	1123	1	JH0771	protein-tyrosine k	801	95.5	2.4	218	2	H70770	probable regulator
729	100	2.5	1125	1	I38004	protein-tyrosine k	802	95.5	2.4	330	2	B82415	probable serine pr
730	100	2.5	1151	2	I38005	M130 antigen precu	803	95.5	2.4	427	2	JC4915	ags protein precu
731	100	2.5	1156	2	A57293	latent transformin	804	95.5	2.4	561	2	T27318	hypothetical prote
732	100	2.5	1251	2	T43251	furin (EC 3.4.21.7	805	95.5	2.4	1042	2	A57534	mucin SAC (clone L
733	100	2.5	1299	2	S34251	X/Y protein - mous	806	95.5	2.4	1135	1	JQ1928	G2-G1 polypoteine
734	99.5	2.5	330	2	I55975	uromodulin precurs	807	95.5	2.4	1270	2	T22615	hypothetical prote
735	99.5	2.5	640	1	A30452	KO8E5.3 protein -	808	95.5	2.4	3191	2	T22945	hypothetical prote
736	99.5	2.5	686	2	S43562	iodide peroxidase	809	95.5	2.4	463	2	T39621	peptidyl prolvl ci
737	99.5	2.5	914	1	S07047	170K lectin precu	810	95	2.4	850	2	S56015	gastric mucin MUC5
738	99.5	2.5	1280	2	A39117	finger protein - A	811	95	2.4	869	1	JC4858	hypothetical prote
739	99.5	2.5	1350	2	S00647	trophozoite cystel	812	95	2.4	989	2	T01519	nitrogen precursor
740	99.5	2.5	1766	2	A42125	probable vitellog	813	95	2.4	1245	1	MMNSND	mucin MUC5B, trach
741	99.5	2.5	1847	2	T18308	probable vitellog	814	95	2.4	1321	2	JE0152	spermadhesin AQN-1
742	99.5	2.5	1984	2	T13171	epithelin/granulin	815	95	2.4	111	2	S21211	hypothetical prote
743	99	2.5	589	2	B38128	acroganin - guine	816	94.5	2.4	643	2	T25473	LDL receptor precu
744	99	2.5	591	1	I48141	plasma protein S p	817	94.5	2.4	736	2	S47645	hypothetical prote
745	99	2.5	675	1	KXMS	leptin receptor, s	818	94.5	2.4	862	1	QRMSLD	hypothetical prote
746	99	2.5	675	1	KXRTS	leptin receptor, s	819	94.5	2.4	1216	2	T26104	protein ZC94.1 [im
747	99	2.5	805	2	S68441	leptin receptor, s	820	94.5	2.4	1416	2	E88550	epidermal growth f
748	99	2.5	892	2	S68439	leptin receptor, s	821	94.5	2.4	1717	1	A45558	insulin-like growt
749	99	2.5	894	2	S68437	leptin receptor, s	822	94.5	2.4	258	1	B37252	platelet-derived g
750	99	2.5	900	2	S68440	leptin receptor, s	823	94	2.4	370	2	JC7998	hypothetical prote
751	99	2.5	1162	2	S68438	two-component hybr	824	94	2.4	634	2	T02594	neuregulin-3 [impo
752	99	2.5	1558	2	AB2457	G-cadherin - sea u	825	94	2.4	736	2	T44447	hypothetical prote
753	99	2.5	2809	2	T30213	hypothetical prote	826	94	2.4	713	2	T06757	subtilisin-like pr
754	98.5	2.5	317	2	T28605	H7R protein - vari	827	94	2.4	899	2	G02428	subtilisin-like pr
755	98.5	2.5	317	2	F72172	B7R protein - vari	828	94	2.4	915	2	JC6148	subtilisin-like pr
756	98.5	2.5	317	2	S36855	PAS-6/7 protein pr	829	94	2.4	932	2	I52527	thrombospondin pre
757	98.5	2.5	427	2	S74211	hypothetical prote	830	94	2.4	1381	2	T31083	neurexin IV - mous
758	98.5	2.5	1178	1	A39804	hypothetical prote	831	94	2.4	1385	2	T14158	
759	98	2.5	82	2	T46510		832	94	2.4				

833	94	2.4	3097	2	T00021	DN-cadherin - frui	906	89.5	2.3	854	1	QRHYLD	LDL receptor precu
834	93.5	2.4	258	2	A45403	insulin-like growt	907	89.5	2.3	1164	2	T01871	RNA-directed DNA p
835	93.5	2.4	317	2	JQ1799	B5R protein precu	908	89.5	2.3	1258	2	A12155	WD-repeat protein
836	93.5	2.4	449	2	T35048	probable ATP /GTP	909	89.5	2.3	1364	2	T00250	MEG2 protein - hu
837	93.5	2.4	456	2	T31483	hypothetical prote	910	89	2.3	319	2	A53502	follicistatin - Afri
838	93.5	2.4	486	2	A49820	PR11 protein - Ara	911	89	2.3	354	2	T22274	hypothetical prote
839	93.5	2.4	612	2	JH0799	laminin-related pr	912	89	2.3	369	2	F81178	histone deacetylase
840	93.5	2.4	739	2	B88553	protein K04H4.2b [913	89	2.3	390	2	C90208	hypothetical prote
841	93.5	2.4	1115	2	S40241	G protein-coupled	914	89	2.3	469	1	NM1V27	exo-alpha-sialidas
842	93.5	2.4	1136	1	S57845	protein-tyrosine k	915	89	2.3	525	2	T21357	hypothetical prote
843	93	2.4	104	2	T19868	hypothetical prote	916	89	2.3	907	2	I50404	p50B/p97 (Lyt-10)
844	93	2.4	329	2	A48805	insulin-like growt	917	89	2.3	1110	1	B42544	G2-C1 polypeptide
845	93	2.4	873	1	I48952	VDL receptor prec	918	89	2.3	1170	2	A40558	chromospondin 1 p
846	93	2.4	995	2	A56599	embryo kinase 5 -	919	88.5	2.2	317	2	T37442	SEV gp42,ps/hr pro
847	93	2.4	2767	1	UIHU	thrombospondin 4	920	88.5	2.2	356	2	T20656	hypothetical prote
848	93	2.4	4545	1	S25111	alpha-2-macroglobu	921	88.5	2.2	438	2	T40509	lim domain protein
849	92.5	2.3	211	2	A46458	human CR1 homolog	922	88.5	2.2	693	2	I37570	zinc finger protei
850	92.5	2.3	736	2	T19366	hypothetical prote	923	88.5	2.2	754	2	T47886	transketolase-like
851	92.5	2.3	756	2	T47656	MDC II protein -	924	88.5	2.2	905	2	S55059	feritin alpha-1 -
852	92.5	2.3	803	1	IJCH3	integrin, band 3 p	925	88.5	2.2	1077	2	T41146	probable cysteine-
853	92.5	2.3	955	2	JC5545	thrombospondin 4	926	88.5	2.2	1096	2	T16875	hypothetical prote
854	92.5	2.3	1367	1	IGHUR1	insulin-like growt	927	88.5	2.2	1170	1	TSHUP1	thrombospondin 1 p
855	92	2.3	334	2	T23027	hypothetical prote	928	88.5	2.2	1978	2	T07081	acetyl-CoA carboxy
856	92	2.3	650	2	A34498	glycoprotein antig	929	88	2.2	621	2	I38467	low density lipopr
857	92	2.3	719	2	T00266	hypothetical prote	930	88	2.2	656	2	JC2005	integrin beta-5 ch
858	92	2.3	915	2	B48225	probable protease	931	88	2.2	798	2	B27079	fibronectin recept
859	92	2.3	964	2	JC5545	integrin beta-4 pr	932	88	2.2	799	2	A38308	integrin beta-5 ch
860	92	2.3	1097	2	S68685	adenylate cyclase	933	88	2.2	962	2	JC5571	subtilisin-like pr
861	92	2.3	1444	2	T18855	angiogenesis inhib	934	88	2.2	1085	2	C96797	unknown protein [i
862	92	2.3	1895	2	T15881	hypothetical prote	935	88	2.2	1175	2	S52417	E-selectin ligand-
863	92	2.3	2533	2	T28675	alpha-5D immobili	936	88	2.2	1192	2	S69000	laminin gamma 2 ch
864	92	2.3	3869	2	A48205	All-1 protein +GFE	937	87.5	2.2	554	2	A45818	cytolysin precuro
865	91.5	2.3	237	2	I47031	insulin-like growt	938	87.5	2.2	580	2	A37107	complement C8 alph
866	91.5	2.3	250	2	T30124	hypothetical prote	939	87.5	2.2	584	1	C8HUA	hypothetical prote
867	91.5	2.3	303	2	H35068	apolipoprotein H-r	940	87.5	2.2	667	2	T01999	iodide peroxidase
868	91.5	2.3	511	2	T17298	hypothetical prote	941	87.5	2.2	914	1	UN0550	hypothetical prote
869	91.5	2.3	588	2	T33815	hypothetical prote	942	87.5	2.2	1807	2	JC6319	receptor protein-t
870	91.5	2.3	640	2	S49932	MET30 protein - ye	943	87.5	2.2	1816	1	S68960	subtilisin-like pr
871	91.5	2.3	1101	2	T16840	hypothetical prote	944	87	2.2	387	2	I38449	extracellular prot
872	91.5	2.3	1161	2	D83076	type 4 fibrial bi	945	87	2.2	706	2	S74610	hypothetical prote
873	91.5	2.3	2144	2	S71490	ashl protein - fru	946	87	2.2	743	2	T40521	hypothetical prote
874	91.5	2.3	2672	2	A48126	translation activa	947	87	2.2	860	2	T16892	hypothetical prote
875	91.5	2.3	2910	2	T42214	otogelin - mouse	948	87	2.2	970	2	I78842	receptor protein-t
876	91	2.3	94	2	PC2013	tissue kallikrein	949	87	2.2	975	2	JC5570	subtilisin-like pr
877	91	2.3	293	2	T09065	hypothetical prote	950	87	2.2	1042	2	T26644	hypothetical prote
878	91	2.3	319	1	I50370	transcription fact	951	87	2.2	1056	2	A53767	mucin MUC5B, trach
879	91	2.3	398	2	E71539	hypothetical prote	952	87	2.2	1134	1	JN0711	protein-tyrosine k
880	91	2.3	435	2	I54182	tumor necrosis fac	953	87	2.2	1945	2	T13937	plexin A - fruit f
881	91	2.3	478	2	S47040	gene t52 protein	954	87	2.2	2481	2	A43908	fibronectin - Afri
882	91	2.3	909	1	QRXLL2	LDL receptor 2 pre	955	87	2.2	2968	2	A44265	trithorax homolog
883	91	2.3	2543	2	T31687	surface antigen - P	956	86.5	2.2	222	2	S72795	hypothetical prote
884	91	2.3	4543	1	A53102	alpha-2-macroglobu	957	86.5	2.2	264	2	T16271	hypothetical prote
885	90.5	2.3	53	2	S17294	epidermal growth f	958	86.5	2.2	336	2	D59074	polyferredoxin 4x2
886	90.5	2.3	330	1	JN0561	urokinase-type pla	959	86.5	2.2	391	2	T34284	hypothetical prote
887	90.5	2.3	642	1	JP0079	LIM protein kinase	960	86.5	2.2	471	2	I79528	alkaline phosphata
888	90.5	2.3	746	1	HYHUMA	mepirin A (EC 3.4.2	961	86.5	2.2	585	2	I46686	complement compone
889	90.5	2.3	776	2	S28258	androgen-regulated	962	86.5	2.2	632	2	T22288	hypothetical prote
890	90.5	2.3	963	2	JEO356	gamma-aminobutyric	963	86.5	2.2	632	2	T21602	hypothetical prote
891	90.5	2.3	1104	2	I38869	transcription fact	964	86.5	2.2	638	2	AF3463	flagellar protein
892	90.5	2.3	1148	1	GNVUNE	M polyprotein prec	965	86.5	2.2	641	2	T71810	type III DNA modif
893	90.5	2.3	1357	2	T16860	hypothetical prote	966	86.5	2.2	700	2	A32392	hypothetical prote
894	90.5	2.3	1436	2	A46496	antigen WC1.1 prec	967	86.5	2.2	734	2	C81399	isocitrate dehydro
895	90.5	2.3	2813	1	VWHU	von Willebrand fac	968	86.5	2.2	734	2	C81399	thrombospondin 2 p
896	90	2.3	156	2	B23863	tissue kallikrein	969	86.5	2.2	1172	2	A42587	E2 glycoprotein pr
897	90	2.3	340	2	T34423	hypothetical prote	970	86.5	2.2	1376	1	JQ1534	ribonucleoside-dip
898	90	2.3	409	2	T11743	pp47 protein - pig	971	86.5	2.2	1418	2	D75281	ovostatin precuro
899	90	2.3	417	2	T29864	hypothetical prote	972	86.5	2.2	1473	2	A20872	alpha-aminoadipyl-
900	90	2.3	522	2	T29767	hypothetical prote	973	86.5	2.2	3712	1	YGC5VC	conserved hypothet
901	90	2.3	577	2	I37057	integrin beta-6 ch	974	86	2.2	455	2	B82525	major surface-labe
902	90	2.3	814	1	I39627	nicotine dehydroge	975	86	2.2	713	2	A35502	hypothetical prote
903	90	2.3	2533	2	T28674	alpha-5D-immobili	976	86	2.2	738	2	S40992	hypothetical prote
904	89.5	2.3	417	2	T39939	DNA binding protei	977	86	2.2	905	2	T23229	hypothetical prote
905	89.5	2.3	748	2	S24134	endopeptidase 2 (E	978	86	2.2	906	2	A71438	probable resistanc

979	86	2.2	933	1	OPRHUT	iodide peroxidase	1052	83.5	2.1	311	2	JC7873	L-thamnose-binding
980	86	2.2	969	1	A39490	subtilisin-like pr	1053	83.5	2.1	344	2	A32141	follicstatin 1 prec
981	86	2.2	1487	2	S48719	phospholipase-A(2)	1054	83.5	2.1	348	2	T28623	hypothetical prote
982	86	2.2	1572	2	T00027	brain-specific ang	1055	83.5	2.1	354	2	G64475	GTP-binding protei
983	86	2.2	1650	2	S53457	dominant autoantig	1056	83.5	2.1	358	1	A55973	transcription fact
984	86	2.2	2233	2	T28669	surface protein 51	1057	83.5	2.1	366	2	I53035	trithorax homolog
985	85.5	2.2	317	2	A38493	ps/hr protein - va	1058	83.5	2.1	491	2	H83770	hypothetical prote
986	85.5	2.2	340	1	B55973	transcription fact	1059	83.5	2.1	579	2	B84192	pyruvate kinase [i
987	85.5	2.2	344	1	A27701	follicstatin precu	1060	83.5	2.1	589	2	C38128	epithelin/granulin
988	85.5	2.2	358	2	B64427	carbamoyl-phosphat	1061	83.5	2.1	697	2	H86457	78.1K hypothetical
989	85.5	2.2	463	1	A36479	milk fat globule m	1062	83.5	2.1	873	2	D88482	protein C5D11.8 [
990	85.5	2.2	515	2	T05863	hypothetical prote	1063	83.5	2.1	1106	2	T13938	gene shuttle craft
991	85.5	2.2	638	2	S22491	acetolactate synth	1064	83.5	2.1	2120	2	T30243	alpha tectorin - c
992	85.5	2.2	663	2	T21010	hypothetical prote	1065	83.5	2.1	2704	2	S09118	G surface protein
993	85.5	2.2	798	2	S01659	integrin beta-1 ch	1066	83.5	2.1	4302	2	A38971	polycystic kidney
994	85.5	2.2	1162	2	PC4184	leptin receptor, O	1067	83.5	2.1	13055	2	T16580	hypothetical prote
995	85.5	2.2	1229	2	H84465	hypothetical prote	1068	83	2.1	304	2	A83513	probable transcrip
996	85.5	2.2	2452	1	RN2Q2L	DNA-directed RNA p	1069	83	2.1	351	2	S20078	NOV protein - chic
997	85.5	2.2	2457	2	T18492	hypothetical prote	1070	83	2.1	372	2	T39244	probable phospho-2
998	85	2.2	200	2	T42678	hypothetical prote	1071	83	2.1	451	2	F83747	denosylmethionine-
999	85	2.2	291	2	I38098	t-plasminogen acti	1072	83	2.1	492	2	D35114	anthranilate synth
1000	85	2.2	318	2	H86342	hypothetical prote	1073	83	2.1	593	1	GYHU	granulin precursor
1001	85	2.2	343	2	S55369	follicstatin - chic	1074	83	2.1	770	2	S04847	leukocyte adhesion
1002	85	2.2	359	1	I51734	transcription fact	1075	83	2.1	771	2	D89447	protein F5YC12.1 [
1003	85	2.2	413	2	T23098	hypothetical prote	1076	83	2.1	771	2	A45839	leukocyte adhesion
1004	85	2.2	542	2	A84554	hypothetical prote	1077	83	2.1	800	2	S54623	probable mitochond
1005	85	2.2	552	2	F83417	hypothetical prote	1078	83	2.1	816	2	C69493	hypothetical prote
1006	85	2.2	606	2	S43118	sulfite reductase	1079	83	2.1	1046	2	F71432	hypothetical prote
1007	85	2.2	638	2	S22490	finger protein - m	1080	83	2.1	1066	2	B95037	hyaluronidase limp
1008	85	2.2	653	2	G96675	acetolactate synth	1081	83	2.1	1111	2	T00324	hypothetical prote
1009	85	2.2	671	1	UYVP19	hypothetical prote	1082	83	2.1	1373	2	JE0095	gastric mucin MUC5
1010	85	2.2	752	2	T26508	noncapsid protein	1083	83	2.1	2116	1	ZLVNSY	genome polyprotein
1011	85	2.2	794	2	F88508	protein H14A12.6 [1084	83	2.1	3020	2	A43932	mucin 2 precursor,
1012	85	2.2	895	2	S74225	leptin receptor, i	1085	82.5	2.1	328	2	F83599	hypothetical prote
1013	85	2.2	1021	2	S26985	probable DNA-direc	1086	82.5	2.1	429	2	A42972	coagulation factor
1014	85	2.2	1078	2	F97907	hyaluronate lyase	1087	82.5	2.1	486	2	S29302	alliin lyase (EC 4
1015	85	2.2	1148	1	JQ1604	M polyprotein prec	1088	82.5	2.1	591	1	C8HUB	complement C8 beta
1016	85	2.2	1533	2	T00344	hypothetical prote	1089	82.5	2.1	753	2	T19338	hypothetical prote
1017	85	2.2	1538	2	S73296	glutamate synthase	1090	82.5	2.1	761	2	E82223	ribonucleoside-dip
1018	85	2.2	2150	2	T32497	hypothetical prote	1091	82.5	2.1	781	2	S43534	integrin beta3 - c
1019	84.5	2.1	271	2	T32783	OX40 antigen precu	1092	82.5	2.1	984	2	T00326	hypothetical prote
1020	84.5	2.1	337	2	I47079	follicstatin - shee	1093	82.5	2.1	1175	2	I57549	adenosine deaminas
1021	84.5	2.1	344	2	I45894	follicstatin - bovi	1094	82.5	2.1	1372	2	A34157	insulin receptor p
1022	84.5	2.1	429	2	T16656	hypothetical prote	1095	82	2.1	188	2	A39787	teratocarcinoma-de
1023	84.5	2.1	494	2	A98683	alkaline phosphata	1096	82	2.1	235	2	AE0114	deoxyribonuclease
1024	84.5	2.1	494	2	E85533	alkaline phosphata	1097	82	2.1	318	2	S65019	chitinase (EC 3.2.
1025	84.5	2.1	505	2	A46570	H+-transporting tw	1098	82	2.1	343	2	S45321	follicstatin - mous
1026	84.5	2.1	615	2	S06546	finger protein (cl	1099	82	2.1	349	2	D72175	G2R protein - vari
1027	84.5	2.1	654	2	T30136	hypothetical prote	1100	82	2.1	432	2	D83904	cabon storage regu
1028	84.5	2.1	696	2	A12849	GDPGF family prote	1101	82	2.1	528	2	B42560	4-chlorobenzoate-C
1029	84.5	2.1	696	2	G97626	hypothetical prote	1102	82	2.1	583	2	T34121	steroid/thyroid/re
1030	84.5	2.1	744	2	A43353	ascites sialoglyco	1103	82	2.1	599	2	B82439	formate-tetrahydro
1031	84.5	2.1	746	2	F87243	isocitrate dehydro	1104	82	2.1	711	2	T27358	hypothetical prote
1032	84.5	2.1	760	2	A01195	meprin A (SC 3.4.2	1105	82	2.1	868	2	T02635	D2 protein homolog
1033	84.5	2.1	788	2	A28547	platelet glycoprot	1106	82	2.1	1530	2	I45944	neurexin 1-alpha -
1034	84.5	2.1	789	2	S28259	androgen-regulated	1107	82	2.1	1609	2	S44821	head-activator bin
1035	84.5	2.1	864	2	T49574	probable carnitine	1108	82	2.1	1661	2	T31330	hypothetical prote
1036	84.5	2.1	917	2	I48950	telencephalin prec	1109	82	2.1	2214	2	T16305	giant protein p619
1037	84.5	2.1	950	2	T28793	diacylglycerol kin	1110	82	2.1	209	2	T02394	hypothetical prote
1038	84	2.1	278	2	T21718	hypothetical prote	1111	81.5	2.1	251	2	A55035	cysteine-rich prot
1039	84	2.1	335	2	T32657	hypothetical prote	1112	81.5	2.1	349	2	S57453	polyferredoxin 4x2
1040	84	2.1	349	2	T36858	gene G4R protein -	1113	81.5	2.1	383	2	D89633	protein F56B3.2 [i
1041	84	2.1	413	2	T34123	hypothetical prote	1114	81.5	2.1	429	2	S01919	knirps protein - f
1042	84	2.1	471	2	A84741	probable myosinas	1115	81.5	2.1	432	2	A25483	env polyprotein, r
1043	84	2.1	520	2	G88846	protein T12A7.2 [i	1116	81.5	2.1	443	2	T29147	hypothetical prote
1044	84	2.1	567	2	T49942	hypothetical prote	1117	81.5	2.1	460	2	S67174	hypothetical prote
1045	84	2.1	972	2	A30363	glycoprotein GP330	1118	81.5	2.1	460	2	A83655	lysine decarboxyla
1046	84	2.1	1034	2	JCS598	mucin - rat	1119	81.5	2.1	482	2	T08674	probable finger pr
1047	84	2.1	1047	2	T34946	probable isoleucyl	1120	81.5	2.1	496	2	S54300	transketolase (EC
1048	84	2.1	1599	2	T16210	hypothetical prote	1121	81.5	2.1	519	2	S54300	transketolase (EC
1049	84	2.1	2153	2	T14893	scavenger receptor	1122	81.5	2.1	604	1	HMNZCD	hemagglutinin - ca
1050	83.5	2.1	202	1	A44247	C4b-binding protei	1123	81.5	2.1	625	2	S35317	hematopoietic grow
1051	83.5	2.1	278	2	AH0282	probable pepetide	1124	81.5	2.1	626	2	S37622	proto-oncogene - m

1125	81.5	2.1	724	2	A48569	antigen Em100 - Ei	1198	80	2.0	644	2	I84634	Tamm-Horsfall prot
1126	81.5	2.1	977	2	S49004	tyrosine kinase Mp	1199	80	2.0	656	1	SN5631	endo-1,4-beta-xyla
1127	81.5	2.1	1187	2	T18355	hypothetical prote	1200	80	2.0	680	2	PN0510	integrin beta-3 ch
1128	81.5	2.1	1210	2	D88013	protein K10B4.1 [i	1201	80	2.0	713	2	JC6012	glutamine-fructose
1129	81.5	2.1	1507	2	A40228	neurexin I-alpha p	1202	80	2.0	741	2	G84888	probable transket
1130	81	2.1	180	2	AE1010	conserved hypothet	1203	80	2.0	746	2	G84505	hypothetical prote
1131	81	2.1	236	2	C81906	hypothetical prote	1204	80	2.0	753	2	JC7386	retinovin - chicke
1132	81	2.1	348	2	A56247	natural killer cel	1205	80	2.0	817	2	T24063	hypothetical prote
1133	81	2.1	428	2	T04472	penicillin binding	1206	80	2.0	902	2	T01127	curly leaf protein
1134	81	2.1	491	2	I40455	maternal transcrip	1207	80	2.0	1138	2	T36406	hypothetical prote
1135	81	2.1	501	2	JC7181	perforin precursor	1208	80	2.0	1184	2	A96638	hypothetical prote
1136	81	2.1	554	2	A31300	jasmonate-induced	1209	80	2.0	1342	2	A36223	kinase-related tra
1137	81	2.1	560	2	S25092	wall-associated se	1210	80	2.0	1385	2	H85669	protein K03H1.5 [1
1138	81	2.1	732	2	T52588	fertilin beta - cr	1211	80	2.0	1409	2	S41028	hypothetical prote
1139	81	2.1	735	2	G02937	ADAM 6 protein pre	1212	80	2.0	2219	2	T27684	hypothetical prote
1140	81	2.1	735	2	I48101	leukocyte adhesion	1213	80	2.0	2229	2	T16199	hypothetical prote
1141	81	2.1	769	1	JC1121	related to tol pro	1214	80	2.0	2643	2	T29149	genome polyprotein
1142	81	2.1	787	2	T49614	integrin beta olig	1215	80	2.0	3140	2	S47508	KGD-bearing platel
1143	81	2.1	799	2	JC4126	brain-derived neur	1216	79.5	2.0	71	2	A59412	conserved hypothet
1144	81	2.1	821	1	A39667	protein-tyrosine k	1217	79.5	2.0	217	2	D90033	insulin-like growt
1145	81	2.1	1166	1	S06142	hypothetical prote	1218	79.5	2.0	254	2	I48599	insulin-like growt
1146	81	2.1	1344	2	H84557	RNA-directed DNA p	1219	79.5	2.0	254	2	JC1464	transaldolase (EC
1147	81	2.1	1365	2	T00833	neurexin III-alpha	1220	79.5	2.0	317	2	D64167	chitinase (EC 3.2.
1148	81	2.1	1438	2	A48216	neurexin III-alpha	1221	79.5	2.0	318	2	S43317	thrombomodulin - b
1149	81	2.1	1471	2	B48218	neurexin III-alpha	1222	79.5	2.0	324	2	S20981	AWJL236 protein -
1150	81	2.1	1578	2	I48216	disease resistance	1223	79.5	2.0	356	2	A25918	hypothetical prote
1151	81	2.1	1895	2	T06609	genome polyprotein	1224	79.5	2.0	391	2	S49300	tubulointerstitial
1152	81	2.1	3898	2	S57437	hypothetical prote	1225	79.5	2.0	457	2	C86464	hypothetical prote
1153	80.5	2.0	371	2	B72461	conserved hypothet	1226	79.5	2.0	474	2	A57480	hypothetical prote
1154	80.5	2.0	390	2	T27256	hemorrhagic protei	1227	79.5	2.0	614	2	T40652	hypothetical prote
1155	80.5	2.0	409	2	B87661	PRL2 protein - Ara	1228	79.5	2.0	661	2	C85758	hypothetical prote
1156	80.5	2.0	416	2	A37877	hypothetical prote	1229	79.5	2.0	690	2	S58083	transketolase (EC
1157	80.5	2.0	431	2	S49821	alkaline phosphata	1230	79.5	2.0	700	1	HYHUMB	meprin A (EC 3.4.2
1158	80.5	2.0	454	2	T26654	protein Fl3M7.11 [1231	79.5	2.0	713	2	I65253	disintegrin-like t
1159	80.5	2.0	471	1	PAECA	hypothetical prote	1232	79.5	2.0	741	2	T05015	probable selenium-
1160	80.5	2.0	479	2	D86182	hypothetical prote	1233	79.5	2.0	868	2	G84674	diacylglycerol kin
1161	80.5	2.0	502	2	T16716	hypothetical prote	1234	79.5	2.0	952	2	T28792	nidogen precursor
1162	80.5	2.0	509	2	T22238	hypothetical prote	1235	79.5	2.0	1161	1	S31213	protein Fl4D16.3 [
1163	80.5	2.0	516	2	S53007	citrate synthase -	1236	79.5	2.0	1178	2	S08405	hypothetical prote
1164	80.5	2.0	555	2	T12028	hypothetical prote	1237	79.5	2.0	1260	2	A86323	sperm tail-specifi
1165	80.5	2.0	570	2	T46261	hypothetical prote	1238	79.5	2.0	1390	2	S51364	hypothetical prote
1166	80.5	2.0	604	2	T15796	hypothetical prote	1239	79.5	2.0	1402	2	T24664	acetyl-CoA carboxy
1167	80.5	2.0	627	2	T00603	hypothetical prote	1240	79.5	2.0	2261	2	T07084	mannose 6-phosphat
1168	80.5	2.0	656	2	B49423	semaphorin I - fru	1241	79.5	2.0	2499	1	A30788	laminin - Hydra vu
1169	80.5	2.0	658	2	A86828	transketolase (EC	1242	79.5	2.0	171	2	S57894	teratocarcinoma-de
1170	80.5	2.0	673	2	A49878	coagulation factor	1243	79	2.0	188	2	A30362	thiosulfate-dithio
1171	80.5	2.0	704	2	A48040	meprin A (EC 3.4.2	1244	79	2.0	192	1	B57143	ribosomal protein
1172	80.5	2.0	741	2	B81143	isocitrate dehydro	1245	79	2.0	206	2	D97285	Wnt-2 protein - Ca
1173	80.5	2.0	742	2	I37225	leucocyte antigen	1246	79	2.0	360	2	S32695	hypothetical prote
1174	80.5	2.0	773	2	I46059	beta-1 integrin su	1247	79	2.0	364	2	T24153	hypothetical prote
1175	80.5	2.0	1055	2	T05663	hypothetical prote	1248	79	2.0	392	2	T33444	hypothetical prote
1176	80.5	2.0	1119	2	A88481	protein C16A3.6 [i	1249	79	2.0	415	2	D87020	probable membrane
1177	80.5	2.0	1245	1	VHW82	structural polypro	1250	79	2.0	587	2	C85044	hypothetical prote
1178	80.5	2.0	1376	1	VGHJ2	E2 glycoprotein pr	1251	79	2.0	602	2	B81420	GTP-binding protei
1179	80.5	2.0	1382	1	INHUR	insulin receptor p	1252	79	2.0	606	2	T22105	hypothetical prote
1180	80.5	2.0	1526	2	T19473	hypothetical prote	1253	79	2.0	630	2	T48369	hypothetical prote
1181	80.5	2.0	1558	2	C89114	protein C37C3.6a [1254	79	2.0	660	2	S71949	metalloproteinase
1182	80.5	2.0	1611	2	G84493	probable retroelem	1255	79	2.0	687	2	T16352	hypothetical prote
1183	80.5	2.0	2167	2	T34395	hypothetical prote	1256	79	2.0	729	2	A45716	leukemia virus cel
1184	80.5	2.0	2262	2	T30890	calcium channel al	1257	79	2.0	738	2	B41730	platelet glycoprot
1185	80	2.0	211	1	CYRTB3	beta-crystallin B3	1258	79	2.0	753	2	B36268	exo-alpha-sialidas
1186	80	2.0	243	2	T27036	hypothetical prote	1259	79	2.0	773	2	JB0387	platelet glycoprot
1187	80	2.0	284	2	T25938	hypothetical prote	1260	79	2.0	788	2	I77349	platelet glycoprot
1188	80	2.0	290	2	T46470	hypothetical prote	1261	79	2.0	790	2	D81668	phenylalanine-tRNA
1189	80	2.0	335	2	A39743	u-plasminogen acti	1262	79	2.0	826	2	A60385	monocyte surface a
1190	80	2.0	395	2	S64299	probable membrane	1263	79	2.0	871	2	T04867	hypothetical prote
1191	80	2.0	437	1	S24802	polyferredoxin 6x2	1264	79	2.0	952	2	T18950	disintegrin and me
1192	80	2.0	437	1	S05478	properdin - mouse	1265	79	2.0	1023	2	T30257	19G Fc binding pro
1193	80	2.0	464	2	H82928	ATP synthase beta	1266	79	2.0				
1194	80	2.0	500	2	A36388	RNA-directed RNA p	1267	79	2.0				
1195	80	2.0	589	2	I38598	zinc finger protei	1268	79	2.0				
1196	80	2.0	642	2	C89124	protein K07C11.9 [1269	79	2.0				
1197	80	2.0	644	1	A40212	uromodulin precurs	1270	79	2.0				

1271	79	2.0	1389	1	RMXRR3	mRNA guanylyltrans	1344	78	2.0	4085	2	S28600	hypothetical prote
1272	79	2.0	1391	2	T20406	hypothetical prote	1345	77.5	2.0	46	2	JT0747	epiregulin - rat
1273	79	2.0	1392	2	A54895	mucin 2, intestina	1346	77.5	2.0	162	2	S68401	epiregulin precurs
1274	79	2.0	1522	2	T00028	brain-specific ang	1347	77.5	2.0	244	2	AB2505	histidine kinase-l
1275	79	2.0	1642	2	T19130	hypothetical prote	1348	77.5	2.0	255	2	H96776	hypothetical prote
1276	79	2.0	1777	2	T04090	nonstructural prote	1349	77.5	2.0	295	2	JC5559	lectin-B - Virgin
1277	79	2.0	1777	2	AC2088	serine/threonine k	1350	77.5	2.0	296	2	G81111	conserved hypothet
1278	78.5	2.0	116	2	S65875	spermadhesin PSP-I	1351	77.5	2.0	400	2	A55647	phyllolopod - fruit
1279	78.5	2.0	307	1	S18523	fructokinase (EC 2	1352	77.5	2.0	402	2	S02099	phosphoribulokinas
1280	78.5	2.0	327	2	A55356	urokinase-type pia	1353	77.5	2.0	407	2	C82428	glucosyl-1-phosphat
1281	78.5	2.0	341	2	I61725	natural killer cell	1354	77.5	2.0	413	4	FOHUE2	retrovirus-related
1282	78.5	2.0	342	2	I57698	follistatin - rat	1355	77.5	2.0	457	2	B85749	ATP-dependent RNA
1283	78.5	2.0	355	2	C70457	hypothetical prote	1356	77.5	2.0	457	2	G90869	ATP-dependent RNA
1284	78.5	2.0	363	1	C55973	transcription fact	1357	77.5	2.0	457	2	B64884	ATP-dependent RNA
1285	78.5	2.0	376	2	E70361	chaperone DnaJ - A	1358	77.5	2.0	469	2	T36362	probable DNA repai
1286	78.5	2.0	389	2	D75180	hypothetical prote	1359	77.5	2.0	488	2	T21701	hypothetical prote
1287	78.5	2.0	401	2	S65138	glycoprotein anti-g	1360	77.5	2.0	546	2	B75375	probable amidase -
1288	78.5	2.0	436	2	S06884	virD2 protein - Ag	1361	77.5	2.0	548	2	S38864	Ig epsilon chain C
1289	78.5	2.0	474	2	B38634	tumor necrosis fac	1362	77.5	2.0	569	2	E85076	probable transposo
1290	78.5	2.0	495	2	A57053	germ cell nuclear	1363	77.5	2.0	645	2	S20138	probable protein k
1291	78.5	2.0	507	2	T06452	probable legumin A	1364	77.5	2.0	717	2	B32838	DNA-directed RNA p
1292	78.5	2.0	517	1	FWPMLA	legumin A precursor	1365	77.5	2.0	721	2	A39707	erythrocyte membra
1293	78.5	2.0	552	2	C45710	R transactivator h	1366	77.5	2.0	729	2	A69202	conserved hypothet
1294	78.5	2.0	600	2	I49281	fertilin alpha pre	1367	77.5	2.0	767	2	E85079	hypothetical prote
1295	78.5	2.0	638	2	D86477	probable CYP-rich	1368	77.5	2.0	809	2	A57283	integrin beta chai
1296	78.5	2.0	658	2	F85024	IL12 receptor comp	1369	77.5	2.0	845	2	G82773	phage-related prot
1297	78.5	2.0	662	2	I37892	hypothetical prote	1370	77.5	2.0	848	2	AF0020	nitrite reductase
1298	78.5	2.0	717	2	T25431	hypothetical prote	1371	77.5	2.0	933	2	A31930	cytotactin - chick
1299	78.5	2.0	748	2	T00732	hypothetical prote	1372	77.5	2.0	1017	2	D75028	h+-transporting AT
1300	78.5	2.0	757	2	T05688	hypothetical prote	1373	77.5	2.0	1079	1	TVFVMI	gag-Rml-env polyP
1301	78.5	2.0	763	2	T49089	hypothetical prote	1374	77.5	2.0	1142	2	A45031	cysteine-rich fibr
1302	78.5	2.0	842	2	T04555	hypothetical prote	1375	77.5	2.0	1323	2	E88257	protein let-23 [im
1303	78.5	2.0	1119	2	T16720	hypothetical prote	1376	77.5	2.0	1374	2	S70712	protein-tyrosine k
1304	78.5	2.0	1121	2	S57058	probable membrane	1377	77.5	2.0	2895	2	T08437	hyperplastic discs
1305	78.5	2.0	1131	2	T30951	hypothetical prote	1378	77.5	2.0	3085	2	T00327	polyprotein - infe
1306	78.5	2.0	1137	2	T18625	atrial natriuretic	1379	77	2.0	194	2	S70663	lectin heavy chain
1307	78.5	2.0	1188	2	JC4889	phosphatidylinosit	1380	77	2.0	230	2	T31722	hypothetical prote
1308	78.5	2.0	3473	1	A46112	genome polyprotein	1381	77	2.0	230	2	A44074	probable EGF-like
1309	78.5	2.0	3473	2	S27927	polyprotein - rice	1382	77	2.0	279	2	T16201	hypothetical prote
1310	78.5	2.0	3864	2	D87757	protein C44E4.1a [1383	77	2.0	317	2	T45984	hypothetical prote
1311	78	2.0	247	2	T27778	hypothetical prote	1384	77	2.0	375	2	F70691	hypothetical prote
1312	78	2.0	334	2	T03157	probable capsid as	1385	77	2.0	452	2	H84772	probable serine ca
1313	78	2.0	360	2	T26037	hypothetical prote	1386	77	2.0	476	2	T19786	hypothetical prote
1314	78	2.0	360	2	G82994	glycine-cleavage s	1387	77	2.0	500	2	AE2032	glycerol kinase [i
1315	78	2.0	372	2	T31060	hypothetical prote	1388	77	2.0	502	2	T41148	trp-asp repeat con
1316	78	2.0	385	2	A81926	hypothetical prote	1389	77	2.0	535	2	T19706	hypothetical prote
1317	78	2.0	401	2	C89102	hypothetical prote	1390	77	2.0	540	1	OYHUCR	natriuretic peptid
1318	78	2.0	415	2	T40553	Trp-Asp repeat pro	1391	77	2.0	591	2	S33542	catechol oxidase (
1319	78	2.0	441	2	E83377	probable alcohol d	1392	77	2.0	713	2	T40729	WD repeat-containi
1320	78	2.0	441	2	AH2930	oxidoreductase Atu	1393	77	2.0	729	2	A49120	protein ZC123.1 [i
1321	78	2.0	446	2	F98351	probable oxidoredu	1394	77	2.0	768	2	A87722	brain-derived neur
1322	78	2.0	454	1	QWST1	tumor necrosis fac	1395	77	2.0	821	1	S06943	neuronal different
1323	78	2.0	468	2	B40228	neurexin I-beta pr	1396	77	2.0	1019	2	JC7538	hypothetical prote
1324	78	2.0	468	2	S26741	T-cell glycoprotei	1397	77	2.0	1302	2	T00038	DNA segregation Ar
1325	78	2.0	482	2	T17250	hypothetical prote	1398	77	2.0	1498	2	B97355	T22111.2 protein -
1326	78	2.0	522	2	A46103	transmembrane glyc	1399	77	2.0	1552	2	G86344	receptor DBC-205 -
1327	78	2.0	523	2	C95303	conserved hypothet	1400	77	2.0	1723	2	S58880	hypothetical prote
1328	78	2.0	527	2	T04329	importin alpha - t	1401	77	2.0	1743	2	T28859	hypothetical prote
1329	78	2.0	539	2	JH0259	prostaglandin-endo	1402	77	2.0	2165	2	T21371	hypothetical prote
1330	78	2.0	723	2	PN0509	integrin beta-3 ch	1403	77	2.0	2584	2	T24158	hypothetical prote
1331	78	2.0	725	2	T27148	hypothetical prote	1404	77	2.0	2606	2	T24157	thryoglobulin prec
1332	78	2.0	843	2	A27131	epidermal growth f	1405	77	2.0	2769	1	UIBO	genome polyprotein
1333	78	2.0	957	2	T15976	hypothetical prote	1406	77	2.0	3033	1	GNVJ8	dysotrophin, musc
1334	78	2.0	989	2	T47503	hypothetical prote	1407	77	2.0	3660	1	S02041	ALR protein - huma
1335	78	2.0	1016	2	G86295	hypothetical prote	1408	77	2.0	4567	2	T03455	ALR protein - huma
1336	78	2.0	1131	2	T38744	hypothetical prote	1409	77	2.0	5262	2	T03454	platelet-aggregati
1337	78	2.0	1245	1	VHVVB	structural polypro	1410	76.5	1.9	71	2	A59413	platelet aggregati
1338	78	2.0	1260	1	TVRTNU	protein-tyrosine k	1411	76.5	1.9	146	2	G95995	phosphoribosylform
1339	78	2.0	1330	1	QGFPE	epidermal growth f	1412	76.5	1.9	216	2	JX0265	platelet aggregati
1340	78	2.0	1339	2	JC4387	epidermal growth f	1413	76.5	1.9	224	2	AD2115	phosphoribosylform
1341	78	2.0	1369	2	S70713	protein-tyrosine k	1414	76.5	1.9	234	2	I48603	insulin-like growt
1342	78	2.0	1658	2	D75489	hypothetical prote	1415	76.5	1.9	264	2	T22380	hypothetical prote
1343	78	2.0	3234	1	S58884	Ran-binding protei	1416	76.5	1.9	272	2	E97451	hypothetical prote

A;Cross-references: GB:D90272
R;Tokunaga, F.; Miyata, T.; Nakamura, T.; Morita, T.; Kuma, K.I.; Miyata, T.; Iwanaga, S.
Eur. J. Biochem. 167, 405-416, 1987
A;Title: Lipopolysaccharide-sensitive serine-protease zymogen (factor C) of horseshoe crab is a novel type of serine protease.
A;Reference number: S00105; MUID:88004461; PMID:3308457
A;Accession: S00105
A;Molecule type: protein
A;Residues: 'S',27-39,'S',41,'T',43-54,'E',691-782;950-977 <TOK>
C;Superfamily: coagulation factor C; C-type lectin homology; complement factor H repeat
C;Keywords: alternative splicing; glycoprotein; hemolymph coagulation; hydrolase; serine
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-690/Product: coagulation factor C heavy chain #status experimental <HCH>
F;136-195/Domain: complement factor H repeat homology <FH01>
F;199-254/Domain: complement factor H repeat homology <FH02>
F;260-321/Domain: complement factor H repeat homology <FH03>
F;436-564/Domain: C-type lectin homology <LCH>
F;576-634/Domain: complement factor H repeat homology <FH04>
F;685-747/Domain: complement factor H repeat homology #status atypical <PH05>
F;691-762/Product: coagulation factor C light chain peptide A #status experimental <PPA>
F;763-1019/Product: coagulation factor C light chain peptide B #status experimental <PPE>
F;763-1015/Domain: trypsin homology <TRY>
F;523,534,624,912/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;767/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;809,865,966/Active site: His, Asp, Ser #status predicted

Query Match 17.0%; Score 672; DB 2; Length 1019;
Best Local Similarity 25.6%; Pred. No. 4.5e-37;
Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;

QY 34 PGAEWNIM---CRECEYDQIE---CVCPRKREVGVYTI PCRCNEBENCDCSLIHPGCT 86
DB 184 PNCQNSFPKPCIRECAKVSSPHGKVNAPSGNMIEGAIL-----RFSCHS-----PYVL 233

QY 87 IFENCKSCR-NGSWGGLT-----CVCPRKREVGVYTI PCRCNEBENCDCSLIHPGCT 103
DB 234 IQGQTLTCQNGQWMSQIQCKKLVCPLDPVNHAHQVIGVEQKYGFQPGTEVTVT 293

QY 104 ---DDFVVKGYCACBR--AGWYGG--DCMR-----CGQVLR--APKG 137
DB 294 CSGNYFLMGFTLTKCPDGSWSGQSPCVKAVDREVDCCSKAVDFLDDYGEFVRHCPAG 353

QY 138 QILLES-----YPLNAHCEWTIRA---KPGFVI-----Q 163
DB 354 CSLTAGTWTGTATYHELSSVCRAIIRAGKLPNSGGVHVVNNPGYSDFLGSLDNGIKSBE 413

QY 164 LRFWMLSLBFDYM-----COYDYVEYRD-----GNDRGQIIRKVCGN--BRPAP 206
DB 414 LKSLARSFRFDYVSSSTAGRSGCPDGFWEVENCVVYTSQRAWERAQGVCTNMAARLAV 473

QY 207 IQS--IGSSLHLVLFHSDG-SKNPDGFH-----AIYEITACSSSPCF 245
DB 474 LDKDLIPSSLTETLRGKGLTTTWIGLHRLDAEKPFVWELMDRSNNVLDNLTFWASGEFG 533

QY 246 HDGTCV-LDKAGS---YKCACLAGYTGQRCENLLBERN---CSDPGPWNVGQKTTGGP 297
DB 534 NETNVCVILRDQLQPVWTKSCFCQSPSSFCACMDLSDRNKAKCDDPOPLENGHATLHGQS 593

QY 298 GLINGRHAIGTGVVSPFCNNSYVLSGNEKRTCCQNGEWSGQPCIK--ACREPKISDLV 355
DB 594 --IDGFVA--GSSIRYSCVHLVLSGTETVCTTNGTWSAPKPRCIKVITCQNPFPVPSYG 649

QY 356 RRRVLPWQVQSRTPPLHQLYSAAFSKQLQ---SAPTKPALPFGD-----LP 400
DB 650 SVEIKE---PSRTNSIRSVGSPFLRLPLPLARAAKPPPKPRSSQSPSTVDLASKVKLP 706

QY 401 MGYCHLHTLOQYECISPFYRLLGSSRRTCLRTKWSGRAPSCIPICCKENITAP-----455
DB 707 EGHYRVGSRAIYTCESRYEYLLSQGRCDNSGNWGRPARSCIPVGRSDSPSPFTWNG 766

QY 456 -KTQGLRWPMQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVAACHVTDLGKVTM 514
DB 767 NSTEIGQWPMQAGISRWLA-----DHNMMWFQCGSLLNEXKIWTAAHCVTYSATAEI 819

QY 515 IKTADLKVVLGKRYFDDRRDEKTIQSLOISAILHPNVDPIILLDADIALKLLDKARIST 574
DB 820 IDPSQFKYLGKYYKDDSDDDYVQVREALEHVNPNYDPGNLFDIALIQLKTPVTLTT 879

QY 575 RVQPICLAASRDLSSTFOESHI-----TVAGMNVLADVRSFGFNKDLTIRSGVSVVDSL 628
DB 880 RVQPICLPT--DITF---REHLKEGTAVVTGCG---LNENNTYSEMIQQAFLPVVAAS 930

QY 629 LCEQHEHGHGIPVSTVDNMFCSWEPAPSDDCTAETGCGIAAVSPGRASPEPRWHLMLGL 688
DB 931 TCEEGYKEADLPLTWTENNFCAGYK-KGRYDACSDDSGG--PLVFADDSRTERRVWVLEGI 987

QY 689 VWSYVDKTCSSH-RLSTAPTKVLPEKDWIER 717
DB 988 VSWGSPSGCGKANQYGGFTKVNFLSWIRQ 1017

RESULT 3
I54763
Ra-reactive factor (EC 3.4.21.-) 1 precursor - human
N;Alternate names: mannose binding protein-associated serine proteinase 1 (MASP-1)
C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: I54763; JN0883
R;Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.
Int. Immunol. 6, 665-669, 1994
A;Title: Molecular characterization of a novel serine protease involved in activation o
A;Reference number: I54763; MUID:94289349; PMID:8018603
A;Accession: I54763
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-699 <SAT>
A;Cross-references: UNIPROT:P48740; GB:D28593; NID:G790963; PIDN:BAA05928.1; PID:G47112
R;Takada, F.; Takayama, Y.; Hattuse, H.; Kawakami, M.
Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
A;Title: A new member of the C1s family of complement proteins found in a bactericidal
A;Reference number: JN0883; MUID:94059062; PMID:8240317
A;Accession: JN0883
A;Molecule type: mRNA
A;Residues: 1-234,'E',236-284,'G',286-498,'K',500-542,'K',544-642,'S',644-699 <TAK>
A;Cross-references: DDBJ:D17525; NID:G439712; PIDN:BAA04477.1; PID:G439713
A;Experimental source: liver
A;Comment: This is a serum bactericidal factor that activates complement C4 and C2 comp.
C;Genetics:
A;Gene: GDB:MASP1; GDB:CRARF; CRARF1; PRSS5; MASP
A;Cross-references: GDB:361104; GDB:330954; OMIM:600521
A;Map position: 3q27-3q28
C;Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein; hydr
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-448,449-699/Product: Ra-reactive factor #status predicted <MAT>
F;19-135/Domain: C1r/C1s repeat homology <C1R1>
F;143-181/Domain: EGF homology <EGF>
F;185-294/Domain: C1r/C1s repeat homology <C1R2>
F;301-362/Domain: complement factor H repeat homology <FH1>
F;367-432/Domain: complement factor H repeat homology <FH2>
F;449-699/Domain: trypsin homology <TRY>
F;49,178,407/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;73-91,143-157,153-166,168-181,185-212,242-260,301-349,329-362,367-414,397-432,436-572
F;159/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;448-449/Cleavage site: Arg-Ile (autolytic) #status predicted
F;490,552,646/Active site: His, Asp, Ser #status predicted

Query Match 12.2%; Score 482; DB 1; Length 699;
Best Local Similarity 24.9%; Pred. No. 1.4e-24;
Matches 178; Conservative 93; Mismatches 215; Indels 228; Gaps 39;

QY 69 CRNEECDCSLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFCACRAGWY---GGD 124
DB 143 CKEDEEELSCDHY-----CHN-----YIGGYCS-CRFGYILHTDNR 180

QY 125 C-MRCQVLRAPKQIILL-----ESYPLNAHCWTTHAKPGFVIQIRFVWLSLEFDYM-- 176


```
QY 174 D-----YMCQDYVEVDGNDNRDQIIRKVCNGERPAPIQISGSSHLVLFHSDGSKNFD 227
Db 241 DIDDHQVHCPCYDQIQI-----YANGKNIGEFQCKQRPDLDTSSNAVDLLFTDGGDSR 296
QY 228 GFHAIY-EETITACSSSPCFHDGTCVLDKAGSYKACLAGVGTQRCNLLERNCSDPGGP 286
Db 297 GWKLRVTTLLIKCPQPKTLDFTIIQNLQPOVQ-----FRDYFTATCK----- 339
QY 287 VNGYQKITGPGGLNGRHAQIGTVVFFCNNSYLVSGNEKRTQQQNGEWSGKQIPIC- IKA 345
Db 340 -QGYQLIEGNOVL-----HSPT-----AVCQDDGTWHRAMPCKIKD 375
QY 346 CREPKLSIDLVRRLVPMQVQSRTPHLQLYSAFQKQKLSQAPTKKPALPFGDL-----PM 401
Db 376 CQQPR-----NLPNGDFRYTTTM 393
QY 402 GYQHLHTLQYECISPFYR-----RLGSSRR-----TCLRTGKNWG-----RAPSCIPICGK 448
Db 394 GUNTYKARIQYCHEPYKMQTRAGSRESEQGVYTCTAQIWNKQKGEKIPCLPVCCK 453
QY 449 IEN-----ITAPKTQGLRMPWQAIIYRTSGVHDGSLHKGAWFLVCSGALVNRVTYV 500
Db 454 PVNPVEQRQRIIGQKAKGNFPQV-----FTNIHG-----RG-----GGALLGDRWIL 498
QY 501 VAAHCVTDLGKVTMIKTADLKVVILGKFYRDDDRDEKTIQSLQ-----ISAILLHPNY-- 552
Db 499 TAAHTLYPKHEAQ-SNASLDVFLG-----HTNVEELMKLGNHPIRRVSVHPDYRQ 548
QY 553 -DPILLADATAILKLDKARISRVQPICLAASRDLSTGFQESHITVAGMNVLAB----- 606
Db 549 DESYNEGDJALLENSVTLGNNLPICLP-----DNDTFYDLGLMGYVSGFGVWEKIAH 605
QY 607 ---VRSPGPKNDTLRSVVVDSLLCEBQEDHGPVSVTDNMFCAWEPAPSDICT 662
Db 606 DLRFVRLP-----VANPQACENWLGRKMRMDVFSQWMFCAQ-HPSLKQDAQ 651
QY 663 AETGGTAANSVFGRASPEPRHMLGLVWSYDKTCSHRLSTAFKTLVFKDWIERNMK 720
Db 652 GDSGGVFAVRDPN-----TDRWATGIVSWGIG-CS-RGYGFTYKVLNVYVDWIKEME 702

RESULT 5
A59271
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
N;Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A59271
R;Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaebler, W.J.; Laureen, S.B.; Poulsen, K.
Nature 386, 506-510, 1997
A;Title: A second serine protease associated with mannan-binding lectin that activates C
A;Reference number: A59271; MUID:97242412; PMID:9087411
A;Accession: A59271
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-686 <JEN>
A;Cross-references: UNIPROT:O00187; GB:Y09926; NID:g4007626; PIDN:CAA71059.1; PID:g40076
A;Experimental source: tissue liver
A;Note: submitted to GenBank, December 1996
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
C;Genetics:
A;Gene: GDB:MASP2
A;Cross-references: GDB:6071500
A;Map position: lp36.2-lp36.3
C;Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine p
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F;19-134/Domain: C1r/C1s repeat homology <C1R1>
F;142-180/Domain: EGF homology <EGF>
F;184-293/Domain: C1r/C1s repeat homology <C1R2>
F;300-361/Domain: complement factor H repeat homology <FHL>
```

F:366-430/Domain: complement factor H repeat homology <FHL>
F:445-679/Domain: tryptase homology <TRY>
F:72-90,142-156,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,
F:158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:444-445/Cleavage site: Arg-Ile (autolytic) #status predicted
F:483,532,633/Active site: His, Asp, Ser #status predicted

Query Match 10.2%; Score 400.5; DB 1; Length 686;
Best Local Similarity 22.7%; Pred. No. 3.9e-19;
Matches 173; Conservative 78; Mismatches 245; Indels 267; Gaps 34;

```
QY 128 CQQLR--APK-----GOILLESYP-----LNAHCEWTTHAKPGFVIQIRFVMLSLEFDY 175
Db 11 CGSVATPLGPKWPEPVFGRLASPGFGEVANDQERRRRLTAPGVRRLRYFTHFDELGH 70
QY 176 MCQDYVEVDGNDNRDQIIRKVCNGE-----RPAP-----IQSGSSHLVLFHSDGS--KN 225
Db 71 LCEYDFVKLSG-----AKVLATLCQOESTDTERAFKQDTFYSLGSLDITFRSDYSNEKP 126
QY 226 FQGEHAIY--EETITACSSSP-----CFHDGTCVLDKAGSYKACLAGVGTQRCNLLERN 274
Db 127 FTGFEAFYAEDIDECQVAPGEAPTCDHH-----CHNHLGGFYCSCRAGYVLRHNRKTC 183
QY 275 -----LEE----- 277
Db 184 CSGQVPTQSRSGELSPYPRYPKLSLSCCTYSISLEEGFSVILDFVESFDVETHPETLCPY 243
QY 278 -----RNCSDP 283
Db 244 DFLKIQTDRREHGFPGKTLPHRIETKSNVTITFTVDESBDHTGMIHYTSTAHAACPPY 303
QY 284 GGPVNGYQKITGPGGLNGRHAQ--IGTVVSPFCNNY-VLSG-----NEKRTCCQNGEW 335
Db 304 MAPPNHG-----VSPVQAKYILKDSFIFCTGYELLOGLHLPLKSFVAVCQKDGW 354
QY 336 SGKQPIC- IKACREPKISDLVRRVRLPMQVQSRTPHLQLYSAFQKQKLSQAPTKKPAL 394
Db 355 DRPMFACSI VDCGP--DDLPSGRV-----EVI TGP----- 383
QY 395 PFGDLPVMGQVHLHTLQYECISPFY--RRLGSSRRITCLRTGKNWG-----RAPSCIPICGK 448
Db 384 -----GVTTYKAVIQSYCEETFTYTMKVDNGKYVCEADGFTWTSKSGKSLPCEPVCGL 436
QY 449 IENITAPKTQGLR-----WPQQAIIYRTSGVHDGSLHKGAWFLVCSGALVNRVTWVVA 502
Db 437 SARTTGRIYGGQAKPGDFPMQVLLIGGT-----AAGALLYDNWVLT 481
QY 503 AHCVTDLGKVTMIKTADLKVVILGKFYRDDDRDEKTIQSLQ-----ISAILLHPNY-DP 554
Db 482 AHAVYE---QKHDSALDIRMG-----TLKRLSPHYTQAWSEAVFIHEGYTHD 526
QY 555 ILLDADIALKLDKARISTRVQPICLAASRDLSTSFQESHITVAGMNVLABVRSPEKXN 614
Db 527 AGPDNDIALIKLNKVNINSNITPICLPKBAESFMRTDDIGTASWG-----LTQGFILA 582
QY 615 DTLRSQVSVVDSLLCEBQEDHGP-VSVTDNMFCAWEPAPSDICTAETGIIAAVSF 673
Db 583 RNLMYVDIPIVDHOKTAAYEKPPYPRGVSVTANMLCAGLE-SGGKDSGCRDSSG--ALVF 639
QY 674 PGRASPEPRHMLGLVWSYDKTCSHRLSTAFKTLVFKDWIE 716
Db 640 --LDSETERFWFGVIVSGMNCGEAGQGVYTKVINIYPWIE 680
```

RESULT 6

S05008

complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S05008
R;Kinoshita, H.; Sakiyama, H.; Tokunaga, K.; Imajob-Ohmi, S.; Hamada, Y.; Isono, K.; Sa-
PEBS Lett. 250, 411-415, 1989
A;Title: Complete primary structure of a calcium-dependent serine proteinase capable of

Db 745 --ELTDHMLCAGPSPSKKXDAQCGDGGPLVCQ-----NEKEQFSIYGLVSWG--EGCG- 794

Qy 700 RLST--AFTKVLFPKDWIERNMK 720

Db 795 RVSKPGVYTKVRLLFTTQNTQ 817

RESULT 8

JC6554

complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004

C;Accession: JC6554

R;Sakai, H.; Nakashima, S.; Yoshimura, S.; Nishimura, Y.; Sakai, N.; Nozawa, Y.

Gene 209, 87-94, 1998

A;Title: Molecular cloning of a cDNA encoding a serine protease homologous to complement

A;Reference number: JC6554; MUID:98192519; PMID:9524231

A;Accession: JC6554

A;Molecule type: mRNA

A;Residues: 1-694 <SAK>

A;Cross-references: UNIPROT:O70542; DDBJ:D88250; NID:g3080541; PIDN:BAA25797.1; PID:g308

C;Comment: This protein is involved in glial cell differentiation and cartilage remodeling

C;Genetics:

A;Gene: x-gsp

C;Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homolog

C;Keywords: differentiation; glycoprotein; hydrolase; serine proteinase

F;1-21/Domain: signal sequence #status predicted <SIG>

F;17-133/Domain: C1r/C1s repeat homology <C1R>

F;22-694/Product: serine protease homolog #status predicted <MAT>

F;141-177/Domain: EGF homology <EGF>

F;300-360/Domain: complement factor H repeat homology <PHR>

F;444-681/Domain: trypsin homology <TRY>

F;180.412/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;481.535.637/Active site: His, Asp, Ser #status predicted

Query Match 8.6%; Score 340.5; DB 2; Length 694;

Best Local Similarity 21.2%; Pred. No. 4e-15;

Matches 167; Conservative 98; Mismatches 244; Indels 277; Gaps 40;

Qy 44 ECCEYDQIECVCGKRE-----VVGYYTTPCCR-----NEE----- 73

Db 69 ENCAYSQVGIISGIEERLQCGRSSKSPNPTVEBFQFPYRNRLQVVFVTSDFSNEERFTG 128

Qy 74 -----NECDCLIHPCGTFIFENCKSCRNCGTGLDDFYVKGFFCAECRAGYGG 123

Db 129 FAAYSADVNECTDFTDVP-CSHF-----CNN-----FIGGYFCS-CPPEYFLH 171

Qy 124 DCMR-----CGOVLRAPKGOILLES-----YPLNHAHCWTIHAKPGFVIQLRFVMLSLEF 173

Db 172 DMRTCGVNCSDVFTALIGEIASPNYPNPYPENSRCVQIRLOEGF--RLVLTIRREDF 229

Qy 174 DYCQDYVEVRDGNR-----DGQIIRKVCNERPAP--IQSIGSSLHLVLFHSDG 222

Db 230 D-----VEPADSEGNCHDSLTFAAKNQOFGPYCGNGFGPLTIKTQSNLTLDIVQTDL 282

Qy 223 SKNFDGFHAIY-----BEITACS-----SSPCFHDTCTVLDKAGSVKCACLAGYTG 268

Db 283 TGQNGKWKLYHGDPIPCPKETSANSIWEPEKAKYVFKD-----VVKITC----- 327

Qy 269 QRCENLEERNCDPGGVNNGYQKINGGGLINGRHAIGTIVVSFFCNNSYVLSGNEKRT 328

Db 328 -----VDGFVEVGNVG-----STSPY-----ST 346

Qy 329 CQONGBWSGK-----QFICIKACREPKISDLVRRVLPQVQSRKPTPLHQLYLSAASFQKQL 384

Db 347 CQNGGWSRLRCQPV---DCGVPE-----PIENGKVEDPDTVFGSV----- 387

Qy 385 QSAPTQKALPFGDLPNGYQHLHTLOQYECISPFY--RRIGSSRRCTCLRTGKWSG----- 437

Db 388 -----IHYTCEEPYYTNEQEGEGEYHCAANGSWNDQLGV 422

Qy 438 RAPSCPIPCG-----KIEN--ITAPKTOGLRFPWQAAIYRRTSGVHDGSLHKGAWFLVC 489

Db 423 ELPKCIPIVCGVTEPFKVOQRIFGGYSTKIQSPFMQVVFESPRGG----- 467

Qy 490 SGALVNERTVVVAACHCVT-DLGKVTMIKTADLKVLGKRYRDDRDEKTIQSIQISAIL 548

Db 468 -GALIDEXVWLTAAHVVEGNSDPVMYVGSSTLKI-----EKLRNAQLITERVII 516

Qy 549 HPNYDP-----ILLDADIAILKLLDKARISTRVQPICLAAASRDILSTSFQESH-----TV 598

Db 517 HFSWKQEDDLNTRTFNDIALVQLKDPVKMGPTVAPICLP---ETFSYDNFSEVDLGLI 573

Qy 599 AGNVLADVRSPGKNKDTLRSGVSVVDSLLCE----EQEDHGIPVSVTDMNMFCAWEP 654

Db 574 SCWG-RTEIRTVIQ---LRGAKLPITSLEKQOVKVENPKARSNDYVFTDNMICAGEKG 629

Qy 655 TAPSDICTAETGIIAAVSPGPRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLFPKDW 714

Db 630 V---DSCEGDSGGAFALPVFN--VKDPKPYVAGLVSWG--KKCG--TYGIYTKVRKNYVDW 680

Qy 715 IERNMK 720

Db 681 ILKTMQ 686

RESULT 9

C1HUS

complement subcomponent C1s (EC 3.4.21.42) precursor [validated] - human

N;Alternate names: C1 esterase precursor

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-May-2004

C;Accession: A40496; A27381; S00224; S05634; A05140; A25396; A38407; B37820

R;Kusumoto, H.; Hitosawa, S.; Salier, J.P.; Hagen, F.S.; Kurachi, K.

Proc. Natl. Acad. Sci. U.S.A. 85, 7307-7311, 1988

A;Title: Human genes for complement components C1r and C1s in a close tail-to-tail array

A;Reference number: A40496; MUID:89017187; PMID:2459702

A;Accession: A40496

A;Molecule type: mRNA

A;Residues: 1-688 <KUS>

A;Cross-references: GB:J04080; NID:g179645; PIDN:AAA51852.1; PID:g179646

R;Tosi, M.; Duponchel, C.; Meo, T.; Julier, C.

Biochemistry 26, 8516-8524, 1987

A;Title: Complete cDNA sequence of human complement C1s and close physical linkage of t

A;Reference number: A27381; MUID:88163522; PMID:2831944

A;Accession: A27381

A;Molecule type: mRNA

A;Residues: 1-688 <TOS>

A;Cross-references: GB:M18767; NID:g179647; PIDN:AAA51853.1; PID:g179648

R;Mackinnon, C.M.; Carter, P.E.; Smyth, S.J.; Dunbar, B.; Fothergill, J.E.

Eur. J. Biochem. 169, 547-553, 1987

A;Title: Molecular cloning of cDNA for human complement component C1s. The complete amir

A;Reference number: S00224; MUID:88082788; PMID:3500856

A;Accession: S00224

A;Molecule type: mRNA

A;Residues: 1-688 <EMBL>

A;Cross-references: EMBL:X06596; NID:g29542; PIDN:CAA29817.1; PID:g763110

A;Accession: S26732

A;Molecule type: protein

A;Residues: 16-38;69-116;170-236;246-262;265-280;282-284;287-308;315-363;384-394;421-431

R;Tosi, M.; Duponchel, C.; Meo, T.; Couture-Tosi, E.

J. Mol. Biol. 208, 709-714, 1989

A;Title: Complement genes C1r and C1s feature an intronless serine protease domain clos

A;Reference number: S05634; MUID:90040704; PMID:2553984

A;Accession: S05634

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 356-513,'G',514-688 <TO2>

R;Carter, P.E.; Dunbar, B.; Fothergill, J.E.

Biochem. J. 215, 565-571, 1983

A;Title: The serine proteinase chain of human complement component C1s. Cyanogen bromid

A;Reference number: A05140; MUID:84104122; PMID:6362661

A;Accession: A05140

A;Molecule type: protein

A;Residues: 438-483,'X',485-500;503-534;542-558;561-572,'A',574-601;617-623;626-644;647

R;Spycher, S.E.; Nick, H.; Rickli, E.E.

A:Pathway: intestinal digestive hydrolase cascade
C:Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding repeat
C:Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen
F:1-784/Product: enteropeptidase heavy chain #status predicted <HCH>
F:22-38/Domain: transmembrane #status predicted <TM>
F:184-221/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:342-504/Domain: MAM homology <MAM>
F:526-631/Domain: C1r/C1s repeat homology <C1r>
F:643-677/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:678-783/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC>
F:785-1019/Product: enteropeptidase light chain #status predicted <LCH>
F:785-1014/Domain: trypsin homology <TRY>
F:116-147, 179, 328, 335, 388, 440, 470, 503, 534, 630, 682, 706, 725, 848, 887, 909, 949/Binding site:
F:772-896, 810-826, 910-977, 941-956, 967-995/Disulfide bonds: #status predicted
F:825, 876, 971/Active site: His, Asp, Ser #status predicted

Query Match 8.4%; Score 331.5; DB 1; Length 1019;
Best Local Similarity 22.9%; Pred. No. 2.4e-14;
Matches 136; Conservative 90; Mismatches 225; Indels 143; Gaps 27;

QY 143 SYPLNAHCWTHAKPGFVIQLRFVMLSLEFDMQYDVEVRDGNRQGIKRCVGN 202
Db SYPLNAHCWTHAKPGFVIQLRFVMLSLEFDMQYDVEVRDGNRQGIKRCVGN 202
QY 545 YPNLAFVCVWILNAQKGNQLHFE-----QEFLENINADVVEIRDGEADSLLLAVTG-- 598
Db YPNLAFVCVWILNAQKGNQLHFE-----QEFLENINADVVEIRDGEADSLLLAVTG-- 598
QY 203 RPAPQSIGSLH-----VLPHSDGSKNF-DGFHAIYEEITACSSSPCFHDGTCV 251
Db RPAPQSIGSLH-----VLPHSDGSKNF-DGFHAIYEEITACSSSPCFHDGTCV 251
QY 599 -PGPVKDVFTNRMVTLITNDVLARGGFKANFTTGYHLGIPE-----PC----- 643
Db -PGPVKDVFTNRMVTLITNDVLARGGFKANFTTGYHLGIPE-----PC----- 643
QY 252 LDKAGSYKC---ACLA-----GYTCQRCENLEERNCSDPGPGVNGYQKITGGPGLNG 302
Db LDKAGSYKC---ACLA-----GYTCQRCENLEERNCSDPGPGVNGYQKITGGPGLNG 302
QY 644 --KADHFQCKNGECVPLNLCGHL--HCDGSDGDEADC-----VRFNGTNNGLVRF 693
Db KADHFQCKNGECVPLNLCGHL--HCDGSDGDEADC-----VRFNGTNNGLVRF 693
QY 303 RHAKIGTVVFFCNNSYVLSGNEKRTCQONGEWSGKQPCIKACREPKISDLVRRVLP 362
Db RHAKIGTVVFFCNNSYVLSGNEKRTCQONGEWSGKQPCIKACREPKISDLVRRVLP 362
QY 694 RIQSIW-----HTACAENWTQTISNDVC-----QLLGL 721
Db RIQSIW-----HTACAENWTQTISNDVC-----QLLGL 721
QY 363 QVQSRRTPLHOLYSAAFSKQKLOSAPTCKPALPFGDLPNGYQHLHTQLQYECISPFYRL 422
Db QVQSRRTPLHOLYSAAFSKQKLOSAPTCKPALPFGDLPNGYQHLHTQLQYECISPFYRL 422
QY 722 GSGNSSKPIFTDGGPF--VKLNTAPD-----GHLIITPSQQLQDSLRL 765
Db GSGNSSKPIFTDGGPF--VKLNTAPD-----GHLIITPSQQLQDSLRL 765
QY 423 GSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSLHK 482
Db GSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSLHK 482
QY 766 QCNHKSC-----GKLAQAQITPKI--VGSNAKEGAWPVVGLY-----YGR--- 807
Db QCNHKSC-----GKLAQAQITPKI--VGSNAKEGAWPVVGLY-----YGR--- 807
QY 483 GAWFLVCSGALNVNRTVVAACHCVTDLGKVTMLKADLVKVLGKFRDDEKTIQSLQ 542
Db GAWFLVCSGALNVNRTVVAACHCVTDLGKVTMLKADLVKVLGKFRDDEKTIQSLQ 542
QY 808 ----LLCGASLVSSDWLWVSAACHV--YGR--NLEPSKWTAILGLHMKSLNLTSPQIVPRL- 858
Db LLCGASLVSSDWLWVSAACHV--YGR--NLEPSKWTAILGLHMKSLNLTSPQIVPRL- 858
QY 543 ISAILHPNVDPIILLDADIAILLKLDKARISTRVQPICLAAASRDLSSTFQESHITVAGWN 602
Db ISAILHPNVDPIILLDADIAILLKLDKARISTRVQPICLAAASRDLSSTFQESHITVAGWN 602
QY 859 IDEIVNPHNRRRKNDIAMHLEFKVNYTDYIQICLPEENQVPPGR--NCSTAGWG 916
Db IDEIVNPHNRRRKNDIAMHLEFKVNYTDYIQICLPEENQVPPGR--NCSTAGWG 916
QY 603 VLADVRSPGFKNDTLRSVVVDSLLCEQEDHGIPIVSVTDNMFCAWEPAPSDICT 662
Db VLADVRSPGFKNDTLRSVVVDSLLCEQEDHGIPIVSVTDNMFCAWEPAPSDICT 662
QY 917 T---VVYQGTANILQEADVPLLSNRCQQQMPY-----NITENMICAGYE-BGGIDSCQ 968
Db T---VVYQGTANILQEADVPLLSNRCQQQMPY-----NITENMICAGYE-BGGIDSCQ 968
QY 663 AETGGIAVSPGRASPERPWHLMGLVSWSYDKTCSHRLSTAFKVLPKDWIE 716
Db AETGGIAVSPGRASPERPWHLMGLVSWSYDKTCSHRLSTAFKVLPKDWIE 716
QY 969 GDSGG-----PLMCQENNRWFLAGVTSFGYKALPNR-PGVYARVSRFTEWIQ 1015
Db GDSGG-----PLMCQENNRWFLAGVTSFGYKALPNR-PGVYARVSRFTEWIQ 1015

RESULT 11
A53663
enteropeptidase (EC 3.4.21.9) precursor [validated] - pig
N:Alternate names: enterokinase
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 07-Oct-1994 #sequence_revision 09-Aug-1996 #text_change 28-Apr-2003
C:Accession: A53663
R:Matsumura, M.; Ichinose, M.; Yahagi, N.; Kakei, N.; Teukada, S.; Miki, K.; Kurokawa, J. Biol. Chem. 269, 19976-19982, 1994
A:Title: Structural characterization of porcine enteropeptidase.
A:Reference number: A53663; MUID:94327548; PMID:8051081
A:Accession: A53663

A:Molecule type: mRNA
A:Residues: 1-1034 <MAT>
A:Cross-references: GB:D30799; NID:g505122; PIDN:BA06459.1; PID:g505123
A:Note: parts of this sequence, including the amino ends of three chains isolated from t
C:Comment: The mechanism of association with the membrane of the intestinal brush border
ated below) or with amino-terminal myristoylation of the heavy chain.
C:Complex: Mature enteropeptidase is variously reported to contain two (heavy and light)
ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involv
C:Function:
A:Description: cleaves activation peptide from trypsinogen to produce active trypsin
A:Pathway: intestinal digestive hydrolase cascade
C:Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding rep
C:Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen
F:22-38/Domain: transmembrane #status predicted <TM>
F:52-117/Product: enteropeptidase mini chain #status predicted <MCH>
F:118-799/Product: enteropeptidase heavy chain #status predicted <HCH>
F:199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:357-519/Domain: MAM homology <MAM>
F:541-646/Domain: C1r/C1s repeat homology <C1r>
F:658-692/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:693-798/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC>
F:800-1034/Product: enteropeptidase light chain #status predicted <LCH>
F:800-1029/Domain: trypsin homology <TRY>
F:116,147,170,194,283,343,350,403,455,485,518,549,645,697,701,721,740,761,804,863,902,96
F:787-911,825-841,925-992,956-971,982-1010/Disulfide bonds: #status predicted
F:840,891,986/Active site: His, Asp, Ser #status predicted

Query Match 8.4%; Score 330.5; DB 1; Length 1034;
Best Local Similarity 22.9%; Pred. No. 2.9e-14;
Matches 137; Conservative 86; Mismatches 224; Indels 151; Gaps 27;

QY 143 SYPLNAHCWTHAKPGFVIQLRFVMLSLEFDMQYDVEVRDGNRQGIKRCVGN 202
Db SYPLNAHCWTHAKPGFVIQLRFVMLSLEFDMQYDVEVRDGNRQGIKRCVGN 202
QY 560 NYPNOAFVCVWILNAQKGNQLHFE-----QEFLENINADVVEIRDGEADSLLLAVTG-- 613
Db NYPNOAFVCVWILNAQKGNQLHFE-----QEFLENINADVVEIRDGEADSLLLAVTG-- 613
QY 203 RPAPQSIGSS---LHVLPHSDGSS-----KNF-DGFHAIYEEITACSSSPCFHD--- 247
Db RPAPQSIGSS---LHVLPHSDGSS-----KNF-DGFHAIYEEITACSSSPCFHD--- 247
QY 614 -PGPVKDVFTNRMVTLITNDVLARGGFKANFTTGYHLGIPE-----PCKDNFQC 665
Db -PGPVKDVFTNRMVTLITNDVLARGGFKANFTTGYHLGIPE-----PCKDNFQC 665
QY 248 --GTCVLDKAGSYKACLAGYTCQRCENLEERNCSDPGPGVNGYQKITGGPGLNGRIA 305
Db GTCVLDKAGSYKACLAGYTCQRCENLEERNCSDPGPGVNGYQKITGGPGLNGRIA 305
QY 666 ENGECVL-----LVNLCDFGSHCKDGSDEAHCVRFNLGNTANNSSLVQFRIQ 711
Db ENGECVL-----LVNLCDFGSHCKDGSDEAHCVRFNLGNTANNSSLVQFRIQ 711
QY 306 KIGTVVFFCNNSYVLSGNEKRTCQONGEWSGKQPCIKACREPKISDLVRRVLP 365
Db KIGTVVFFCNNSYVLSGNEKRTCQONGEWSGKQPCIKACREPKISDLVRRVLP 365
QY 712 SIW-----HTACAENWTQTISDDVC-----QLLGLGTG 739
Db SIW-----HTACAENWTQTISDDVC-----QLLGLGTG 739
QY 366 SRETPLHOLYSAAFSKQKLOSAPTCKPALPFGDLPNGYQHLHTQLQYECISPFYRLGSS 425
Db SRETPLHOLYSAAFSKQKLOSAPTCKPALPFGDLPNGYQHLHTQLQYECISPFYRLGSS 425
QY 740 NSSMPFFSSGGGPF--VKLNTAPNGSLILTASE-----QCFEDSLILLQCN 783
Db NSSMPFFSSGGGPF--VKLNTAPNGSLILTASE-----QCFEDSLILLQCN 783
QY 426 RRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLR-----WPQAAIYRRTSGVHDGS 479
Db RRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLR-----WPQAAIYRRTSGVHDGS 479
QY 784 HKSC---GK-----KQVQAEVSPKIVGGNDSREGAWPVVVALY-----YNGQ 822
Db HKSC---GK-----KQVQAEVSPKIVGGNDSREGAWPVVVALY-----YNGQ 822
QY 480 LHKGAFLVCSGALNVNRTVVAACHCVTDLGKVTMLKADLVKVLGKFRDDEKTIQ 539
Db LHKGAFLVCSGALNVNRTVVAACHCVTDLGKVTMLKADLVKVLGKFRDDEKTIQ 539
QY 823 -----LLCGASLVSSDWLWVSAACHV--YGR--NLEPSKWTAILG-LHMTSLTSPQIV 870
Db -----LLCGASLVSSDWLWVSAACHV--YGR--NLEPSKWTAILG-LHMTSLTSPQIV 870
QY 540 SIQISAILHPNVDPIILLDADIAILLKLDKARISTRVQPICLAAASRDLSSTFQESH- TV 598
Db SIQISAILHPNVDPIILLDADIAILLKLDKARISTRVQPICLAAASRDLSSTFQESH- TV 598
QY 871 TRLIDEIVNPHNRRRKNDIAMHLEFKVNYTDYIQICLPEENQV---PPGGRICSI 927
Db TRLIDEIVNPHNRRRKNDIAMHLEFKVNYTDYIQICLPEENQV---PPGGRICSI 927
QY 599 AGNVLADVRSFGFKNDTLRSVVVDSLLCEQEDHGIPIVSVTDNMFCAWEPAPSD 658
Db AGNVLADVRSFGFKNDTLRSVVVDSLLCEQEDHGIPIVSVTDNMFCAWEPAPSD 658
QY 928 AGWKGVIYQSPA---DILQEADVPLLSNRCQQQMPY-----NITENMWCAQYE-EGGI 979
Db AGWKGVIYQSPA---DILQEADVPLLSNRCQQQMPY-----NITENMWCAQYE-EGGI 979
QY 659 DICTAETGGIAVSPGRASPERPWHLMGLVSWSYDKTCSHRLSTAFKVLPKDWIE 716
Db DICTAETGGIAVSPGRASPERPWHLMGLVSWSYDKTCSHRLSTAFKVLPKDWIE 716
QY 980 DSCQDGGSG-----PLMCLENNRWLLAGVTSFGYKALPNR-PGVYARVPKTEWIQ 1030
Db DSCQDGGSG-----PLMCLENNRWLLAGVTSFGYKALPNR-PGVYARVPKTEWIQ 1030

RESULT 12

JX0210
Protein C (activated) (EC 3.4.21.69) precursor - mouse
N;Alternate names: vitamin K-dependent serine proteinase
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JX0210
R;Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A;Title: Isolation and characterization of a mouse protein C cDNA.
A;Reference number: JX0210; MUID:92316897; PMID:1618739
A;Accession: JX0210
A;Molecule type: mRNA
A;Residues: 1-461 <TAD>
A;Cross-references: UNIPROT:P33587; GB:D10445; NID:g2203085; PIDN:BAA01235.1; PID:g2203086
A;Experimental source: liver
C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
B.
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
F;1-33/Domain: signal sequence #status predicted <SIG>
F;27-85/Domain: Gla domain homology <GLA>
F;34-41/Domain: propeptide #status predicted <PRO>
F;42-196/Domain: protein C #status predicted <PC>
F;42-196/Domain: light chain #status predicted <PCL>
F;91-130/Domain: EGF homology <EG1>
F;139-174/Domain: EGF homology <EG2>
F;199-461/Domain: heavy chain #status predicted <PCH>
F;199-211/Domain: activation peptide #status predicted <ACT>
F;212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>
F;212-445/Domain: trypsin homology <TRY>
F;47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;121-130,139-159,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat
F;214,290,355/Binding site: carbohydrate (Aen) (covalent) #status predicted
F;253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 8.1%; Score 320; DB 1; Length 461;
Best Local Similarity 23.9%; Pred. No. 6e-14;
Matches 145; Conservative 70; Mismatches 174; Indels 218; Gaps 29;

QY 152 WTI-----HAKPGF-----VIOLRFVMLSLFEDYMCQYDVEYRDNDRDQIILKRV 198
DB 14 WGISSIPALHPDPVFSSEHQAQVLRVRRANSFLF-----EMRPG-SLERECWEEI 62

QY 199 CGNERPAPI-QSIGSSHLVLFHSDGSKNFDFGHAIYEETACSSPFCFHDGTCVLDKAGS 257
DB 63 CDFEERAQEIFQNVEDTLAFWI-----KYFDGQCSAPPLDHCQDSFCCGHGTCT-DGIGS 116

QY 258 YKACLAGYTGQRCENLLBERNSCDPGPVNGVKITGGPL-----INGRHAKITGVV 311
DB 117 FSCGCDKGWEGKFCQQLRFPQC-----RVNNGGCLHYCLEESNGRCA----- 160

QY 312 SPFCNNSYVLSGNEKR-----TCQNGEWSGKQPIKACREPISDLVRRVLPQV 364
DB 161 ----CAGYELADHMECKSTVNPFCGKGRWIEK-----KKKIL----- 196

QY 365 QSRETPHLHOLYSAFQSKQLQSAPTKKPALPFGDLPWGYHLTLQYECISPFYRRLGS 424
DB 197 -KEDTUL-----EDELPPD----- 210

QY 425 SRRTLRTGWSGRAPSCIPICOKIENITAPKTQGLRWPMQAAYVRTSGVHDGSLHKA 484
DB 211 -----RIVNGTLTK-QG-DSPQAAIL-----DSKKK-- 235

QY 485 WELVCSGALVNERTVVVAACHVTDLCKVMTKADLKVVLKGYRDRDRDEKTIQSLQIS 544
DB 236 --LACGVLHTSWLTAACHVEGTGKLT-----VRLGEY--DLRRDRHWELDLDIK 283

QY 545 AILTHNPYDPLLDADIALIKLADKARISTRVOPICL-----AASRDLSTSFQESHITVAG 600
DB 284 EILVHNPYTRSSDNDIALRLAQPATLSKTIPICLPNNGLAQQLTQAGETVVT--G 341

QY 601 WNVLADVRSPGPKNDTL-----RSGVVSVVDSLLCEEQHEHDGIPVSVTDNMF 649

DB 342 WGYQSDRIKDRNRRTFILTIRIPLVARNECEVMKNV-----VSENMLC 387
QY 650 ASMEPTAPSDICTAETGGIAAASFPGRASPEPRWHLMLGLVSWGYDKTCSHRLSTA-PTKV 708
DB 388 AGIIGNT-RDACDGDGGPMVFFRG-----TWFLVGLVSWG--EGCGHTNNGYITKV 438
QY 709 LPFKDWI 715
DB 439 GSYLKI 445

RESULT 13
A43090
enteropeptidase (EC 3.4.21.9) precursor [validated] - bovine
N;Alternate names: enterokinase
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A43090; A48874; A61436
R;Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A;Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease comp
A;Reference number: A43090; MUID:94329561; PMID:8052624
A;Accession: A43090
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDDBJ
A;Molecule type: mRNA
A;Residues: 1-1035 <KIT>
A;Cross-references: UNIPROT:P98072; GB:U09859; NID:g746410; PIDN:AAB40026.1; PID:g74641
A;Experimental source: small intestine
R;LaVallie, E.R.; Rehentulla, A.; Racie, L.A.; DiBlasio, E.A.; Ferenz, C.; Grant, K.L.;
J. Biol. Chem. 268, 23311-23317, 1993
A;Title: Cloning and functional expression of a cDNA encoding the catalytic subunit of
A;Reference number: A48874; MUID:94043122; PMID:8226855
A;Accession: A48874
A;Molecule type: mRNA
A;Residues: 801-1035 <LAV>
A;Cross-references: GB:U19663; NID:9416131; PIDN:AAA16035.1; PID:g416132
A;Note: Parts of this sequence, including the amino end of the mature protein, were con
R;Light, A.; Janska, H.
J. Protein Chem. 10, 475-480, 1991
A;Title: The amino-terminal sequence of the catalytic subunit of bovine enterokinase.
A;Reference number: A61436; MUID:92189715; PMID:1799406
A;Accession: A61436
A;Molecule type: protein
A;Residues: 801-807, 'Y', 809-827 <LIG>
C;Comment: The mechanism of association with the membrane of the intestinal brush borde
embrane attachment using a signal-anchor sequence
C;Comment: Conversion from membrane-bound to soluble forms may involve further processin
l-fide linked
C;Function:
A;Description: cleaves propeptide from trypsinogen to produce active trypsin
A;Pathway: intestinal digestive hydrolase cascade
C;Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding re
C;Keywords: glycoprotein; hydrolase; intestine; serine proteinase; transmembrane protei
F;22-38/Domain: transmembrane #status predicted <TRM>
F;52-117/Product: enteropeptidase mini chain #status predicted <MCH>
F;118-800/Product: enteropeptidase heavy chain #status predicted <HCH>
F;199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;358-520/Domain: MM homology <MM>
F;542-647/Domain: C1r/C1s repeat homology <C1r>
F;659-693/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;694-799/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SR
F;801-1035/Product: enteropeptidase light chain #status predicted <LCH>
F;801-1030/Domain: trypsin homology <TRY>
F;116,147,170,194,233,263,264,404,456,486,519,550,646,698,722,741,762,864,903,965/Bindi
F;788-912,826-926,957-972,983-1011/Disulfide bonds: #status predicted
F;841,892,987/Active site: His, Asp, Ser #status predicted

Query Match 8.0%; Score 317.5; DB 1; Length 1035;
Best Local Similarity 24.6%; Pred. No. 2.1e-13;
Matches 146; Conservative 80; Mismatches 225; Indels 143; Gaps 30;

This Page Blank (uspto)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 8, 2005, 16:05:58 ; Search time 62 Seconds
(without alignments)
3874.051 Million cell updates/sec

Perfect score: 3945
Sequence: 1 MELGCWTQLGLTFLQLLLIS.....LSTAFKVLFPKDWIERNWK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1428581 seqs, 333598853 residues

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published Applications AA.*

1: /cgn2_6/protdata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/protdata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/protdata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/protdata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/protdata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/protdata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/protdata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/protdata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/protdata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/protdata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/protdata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/protdata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/protdata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/protdata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/protdata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/protdata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/protdata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/protdata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/protdata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/protdata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
27	3945	100.0	720	10	US-09-997-428-231
562	3945	100.0	720	14	US-10-174-587-170
626	3945	100.0	720	14	US-10-063-742-38
741	3945	100.0	720	17	US-10-972-317-38
742	3939	99.8	720	14	US-10-004-551-4
743	3939	99.8	720	14	US-10-098-871-26
744	3921.5	99.4	737	16	US-10-408-765A-1796
745	3500.5	88.7	649	15	US-10-274-639-17
746	3500.5	88.7	649	15	US-10-333-574-17
747	3089.5	78.3	567	14	US-10-004-551-2
748	2946.5	74.7	570	13	US-10-067-422-9
749	2413	61.2	455	11	US-09-833-245-1401
750	1708.5	43.3	323	11	US-09-833-245-1402
751	672	17.0	1019	14	US-10-183-992-4

752	665	16.9	1019	14	US-10-183-992-8	Sequence 8, Appli
753	665	16.9	1019	16	US-10-638-125-4	Sequence 4, Appli
754	665	16.9	1083	14	US-10-183-992-6	Sequence 6, Appli
755	665	16.9	1083	16	US-10-638-125-2	Sequence 2, Appli
756	476	12.1	699	15	US-10-388-322-2	Sequence 2, Appli
757	471	11.9	728	14	US-10-148-671-5	Sequence 5, Appli
758	469.5	11.9	679	9	US-09-874-198-6	Sequence 6, Appli
759	469.5	11.9	679	9	US-09-874-238-6	Sequence 6, Appli
760	468	11.9	728	15	US-10-388-322-4	Sequence 4, Appli
761	403.5	10.2	688	9	US-09-874-198-7	Sequence 7, Appli
762	403.5	10.2	688	9	US-09-874-238-7	Sequence 7, Appli
763	403.5	10.2	705	9	US-09-808-602-94	Sequence 94, Appli
764	403.5	10.2	705	10	US-09-800-198-81	Sequence 81, Appli
765	403.5	10.2	705	15	US-10-257-021-66	Sequence 66, Appli
766	401.5	10.2	686	9	US-09-874-198-2	Sequence 2, Appli
767	401.5	10.2	686	9	US-09-874-238-2	Sequence 2, Appli
768	400.5	10.2	686	15	US-10-388-322-3	Sequence 3, Appli
769	400.5	10.2	686	15	US-10-332-713-2	Sequence 2, Appli
770	398.5	10.1	671	15	US-10-332-713-3	Sequence 3, Appli
771	336	8.5	760	9	US-09-925-301-1024	Sequence 1024, Ap
772	334	8.5	673	9	US-09-874-198-8	Sequence 8, Appli
773	334	8.5	673	9	US-09-874-238-8	Sequence 8, Appli
774	332	8.4	855	15	US-10-072-012-354	Sequence 354, App
775	332	8.4	855	15	US-10-072-012-420	Sequence 420, App
776	332	8.4	855	15	US-10-037-417-132	Sequence 132, App
777	331.5	8.4	1019	10	US-09-776-191-64	Sequence 64, Appli
778	331.5	8.4	1019	14	US-10-157-031-267	Sequence 267, App
779	331.5	8.4	1019	15	US-10-156-214A-31	Sequence 31, Appli
780	331.5	8.4	1019	16	US-10-729-807-37	Sequence 37, Appli
781	330.5	8.4	1019	16	US-10-408-765A-2243	Sequence 2243, Ap
782	329.5	8.4	3389	15	US-10-016-248-47	Sequence 47, Appli
783	329.5	8.4	3389	16	US-10-408-765A-2286	Sequence 2286, Ap
784	329.5	8.4	3508	15	US-10-016-248-46	Sequence 46, Appli
785	329	8.3	3564	15	US-10-016-248-45	Sequence 45, Appli
786	328.5	8.3	1274	15	US-10-467-042-11	Sequence 11, Appli
787	328.5	8.3	1783	14	US-10-276-934-12	Sequence 12, Appli
788	328.5	8.3	1800	14	US-10-276-934-10	Sequence 10, Appli
789	328.5	8.3	1826	14	US-10-276-934-9	Sequence 9, Appli
790	328.5	8.3	2008	14	US-10-276-934-11	Sequence 11, Appli
791	328.5	8.3	2306	14	US-10-276-934-14	Sequence 14, Appli
792	328.5	8.3	2352	14	US-10-276-934-13	Sequence 13, Appli
793	328	8.3	762	16	US-10-729-807-1	Sequence 1, Appli
794	328	8.3	851	15	US-10-276-774-1798	Sequence 1798, Ap
795	328	8.3	851	15	US-10-296-115-1143	Sequence 1143, Ap
796	328	8.3	855	15	US-10-295-027-1185	Sequence 1185, Ap
797	328	8.3	855	15	US-10-072-012-353	Sequence 353, App
798	328	8.3	855	15	US-10-072-012-412	Sequence 412, App
799	328	8.3	855	15	US-10-072-012-419	Sequence 419, App
800	327.5	8.3	449	9	US-09-925-302-612	Sequence 612, App
801	327.5	8.3	449	10	US-09-925-302-612	Sequence 612, App
802	327	8.3	688	15	US-10-453-827-884	Sequence 884, App
803	327	8.3	757	15	US-10-072-012-44	Sequence 44, Appli
804	327	8.3	855	10	US-09-776-191-2	Sequence 2, Appli
805	327	8.3	855	14	US-10-099-700A-2	Sequence 2, Appli
806	327	8.3	855	14	US-10-190-030B-2	Sequence 2, Appli
807	327	8.3	855	14	US-10-302-840A-2	Sequence 2, Appli
808	327	8.3	855	14	US-10-267-219-2	Sequence 2, Appli
809	327	8.3	855	14	US-10-112-221A-2	Sequence 2, Appli
810	327	8.3	855	14	US-10-104-271-2	Sequence 2, Appli
811	327	8.3	855	15	US-10-147-211A-2	Sequence 2, Appli
812	327	8.3	855	15	US-10-156-214A-2	Sequence 2, Appli
813	327	8.3	855	15	US-10-072-012-352	Sequence 352, App
814	327	8.3	855	15	US-10-072-012-411	Sequence 411, App
815	327	8.3	855	15	US-10-072-012-418	Sequence 418, App
816	327	8.3	855	15	US-10-600-187-2	Sequence 2, Appli
817	319.5	8.1	455	15	US-10-406-031-17	Sequence 17, Appli
818	318	8.1	2669	15	US-10-016-248-4	Sequence 4, Appli
819	318	8.1	3104	15	US-10-016-248-2	Sequence 2, Appli
820	314.5	8.0	454	15	US-10-406-031-11	Sequence 11, Appli
821	314	8.0	855	9	US-09-900-751-2	Sequence 2, Appli
822	314	8.0	855	15	US-10-072-012-355	Sequence 355, App
823	314	8.0	855	15	US-10-072-012-413	Sequence 413, App
824	313	7.9	855	15	US-10-072-012-356	Sequence 356, App

825	313	7.9	855	15	US-10-072-012-414	Sequence 414, App	981	280	7.1	562	15	US-10-411-049-26	Sequence 26, Appl
826	313	7.9	855	15	US-10-072-012-417	Sequence 417, App	982	280	7.1	562	16	US-10-410-930-26	Sequence 26, Appl
827	312	7.9	419	15	US-10-168-407-5	Sequence 5, Appl	983	280	7.1	562	16	US-10-410-937-26	Sequence 26, Appl
828	312	7.9	467	15	US-10-406-031-8	Sequence 8, Appl	984	280	7.1	562	16	US-10-411-012-26	Sequence 26, Appl
829	312	7.9	1031	15	US-10-451-168-80	Sequence 80, Appl	985	280	7.1	562	16	US-10-287-994-26	Sequence 26, Appl
830	311	7.9	419	15	US-10-168-407-3	Sequence 3, Appl	986	280	7.1	562	16	US-10-410-913-26	Sequence 26, Appl
831	311	7.9	419	15	US-10-168-407-6	Sequence 6, Appl	987	280	7.1	562	17	US-10-741-600-911	Sequence 911, App
832	310.5	7.9	415	15	US-10-670-628-2	Sequence 2, Appl	988	280	7.1	562	17	US-10-410-980-26	Sequence 26, Appl
833	310.5	7.9	419	10	US-09-997-623-4	Sequence 4, Appl	989	279.5	7.1	932	14	US-10-097-340-312	Sequence 312, App
834	310.5	7.9	419	10	US-09-978-917A-4	Sequence 4, Appl	990	279	7.1	932	15	US-10-363-937-6	Sequence 6, Appl
835	310.5	7.9	419	14	US-10-182-263-1	Sequence 1, Appl	991	279	7.1	970	9	US-09-888-615-101	Sequence 101, App
836	310.5	7.9	419	15	US-10-168-407-1	Sequence 1, Appl	992	278.5	7.1	264	10	US-09-978-418-34	Sequence 34, Appl
837	310.5	7.9	453	15	US-10-406-031-14	Sequence 14, Appl	993	278.5	7.1	466	14	US-10-017-122-2	Sequence 2, Appl
838	310.5	7.9	461	10	US-09-997-623-2	Sequence 2, Appl	994	278.5	7.1	466	15	US-10-375-741-14	Sequence 14, Appl
839	310.5	7.9	461	10	US-09-978-917A-2	Sequence 2, Appl	995	278.5	7.1	481	16	US-10-741-601-501	Sequence 501, App
840	310.5	7.9	461	14	US-10-182-263-2	Sequence 2, Appl	996	278.5	7.1	481	16	US-10-741-601-502	Sequence 502, App
841	310.5	7.9	461	15	US-10-168-407-2	Sequence 2, Appl	997	278.5	7.1	701	16	US-10-617-619-6	Sequence 6, Appl
842	310	7.9	419	14	US-10-182-263-6	Sequence 6, Appl	998	278	7.0	488	15	US-10-406-031-27	Sequence 27, Appl
843	310	7.9	419	15	US-10-168-407-4	Sequence 4, Appl	999	278	7.0	1113	15	US-10-464-368-78	Sequence 78, Appl
844	309.5	7.8	799	15	US-10-072-012-410	Sequence 410, App	1000	277.5	7.0	476	17	US-10-494-004-1	Sequence 1, Appl
845	309.5	7.8	799	15	US-10-072-012-416	Sequence 416, App	1001	276.5	7.0	426	10	US-09-951-121A-1	Sequence 1, Appl
846	309	7.8	419	14	US-10-182-263-3	Sequence 3, Appl	1002	276.5	7.0	426	10	US-09-848-107-1	Sequence 1, Appl
847	309	7.8	419	14	US-10-182-263-5	Sequence 5, Appl	1003	276.5	7.0	426	14	US-10-295-682-1	Sequence 1, Appl
848	308	7.8	419	14	US-10-182-263-4	Sequence 4, Appl	1004	276.5	7.0	655	14	US-10-172-721-28	Sequence 28, Appl
849	301.5	7.6	229	10	US-09-825-751A-72	Sequence 72, Appl	1005	276	7.0	249	9	US-09-961-721-5	Sequence 5, Appl
850	299.5	7.6	467	15	US-10-406-031-2	Sequence 2, Appl	1006	276	7.0	249	14	US-10-170-789-46	Sequence 46, Appl
851	298	7.6	397	15	US-10-104-047-3904	Sequence 3904, Ap	1007	276	7.0	251	9	US-09-961-721-4	Sequence 4, Appl
852	296	7.5	229	15	US-10-051-874-101	Sequence 101, App	1008	276	7.0	251	14	US-10-170-789-45	Sequence 45, Appl
853	296	7.5	230	10	US-09-981-151A-96	Sequence 87, Appl	1009	276	7.0	259	15	US-10-107-782-214	Sequence 214, App
854	296	7.5	230	10	US-09-981-151A-96	Sequence 96, Appl	1010	276	7.0	259	15	US-10-038-854-100	Sequence 100, App
855	296	7.5	230	14	US-10-032-189-66	Sequence 66, Appl	1011	276	7.0	396	16	US-10-700-778-1	Sequence 1, Appl
856	296	7.5	230	15	US-10-074-978A-221	Sequence 221, App	1012	275.5	7.0	405	15	US-10-360-101-225	Sequence 225, App
857	296	7.5	230	15	US-10-074-978A-222	Sequence 222, App	1013	275.5	7.0	406	10	US-09-782-587B-1	Sequence 1, Appl
858	296	7.5	230	15	US-10-055-569A-96	Sequence 96, Appl	1014	275.5	7.0	406	10	US-09-782-587B-3	Sequence 3, Appl
859	296	7.5	230	15	US-10-042-865-155	Sequence 155, App	1015	275.5	7.0	406	14	US-10-109-498-1	Sequence 1, Appl
860	296	7.5	230	15	US-10-072-012-804	Sequence 804, App	1016	275.5	7.0	406	14	US-10-285-032-1	Sequence 1, Appl
861	296	7.5	230	15	US-10-072-012-812	Sequence 812, App	1017	275.5	7.0	406	14	US-10-727-1	Sequence 1, Appl
862	296	7.5	230	15	US-10-037-417-135	Sequence 135, App	1018	275.5	7.0	406	15	US-10-386-898-7	Sequence 7, Appl
863	293	7.4	986	14	US-10-114-153-80	Sequence 50, Appl	1019	275.5	7.0	406	15	US-10-383-898-1	Sequence 1, Appl
864	291.5	7.4	516	17	US-10-741-600-909	Sequence 909, App	1020	275.5	7.0	406	15	US-10-617-500-1	Sequence 1, Appl
865	291	7.4	376	15	US-10-406-031-31	Sequence 31, Appl	1021	275.5	7.0	406	15	US-10-263-205B-2	Sequence 2, Appl
866	289.5	7.3	658	10	US-09-776-191-10	Sequence 10, Appl	1022	275.5	7.0	406	16	US-10-617-619-1	Sequence 1, Appl
867	289.5	7.3	658	15	US-10-156-214A-10	Sequence 10, Appl	1023	275.5	7.0	406	16	US-10-701-294-1	Sequence 1, Appl
868	289.5	7.3	802	10	US-09-776-191-8	Sequence 8, Appl	1024	275.5	7.0	406	16	US-10-669-537-1	Sequence 1, Appl
869	289.5	7.3	802	15	US-10-156-214A-8	Sequence 8, Appl	1025	275.5	7.0	406	16	US-10-738-777-2	Sequence 2, Appl
870	288.5	7.3	802	9	US-09-888-615-113	Sequence 113, App	1026	275.5	7.0	406	17	US-10-900-490-1	Sequence 1, Appl
904	288.5	7.3	802	14	US-10-167-749-169	Sequence 169, App	1027	275.5	7.0	406	17	US-10-725-843-3	Sequence 3, Appl
940	288.5	7.3	802	15	US-10-170-481A-169	Sequence 169, App	1028	275.5	7.0	444	15	US-10-411-037-8	Sequence 8, Appl
942	288.5	7.3	802	15	US-10-210-028-169	Sequence 169, App	1029	275.5	7.0	444	15	US-10-382-248-34	Sequence 34, Appl
947	288.5	7.3	802	15	US-10-162-521A-169	Sequence 169, App	1030	275.5	7.0	444	15	US-10-411-026-8	Sequence 8, Appl
959	288.5	7.3	802	17	US-10-918-851-169	Sequence 169, App	1031	275.5	7.0	444	15	US-10-411-049-8	Sequence 8, Appl
959	288.5	7.3	802	17	US-10-803-667-169	Sequence 169, App	1032	275.5	7.0	444	15	US-10-263-205B-3	Sequence 3, Appl
960	288.5	7.3	802	17	US-10-897-359-169	Sequence 169, App	1033	275.5	7.0	444	16	US-10-410-930-8	Sequence 8, Appl
961	288.5	7.3	802	17	US-10-893-802-169	Sequence 169, App	1034	275.5	7.0	444	16	US-10-410-997-8	Sequence 8, Appl
962	288.5	7.3	802	17	US-10-897-360-169	Sequence 169, App	1035	275.5	7.0	444	16	US-10-410-997-8	Sequence 8, Appl
963	288.5	7.3	902	15	US-10-333-743-3	Sequence 3, Appl	1036	275.5	7.0	444	16	US-10-411-012-8	Sequence 8, Appl
964	288.5	7.3	902	15	US-10-600-187-10	Sequence 10, Appl	1037	275.5	7.0	444	16	US-10-287-994-8	Sequence 8, Appl
965	288.5	7.3	902	16	US-10-297-987B-11	Sequence 11, Appl	1038	275.5	7.0	444	16	US-10-410-913-8	Sequence 8, Appl
966	287	7.3	467	15	US-10-406-031-5	Sequence 5, Appl	1039	275.5	7.0	444	16	US-10-738-777-3	Sequence 3, Appl
967	283	7.2	925	16	US-10-865-978-25	Sequence 25, Appl	1040	275.5	7.0	444	17	US-10-410-980-8	Sequence 8, Appl
968	281	7.1	488	14	US-10-348-504-44	Sequence 44, Appl	1041	275.5	7.0	459	16	US-10-741-601-503	Sequence 503, App
969	281	7.1	488	14	US-10-407-123-27	Sequence 27, Appl	1042	275.5	7.0	459	16	US-10-741-601-504	Sequence 504, App
970	280	7.1	527	10	US-09-987-457-18	Sequence 18, Appl	1043	275.5	7.0	641	16	US-10-617-619-8	Sequence 8, Appl
971	280	7.1	527	10	US-09-987-455-19	Sequence 19, Appl	1044	275.5	7.0	671	17	US-10-841-250-6	Sequence 6, Appl
972	280	7.1	527	15	US-10-360-101-203	Sequence 203, App	1045	275.5	7.0	679	16	US-10-617-619-11	Sequence 11, Appl
973	280	7.1	527	15	US-10-432-842-1	Sequence 1, Appl	1046	275	7.0	1113	17	US-10-926-083-4	Sequence 4, Appl
974	280	7.1	562	9	US-09-969-271-7	Sequence 7, Appl	1047	273	6.9	560	9	US-09-912-559-3	Sequence 3, Appl
975	280	7.1	562	9	US-09-974-298-145	Sequence 145, App	1048	273	6.9	560	9	US-09-912-559-4	Sequence 4, Appl
976	280	7.1	562	14	US-10-193-656-8	Sequence 8, Appl	1049	273	6.9	560	14	US-10-172-712-32	Sequence 32, Appl
977	280	7.1	562	14	US-10-443-701-4	Sequence 4, Appl	1050	273	6.9	560	15	US-10-391-215-5	Sequence 5, Appl
978	280	7.1	562	15	US-10-411-037-26	Sequence 26, Appl	1051	273	6.9	560	15	US-10-391-215-6	Sequence 6, Appl
979	280	7.1	562	15	US-10-411-026-26	Sequence 26, Appl	1052	273	6.9	560	15	US-10-391-215-7	Sequence 7, Appl
980	280	7.1	562	15	US-10-410-962-26	Sequence 26, Appl	1053	273	6.9	560	15	US-10-391-215-8	Sequence 8, Appl

1054	273	6.9	560	17	US-10-930-754-3	Sequence 3, Appli	1127	261.5	6.6	415	9	US-09-118-748-2	Sequence 2, Appli
1055	273	6.9	560	17	US-10-930-754-4	Sequence 4, Appli	1128	261.5	6.6	443	17	US-10-741-600-830	Sequence 830, App
1056	272.5	6.9	296	14	US-10-148-671-17	Sequence 17, Appl	1129	261	6.6	431	14	US-10-193-656-4	Sequence 4, Appli
1057	272	6.9	488	15	US-10-712-332-1	GENERAL INFORMA	1130	260.5	6.6	437	15	US-10-712-332-2	GENERAL INFORMA
1058	271.5	6.9	244	14	US-10-097-340-169	Sequence 169, App	1131	260	6.6	431	15	US-10-282-174-562	Sequence 562, App
1059	271.5	6.9	244	14	US-10-282-907-2	Sequence 2, Appli	1132	260	6.6	431	17	US-10-600-009-562	Sequence 562, App
1060	271.5	6.9	244	14	US-10-301-882-97	Sequence 97, Appl	1133	259.5	6.6	991	16	US-10-865-978-34	Sequence 34, Appl
1061	271.5	6.9	244	15	US-10-295-027-530	Sequence 530, App	1134	259	6.6	227	13	US-10-045-367A-4	Sequence 4, Appli
1062	271.5	6.9	244	15	US-10-173-999-131	Sequence 131, App	1135	259	6.6	227	14	US-10-170-789-54	Sequence 54, Appl
1063	271.5	6.9	244	15	US-10-344-394-25	Sequence 25, Appl	1136	258.5	6.6	411	9	US-09-880-503-3	Sequence 3, Appli
1064	271.5	6.9	244	16	US-10-757-262-28	Sequence 28, Appl	1137	258.5	6.6	411	15	US-10-407-821-2	Sequence 2, Appli
1065	271.5	6.9	1006	15	US-10-210-130-62	Sequence 62, Appl	1138	257.5	6.5	591	16	US-10-865-978-17	Sequence 17, Appl
1066	271	6.9	650	15	US-10-401-077-1	Sequence 1, Appli	1139	257	6.5	215	15	US-10-051-874-102	Sequence 102, App
1067	269	6.8	462	16	US-10-416-952-2	Sequence 2, Appli	1140	257	6.5	217	10	US-09-981-151A-88	Sequence 88, Appl
1068	269	6.8	643	9	US-09-808-602-103	Sequence 103, App	1141	257	6.5	217	10	US-09-981-151A-97	Sequence 97, Appl
1069	269	6.8	643	10	US-09-800-198-86	Sequence 86, Appl	1142	257	6.5	217	14	US-10-032-189-67	Sequence 67, Appl
1070	269	6.8	643	15	US-10-099-322-113	Sequence 113, App	1143	257	6.5	217	15	US-10-074-978A-223	Sequence 223, App
1071	269	6.8	643	15	US-10-044-564-113	Sequence 113, App	1144	257	6.5	217	15	US-10-055-569A-97	Sequence 97, Appl
1072	267	6.8	462	15	US-10-411-037-10	Sequence 10, Appl	1145	257	6.5	217	15	US-10-042-865-156	Sequence 156, App
1073	267	6.8	462	15	US-10-411-026-10	Sequence 10, Appl	1146	257	6.5	217	15	US-10-072-012-805	Sequence 805, App
1074	267	6.8	462	15	US-10-410-962-10	Sequence 10, Appl	1147	257	6.5	217	15	US-10-072-012-813	Sequence 813, App
1075	267	6.8	462	15	US-10-411-049-10	Sequence 10, Appl	1148	257	6.5	217	15	US-10-037-417-136	Sequence 136, App
1076	267	6.8	462	16	US-10-410-930-10	Sequence 10, Appl	1149	257	6.5	529	16	US-10-398-037-2	Sequence 2, Appli
1077	267	6.8	462	16	US-10-410-937-10	Sequence 10, Appl	1150	257	6.5	1039	16	US-10-865-978-30	Sequence 30, Appl
1078	267	6.8	462	16	US-10-411-012-10	Sequence 10, Appl	1151	256	6.5	207	15	US-10-004-378A-147	Sequence 147, App
1079	267	6.8	462	16	US-10-287-994-10	Sequence 10, Appl	1152	255.5	6.5	244	9	US-09-796-294-11	Sequence 11, Appl
1080	267	6.8	462	16	US-10-410-913-10	Sequence 10, Appl	1153	255.5	6.5	244	14	US-10-461-787-11	Sequence 11, Appl
1081	267	6.8	462	17	US-10-410-980-10	Sequence 10, Appl	1154	255.5	6.5	441	17	US-10-741-600-829	Sequence 829, App
1082	265	6.7	419	15	US-10-382-248-36	Sequence 36, Appl	1155	254.5	6.5	437	15	US-10-712-332-3	GENERAL INFORMA
1083	264.5	6.7	900	16	US-10-865-978-15	Sequence 15, Appl	1156	254	6.4	431	9	US-09-264-4688-1	Sequence 1, Appli
1084	264	6.7	431	14	US-10-247-671-149	Sequence 149, App	1157	253.5	6.4	464	9	US-09-808-602-95	Sequence 95, Appl
1085	263	6.7	431	13	US-10-076-421-2	Sequence 2, Appli	1158	253.5	6.4	487	9	US-09-808-602-93	Sequence 93, Appl
1086	263	6.7	431	14	US-10-171-311-184	Sequence 184, App	1159	253.5	6.4	487	10	US-09-800-198-80	Sequence 80, Appl
1087	263	6.7	431	14	US-10-301-822-161	Sequence 161, App	1160	253.5	6.4	1043	15	US-10-016-248-48	Sequence 48, Appl
1088	263	6.7	431	14	US-10-131-985-21	Sequence 21, Appl	1161	253.5	6.4	1048	15	US-10-016-248-49	Sequence 49, Appl
1089	263	6.7	431	15	US-10-295-027-114	Sequence 414, App	1162	253	6.4	273	14	US-10-148-671-25	Sequence 25, Appl
1090	263	6.7	431	15	US-10-295-027-1275	Sequence 1275, Ap	1163	252.5	6.4	452	9	US-09-808-602-21	Sequence 21, Appl
1091	263	6.7	431	15	US-10-411-037-34	Sequence 34, Appl	1164	252	6.4	719	16	US-10-865-978-16	Sequence 16, Appl
1092	263	6.7	431	15	US-10-411-026-34	Sequence 34, Appl	1165	252	6.4	889	16	US-10-865-978-22	Sequence 22, Appl
1093	263	6.7	431	15	US-10-410-962-34	Sequence 34, Appl	1166	251.5	6.4	487	9	US-09-808-602-17	Sequence 17, Appl
1094	263	6.7	431	15	US-10-411-049-34	Sequence 34, Appl	1167	251.5	6.4	487	9	US-09-808-602-19	Sequence 19, Appl
1095	263	6.7	431	16	US-10-410-930-34	Sequence 34, Appl	1168	251.5	6.4	487	10	US-09-800-198-17	Sequence 17, Appl
1096	263	6.7	431	16	US-10-410-997-34	Sequence 34, Appl	1169	251.5	6.4	487	10	US-09-800-198-19	Sequence 19, Appl
1097	263	6.7	431	16	US-10-411-012-34	Sequence 34, Appl	1170	251	6.4	433	16	US-10-372-966-5	Sequence 5, Appli
1098	263	6.7	431	16	US-10-287-994-34	Sequence 34, Appl	1171	249.5	6.3	403	9	US-09-880-503-6	Sequence 6, Appli
1099	263	6.7	431	16	US-10-410-913-34	Sequence 34, Appl	1172	249.5	6.3	822	9	US-09-147-947-6	Sequence 6, Appli
1100	263	6.7	431	17	US-10-741-600-1265	Sequence 1265, Ap	1173	249.5	6.3	875	16	US-10-757-262-34	Sequence 34, Appl
1101	263	6.7	431	17	US-10-741-600-1266	Sequence 1266, Ap	1174	249.5	6.3	875	17	US-10-843-239-2	Sequence 2, Appli
1102	263	6.7	431	17	US-10-901-417-21	Sequence 21, Appl	1175	249.5	6.3	986	9	US-09-285-385C-19	Sequence 19, Appl
1103	263	6.7	431	17	US-10-410-980-34	Sequence 34, Appl	1176	249	6.3	235	10	US-09-776-191-6	Sequence 6, Appli
1104	263	6.7	431	17	US-10-645-756-38	Sequence 38, Appl	1177	249	6.3	235	15	US-10-156-214A-6	Sequence 6, Appli
1105	263	6.7	437	13	US-10-087-192-594	Sequence 594, App	1178	249	6.3	251	11	US-09-789-210-47	Sequence 47, Appl
1106	262.5	6.7	415	16	US-10-466-988A-2	Sequence 2, Appli	1179	249	6.3	263	9	US-09-888-615-96	Sequence 96, Appl
1107	262.5	6.7	456	15	US-10-038-854-25	Sequence 95, Appl	1180	248.5	6.3	250	10	US-09-898-837A-45	Sequence 45, Appl
1108	262.5	6.7	456	15	US-10-038-854-96	Sequence 96, Appl	1181	248.5	6.3	250	11	US-09-789-210-51	Sequence 51, Appl
1109	262.5	6.7	461	9	US-09-884-901-3	Sequence 3, Appli	1182	248.5	6.3	251	10	US-09-898-837A-41	Sequence 41, Appl
1110	262.5	6.7	461	14	US-10-132-829-5	Sequence 5, Appli	1183	248	6.3	230	11	US-09-789-210-62	Sequence 62, Appl
1111	262.5	6.7	461	14	US-10-234-406-5	Sequence 6, Appli	1184	248	6.3	231	15	US-10-600-187-6	Sequence 6, Appli
1112	262.5	6.7	461	14	US-10-234-406-8	Sequence 8, Appli	1185	248	6.3	638	9	US-09-808-602-102	Sequence 102, App
1113	262.5	6.7	461	14	US-10-133-907-5	Sequence 5, Appli	1186	248	6.3	638	10	US-09-800-198-85	Sequence 85, Appl
1114	262.5	6.7	461	15	US-10-038-854-32	Sequence 92, Appl	1187	248	6.3	638	15	US-10-099-322-111	Sequence 111, App
1115	262.5	6.7	461	15	US-10-038-854-93	Sequence 93, Appl	1188	248	6.3	638	15	US-10-044-564-111	Sequence 111, App
1116	262.5	6.7	461	15	US-10-038-854-94	Sequence 94, Appl	1189	248	6.3	638	15	US-10-403-161-50	Sequence 50, Appl
1117	262.5	6.7	461	15	US-10-239-498A-5	Sequence 5, Appli	1190	248	6.3	638	15	US-10-287-226-400	Sequence 400, App
1118	262.5	6.7	461	17	US-10-741-600-832	Sequence 832, App	1191	248	6.3	638	15	US-10-287-226-558	Sequence 558, App
1119	262.5	6.7	696	17	US-10-841-250-8	Sequence 8, Appli	1192	248	6.3	638	16	US-10-741-601-303	Sequence 303, App
1120	262.5	6.7	1042	10	US-09-776-191-41	Sequence 62, Appl	1193	248	6.3	638	17	US-10-741-600-854	Sequence 854, App
1121	262.5	6.7	1042	15	US-10-156-214A-29	Sequence 29, Appl	1194	247.5	6.3	635	16	US-10-741-601-304	Sequence 304, App
1122	262.5	6.7	1042	16	US-10-865-978-2	Sequence 2, Appli	1195	247.5	6.3	635	17	US-10-741-600-855	Sequence 855, App
1123	262.5	6.7	1042	17	US-10-926-083-2	Sequence 2, Appli	1196	247	6.3	455	16	US-10-865-978-18	Sequence 18, Appl
1124	262.5	6.7	1044	16	US-10-865-978-9	Sequence 9, Appli	1197	247	6.3	619	15	US-10-403-161-52	Sequence 52, Appl
1125	262.5	6.7	1076	15	US-10-276-774-2345	Sequence 26, Appl	1198	247	6.3	619	15	US-10-287-226-404	Sequence 404, App
1126	262	6.6	280	14	US-10-148-671-26	Sequence 26, Appl	1199	247	6.3	623	15	US-10-403-161-48	Sequence 48, Appl

1200	247	6.3	638	15	US-10-099-322-30	Sequence 30, Appl	1273	239.5	6.1	3567	15	US-10-107-782-47	Sequence 47, Appl
1201	247	6.3	638	15	US-10-044-564-30	Sequence 30, Appl	1274	239.5	6.1	3594	9	US-09-911-842-4	Sequence 4, Appl
1202	247	6.3	638	15	US-10-403-161-46	Sequence 46, Appl	1275	239.5	6.1	3594	13	US-10-150-821-4	Sequence 4, Appl
1203	247	6.3	638	15	US-10-287-226-402	Sequence 402, App	1276	239	6.1	328	9	US-09-888-615-91	Sequence 91, Appl
1204	247	6.3	764	14	US-10-177-293-27	Sequence 27, Appl	1277	239	6.1	1093	15	US-10-156-214A-20	Sequence 20, Appl
1205	247	6.3	764	15	US-10-236-031B-44	Sequence 44, Appl	1278	238.5	6.0	482	17	US-10-741-600-910	Sequence 910, App
1206	247	6.3	986	10	US-09-918-715-242	Sequence 242, App	1279	238	6.0	263	15	US-10-094-886-128	Sequence 128, App
1207	247	6.3	986	15	US-10-366-345-33	Sequence 33, Appl	1280	238	6.0	335	10	US-09-987-457-13	Sequence 13, Appl
1208	246.5	6.2	259	11	US-09-789-210-52	Sequence 52, Appl	1281	238	6.0	335	10	US-09-987-455-14	Sequence 14, Appl
1209	246.5	6.2	259	16	US-10-872-198-5	Sequence 5, Appl	1282	238	6.0	343	10	US-09-987-457-15	Sequence 15, Appl
1210	246.5	6.2	259	17	US-10-872-198A-5	Sequence 5, Appl	1283	238	6.0	343	10	US-09-987-455-16	Sequence 16, Appl
1211	246.5	6.2	347	9	US-09-977-577-3	Sequence 3, Appl	1284	238	6.0	347	9	US-09-977-577-1	Sequence 1, Appl
1212	246.5	6.2	347	17	US-10-885-784-3	Sequence 3, Appl	1285	238	6.0	347	17	US-10-885-784-1	Sequence 1, Appl
1213	246.5	6.2	622	14	US-10-020-141-8	Sequence 8, Appl	1286	238	6.0	379	16	US-10-865-978-19	Sequence 19, Appl
1214	246.5	6.2	622	14	US-10-017-631-2	Sequence 2, Appl	1287	237.5	6.0	255	10	US-09-813-432-41	Sequence 41, Appl
1215	246.5	6.2	622	14	US-10-214-932-116	Sequence 116, App	1288	237.5	6.0	255	15	US-10-174-364-41	Sequence 41, Appl
1216	246.5	6.2	622	14	US-10-172-712-29	Sequence 29, Appl	1289	237.5	6.0	255	15	US-10-246-583-41	Sequence 41, Appl
1217	246.5	6.2	622	16	US-10-872-198-149	Sequence 149, App	1290	237.5	6.0	255	16	US-10-689-832-41	Sequence 41, Appl
1218	246.5	6.2	639	17	US-10-792-498-16	Sequence 16, Appl	1291	237.5	6.0	3568	15	US-10-028-248A-8	Sequence 8, Appl
1219	246.5	6.2	639	17	US-10-792-498-17	Sequence 17, Appl	1292	237.5	6.0	3568	15	US-10-107-782-8	Sequence 8, Appl
1220	246	6.2	812	10	US-09-825-751A-71	Sequence 71, Appl	1293	237.5	6.0	3570	15	US-10-028-248A-6	Sequence 6, Appl
1221	245.5	6.2	638	15	US-10-099-322-112	Sequence 112, App	1294	236.5	6.0	3570	15	US-10-107-782-6	Sequence 6, Appl
1222	245.5	6.2	638	15	US-10-044-564-112	Sequence 112, App	1295	236.5	6.0	308	10	US-09-987-457-16	Sequence 16, Appl
1223	245.5	6.2	823	15	US-10-112-944-309	Sequence 309, App	1296	236.5	6.0	308	10	US-09-987-455-17	Sequence 17, Appl
1224	245	6.2	445	15	US-10-360-101-266	Sequence 266, App	1297	236.5	6.0	331	10	US-09-987-457-11	Sequence 11, Appl
1225	244.5	6.2	269	9	US-09-981-123-2	Sequence 2, Appl	1298	236.5	6.0	331	10	US-09-987-455-12	Sequence 12, Appl
1226	244.5	6.2	280	14	US-10-148-671-23	Sequence 23, Appl	1299	236.5	6.0	339	10	US-09-987-457-12	Sequence 12, Appl
1227	244.5	6.2	292	14	US-10-029-386-31995	Sequence 31995, A	1300	236.5	6.0	339	10	US-09-987-455-13	Sequence 13, Appl
1228	244	6.2	322	15	US-10-051-874-96	Sequence 96, Appl	1301	236.5	6.0	343	10	US-09-987-457-14	Sequence 14, Appl
1229	244	6.2	477	17	US-10-494-004-2	Sequence 2, Appl	1302	236.5	6.0	343	10	US-09-987-455-15	Sequence 15, Appl
1230	244	6.2	638	15	US-10-099-322-114	Sequence 114, App	1303	236.5	6.0	354	10	US-09-987-457-10	Sequence 10, Appl
1231	244	6.2	638	15	US-10-044-564-114	Sequence 114, App	1304	236.5	6.0	354	10	US-09-987-455-11	Sequence 11, Appl
1232	244	6.2	638	15	US-10-287-226-672	Sequence 672, App	1305	236.5	6.0	372	9	US-09-084-491A-3	Sequence 3, Appl
1233	243	6.2	273	15	US-10-028-248A-63	Sequence 63, Appl	1306	236.5	6.0	372	13	US-10-102-704-3	Sequence 3, Appl
1234	243	6.2	273	15	US-10-107-782-63	Sequence 63, Appl	1307	236.5	6.0	377	10	US-09-987-455-8	Sequence 8, Appl
1235	243	6.2	282	15	US-10-051-874-97	Sequence 97, Appl	1308	236.5	6.0	416	15	US-10-099-322-138	Sequence 138, App
1236	242.5	6.1	232	15	US-10-156-214A-276	Sequence 276, App	1309	236.5	6.0	416	15	US-10-044-564-138	Sequence 138, App
1237	242.5	6.1	326	16	US-10-865-978-37	Sequence 37, Appl	1310	236.5	6.0	871	9	US-09-893-238-19	Sequence 19, Appl
1238	242.5	6.1	1019	15	US-10-016-248-99	Sequence 99, Appl	1311	236.5	6.0	1013	15	US-09-942-368-3	Sequence 3, Appl
1239	242.5	6.1	3571	16	US-10-603-283-2	Sequence 2, Appl	1312	236.5	6.0	1013	15	US-10-016-248-95	Sequence 95, Appl
1240	242	6.1	322	15	US-10-114-270-134	Sequence 134, App	1313	236.5	6.0	1350	9	US-09-893-238-17	Sequence 17, Appl
1241	242	6.1	730	9	US-09-850-048A-2	Sequence 2, Appl	1314	236	6.0	252	14	US-10-148-671-21	Sequence 21, Appl
1242	241.5	6.1	416	9	US-09-815-876-2	Sequence 2, Appl	1315	236	6.0	275	14	US-10-117-323-27	Sequence 27, Appl
1243	241.5	6.1	823	15	US-10-016-248-98	Sequence 98, Appl	1316	236	6.0	411	16	US-10-372-966-6	Sequence 6, Appl
1244	241	6.1	346	9	US-09-977-577-8	Sequence 8, Appl	1317	236	6.0	992	15	US-10-016-248-40	Sequence 40, Appl
1245	241	6.1	346	9	US-10-885-784-8	Sequence 8, Appl	1318	235.5	6.0	325	14	US-10-311-955-2	Sequence 2, Appl
1246	241	6.1	986	9	US-09-850-048A-8	Sequence 4, Appl	1319	235	6.0	293	14	US-10-148-671-18	Sequence 18, Appl
1247	240.5	6.1	278	10	US-09-813-432-12	Sequence 12, Appl	1320	234.5	5.9	556	9	US-09-729-674-92	Sequence 92, Appl
1248	240.5	6.1	278	10	US-09-813-432-43	Sequence 43, Appl	1321	234.5	5.9	556	16	US-10-913-553-92	Sequence 92, Appl
1249	240.5	6.1	278	15	US-10-174-364-12	Sequence 12, Appl	1322	234.5	5.9	624	15	US-10-004-378A-143	Sequence 143, App
1250	240.5	6.1	278	15	US-10-174-364-43	Sequence 43, Appl	1323	234	5.9	296	15	US-10-051-874-99	Sequence 99, Appl
1251	240.5	6.1	278	15	US-10-246-583-12	Sequence 12, Appl	1324	234	5.9	296	15	US-10-051-874-99	Sequence 99, Appl
1252	240.5	6.1	278	15	US-10-246-583-43	Sequence 43, Appl	1325	233.5	5.9	253	11	US-09-789-210-72	Sequence 72, Appl
1253	240.5	6.1	278	16	US-10-689-832-12	Sequence 12, Appl	1326	233.5	5.9	253	15	US-10-600-187-8	Sequence 8, Appl
1254	240.5	6.1	278	16	US-10-689-832-43	Sequence 43, Appl	1327	233.5	5.9	268	10	US-09-987-457-17	Sequence 17, Appl
1255	240.5	6.1	430	16	US-10-372-966-4	Sequence 4, Appl	1328	233.5	5.9	268	10	US-09-987-455-18	Sequence 18, Appl
1256	240.5	6.1	970	15	US-10-016-248-42	Sequence 42, Appl	1329	233.5	5.9	275	14	US-10-131-409-20	Sequence 20, Appl
1257	240.5	6.1	3571	9	US-09-911-842-2	Sequence 2, Appl	1330	233.5	5.9	275	15	US-10-139-854-20	Sequence 20, Appl
1258	240.5	6.1	3571	13	US-10-150-821-2	Sequence 2, Appl	1331	233.5	5.9	275	15	US-10-150-813-20	Sequence 20, Appl
1259	240	6.1	242	17	US-10-926-083-34	Sequence 34, Appl	1332	233.5	5.9	273	15	US-10-150-811-20	Sequence 20, Appl
1260	240	6.1	1128	9	US-09-888-615-97	Sequence 97, Appl	1333	233	5.9	273	15	US-10-028-248A-64	Sequence 64, Appl
1261	240	6.1	1128	15	US-10-399-645-8	Sequence 8, Appl	1334	233	5.9	273	15	US-10-107-782-64	Sequence 64, Appl
1262	239.5	6.1	406	9	US-09-977-577-2	Sequence 2, Appl	1335	232.5	5.9	259	15	US-10-165-442-2	Sequence 2, Appl
1263	239.5	6.1	406	16	US-10-764-649-6	Sequence 6, Appl	1336	232.5	5.9	259	16	US-10-699-393-2	Sequence 2, Appl
1264	239.5	6.1	406	17	US-10-885-784-2	Sequence 2, Appl	1337	232.5	5.9	295	15	US-10-165-442-1	Sequence 1, Appl
1265	239.5	6.1	416	9	US-09-804-156-13	Sequence 13, Appl	1338	232.5	5.9	295	16	US-10-699-393-1	Sequence 1, Appl
1266	239.5	6.1	416	13	US-10-067-761-13	Sequence 13, Appl	1339	232.5	5.9	1013	9	US-09-942-366-5	Sequence 5, Appl
1267	239.5	6.1	416	14	US-10-319-519-13	Sequence 13, Appl	1340	232.5	5.9	1013	9	US-09-285-385C-20	Sequence 20, Appl
1268	239.5	6.1	1015	9	US-09-285-385C-2	Sequence 2, Appl	1341	232	5.9	416	15	US-10-099-322-137	Sequence 137, App
1269	239.5	6.1	1015	15	US-10-016-248-97	Sequence 97, Appl	1342	232	5.9	416	15	US-10-044-564-137	Sequence 137, App
1270	239.5	6.1	3557	15	US-10-295-027-430	Sequence 430, App	1343	232	5.9	638	14	US-10-316-253-82	Sequence 82, Appl
1271	239.5	6.1	3557	15	US-10-295-027-1297	Sequence 1297, Ap	1344	232	5.9	638	15	US-10-099-322-115	Sequence 115, App
1272	239.5	6.1	3567	15	US-10-028-248A-47	Sequence 47, Appl	1345	232	5.9	638	15	US-10-044-564-115	Sequence 115, App

1346	232	5.9	638	15	US-10-287-226-671	Sequence 671, Appl	1419	226	5.7	423	14	US-10-254-289-2	Sequence 2, Appli
1347	232	5.9	839	16	US-10-399-455-11	Sequence 11, Appl	1420	226	5.7	423	15	US-10-156-214A-39	Sequence 39, Appl
1348	231.5	5.9	417	9	US-09-820-002-4	Sequence 4, Appli	1421	226	5.7	432	10	US-09-888-257A-7	Sequence 7, Appli
1349	231.5	5.9	417	14	US-10-274-031-4	Sequence 4, Appli							
1350	231	5.9	1012	9	US-09-285-3850-4	Sequence 4, Appli							
1351	231	5.9	1012	15	US-10-016-248-96	Sequence 96, Appl							
1352	231	5.9	1958	15	US-10-467-433-18	Sequence 18, Appl							
1353	230.5	5.8	259	15	US-10-165-442-4	Sequence 4, Appli							
1354	230.5	5.8	259	16	US-10-699-393-4	Sequence 4, Appli							
1355	230.5	5.8	267	14	US-10-131-409-83	Sequence 83, Appl							
1356	230.5	5.8	267	15	US-10-139-854-83	Sequence 83, Appl							
1357	230.5	5.8	267	15	US-10-150-813-83	Sequence 83, Appl							
1358	230.5	5.8	267	15	US-10-150-811-83	Sequence 83, Appl							
1359	230.5	5.8	279	9	US-09-858-332-15	Sequence 15, Appl							
1360	230.5	5.8	295	15	US-10-165-442-3	Sequence 3, Appli							
1361	230.5	5.8	295	16	US-10-699-393-3	Sequence 3, Appli							
1362	230.5	5.8	352	9	US-09-808-602-105	Sequence 105, App							
1363	230	5.8	352	17	US-10-926-083-31	Sequence 31, Appl							
1364	230	5.8	329	11	US-09-777-577-9	Sequence 9, Appli							
1365	229.5	5.8	329	9	US-09-885-784-9	Sequence 9, Appli							
1366	229.5	5.8	329	17	US-10-885-784-9	Sequence 9, Appli							
1367	229.5	5.8	352	9	US-09-888-615-95	Sequence 95, Appl							
1368	229.5	5.8	389	15	US-10-210-130-156	Sequence 156, App							
1369	229.5	5.8	624	15	US-10-004-378A-145	Sequence 145, App							
1370	229	5.8	845	15	US-10-273-505-8	Sequence 8, Appli							
1371	229	5.8	845	15	US-10-072-012-415	Sequence 415, App							
1372	228.5	5.8	235	9	US-09-988-975A-6	Sequence 6, Appli							
1373	228.5	5.8	343	15	US-10-162-335-86	Sequence 86, Appl							
1374	228.5	5.8	356	15	US-10-343-953-4	Sequence 4, Appli							
1375	228	5.8	287	15	US-10-114-270-130	Sequence 130, App							
1376	228	5.8	328	15	US-10-467-042-7	Sequence 7, Appli							
1377	228	5.8	812	9	US-09-788-142-1	Sequence 1, Appli							
1378	228	5.8	812	9	US-09-761-120-1	Sequence 1, Appli							
1379	228	5.8	812	9	US-09-873-676-81	Sequence 81, Appl							
1380	228	5.8	812	9	US-09-335-325-1	Sequence 1, Appli							
1381	228	5.8	812	14	US-10-131-241-1	Sequence 1, Appli							
1382	228	5.8	812	14	US-10-127-066-1	Sequence 1, Appli							
1383	228	5.8	812	15	US-10-402-364-1	Sequence 1, Appli							
1384	228	5.8	812	15	US-10-401-108-1	Sequence 1, Appli							
1385	227.5	5.8	251	15	US-10-344-394-27	Sequence 27, Appl							
1386	227.5	5.8	267	17	US-10-480-988-20	Sequence 20, Appl							
1387	227.5	5.8	296	9	US-09-888-615-85	Sequence 85, Appl							
1388	227.5	5.8	305	9	US-09-885-441-57	Sequence 57, Appl							
1389	227.5	5.8	305	14	US-10-239-663-56	Sequence 56, Appl							
1390	227.5	5.8	305	15	US-10-424-836-57	Sequence 57, Appl							
1391	227.5	5.8	334	9	US-09-885-441-56	Sequence 56, Appl							
1392	227.5	5.8	334	15	US-10-424-836-56	Sequence 56, Appl							
1393	227	5.8	241	10	US-09-776-131-50	Sequence 50, Appl							
1394	227	5.8	241	14	US-10-099-700A-4	Sequence 4, Appli							
1395	227	5.8	241	14	US-10-092-004A-2	Sequence 2, Appli							
1396	227	5.8	241	14	US-10-190-030B-4	Sequence 4, Appli							
1397	227	5.8	241	14	US-10-302-840A-4	Sequence 4, Appli							
1398	227	5.8	241	14	US-10-267-219-4	Sequence 4, Appli							
1399	227	5.8	241	14	US-10-112-221A-4	Sequence 4, Appli							
1400	227	5.8	241	14	US-10-104-271-4	Sequence 4, Appli							
1401	227	5.8	241	15	US-10-147-211A-4	Sequence 4, Appli							
1402	227	5.8	285	14	US-10-040-647-26	Sequence 26, Appl							
1403	227	5.8	309	16	US-10-297-987B-27	Sequence 27, Appl							
1404	227	5.8	324	15	US-10-051-874-98	Sequence 98, Appl							
1405	226.5	5.7	308	17	US-10-884-163-20	Sequence 20, Appl							
1406	226.5	5.7	454	14	US-10-357-175-2	Sequence 2, Appli							
1407	226.5	5.7	454	15	US-10-455-720-2	Sequence 2, Appli							
1408	226.5	5.7	761	9	US-09-147-947-4	Sequence 4, Appli							
1409	226.5	5.7	761	17	US-10-843-299-4	Sequence 4, Appli							
1410	226.5	5.7	2787	9	US-09-893-238-15	Sequence 15, Appl							
1411	226	5.7	243	16	US-10-297-987B-10	Sequence 10, Appl							
1412	226	5.7	288	9	US-09-888-615-115	Sequence 115, App							
1413	226	5.7	290	15	US-10-274-639-15	Sequence 15, Appl							
1414	226	5.7	290	15	US-10-333-574-15	Sequence 15, Appl							
1415	226	5.7	317	15	US-10-296-115-1148	Sequence 1148, Ap							
1416	226	5.7	406	9	US-09-851-588-6	Sequence 6, Appli							
1417	226	5.7	423	10	US-09-776-191-72	Sequence 72, Appl							
1418	226	5.7	423	14	US-10-264-820-23	Sequence 23, Appl							

Search completed: May 8, 2005, 16:10:51
Job time : 80 secs

This Page Blank (uspto)

GenCore version 5.1.6

OM protein - protein search, using sw model
Run on: May 8, 2005, 16:10:59 ; Search time 54 Seconds
(without alignments)
5156.805 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 720

Sequence: 1 MELGQWTGLTFLQLLLIS.....LSTAFKVLPPKDWIERNMK 720

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Database : A Geneseq16Dec04:*

1: geneseqp1980a:*

2: geneseqp1990a:*

3: geneseqp2000a:*

4: geneseqp2001a:*

5: geneseqp2002a:*

6: geneseqp2003a:*

7: geneseqp2003bs:*

8: geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
-----	-------	-------	--------	----	----	-------------

RESULT 1						
----------	--	--	--	--	--	--

ID	AAV66695	standard; protein; 720 AA.
----	----------	----------------------------

DE	Membrane-bound protein PRO1344.
----	---------------------------------

PN	WO9963088-A2.
----	---------------

PD	09-DEC-1999.
----	--------------

PA	(GETH) GENENTECH INC.
----	------------------------

Query Match	100.0%;	Score 720;	DB 3;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 2					
----------	--	--	--	--	--

ID	AAU29108	standard; protein; 720 AA.
----	----------	----------------------------

DE	Human PRO polypeptide sequence #85.
----	-------------------------------------

PN	WO20016848-A2.
----	----------------

PD	20-SEP-2001.
----	--------------

PA	(GETH) GENENTECH INC.
----	------------------------

Query Match	100.0%;	Score 720;	DB 4;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 3					
----------	--	--	--	--	--

ID	AA887544	standard; protein; 720 AA.
----	----------	----------------------------

DE	Human PRO1344.
----	----------------

PN	WO200116318-A2.
----	-----------------

PD	08-MAR-2001.
----	--------------

PA	(GETH) GENENTECH INC.
----	------------------------

Query Match	100.0%;	Score 720;	DB 4;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 4					
----------	--	--	--	--	--

ID	AA865218	standard; protein; 720 AA.
----	----------	----------------------------

DE	Human PRO1344 (UNQ699) protein sequence SEQ ID NO:231.
----	--

PN	WO200073454-A1.
----	-----------------

PD	07-DEC-2000.
----	--------------

PA	(GETH) GENENTECH INC.
----	------------------------

Query Match	100.0%;	Score 720;	DB 4;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 5					
----------	--	--	--	--	--

ID	ABG95869	standard; protein; 720 AA.
----	----------	----------------------------

DE	Human secreted/transmembrane protein PRO1344.
----	---

PN	US2002119130-A1.
----	------------------

PD	29-AUG-2002.
----	--------------

PA	(GETH) GENENTECH INC.
----	------------------------

Query Match	100.0%;	Score 720;	DB 5;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 6					
----------	--	--	--	--	--

ID	ABU58484	standard; protein; 720 AA.
----	----------	----------------------------

DE	Human PRO polypeptide #85.
----	----------------------------

PN	US2003027272-A1.
----	------------------

PD	06-FEB-2003.
----	--------------

Query Match	100.0%;	Score 720;	DB 6;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 7					
----------	--	--	--	--	--

ID	ABU8032	standard; protein; 720 AA.
----	---------	----------------------------

DE	Novel human secreted and transmembrane protein PRO1344.
----	---

PN	US2003032127-A1.
----	------------------

PD	13-FEB-2003.
----	--------------

Query Match	100.0%;	Score 720;	DB 6;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 8					
----------	--	--	--	--	--

ID	ABU84347	standard; protein; 720 AA.
----	----------	----------------------------

DE	Human secreted/transmembrane protein (PRO) #85.
----	---

PN	US2003032112-A1.
----	------------------

PD	13-FEB-2003.
----	--------------

Query Match	100.0%;	Score 720;	DB 6;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 9					
----------	--	--	--	--	--

ID	ABR66221	standard; protein; 720 AA.
----	----------	----------------------------

DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.
----	--

PN	US2003027278-A1.
----	------------------

PD	06-FEB-2003.
----	--------------

Query Match	100.0%;	Score 720;	DB 6;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 10					
-----------	--	--	--	--	--

ID	ABR65611	standard; protein; 720 AA.
----	----------	----------------------------

DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.
----	--

PN	US2003036159-A1.
----	------------------

PD	20-FEB-2003.
----	--------------

Query Match	100.0%;	Score 720;	DB 6;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 11					
-----------	--	--	--	--	--

ID	ABU99551	standard; protein; 720 AA.
----	----------	----------------------------

DE	Human secreted/transmembrane protein (PRO) #85.
----	---

PN	US2003040070-A1.
----	------------------

PD	27-FEB-2003.
----	--------------

Query Match	100.0%;	Score 720;	DB 6;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 12					
-----------	--	--	--	--	--

ID	ABU58033	standard; protein; 720 AA.
----	----------	----------------------------

DE	Human PRO polypeptide #65.
----	----------------------------

PN	US2003027163-A1.
----	------------------

PD	06-FEB-2003.
----	--------------

Query Match	100.0%;	Score 720;	DB 6;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 13					
-----------	--	--	--	--	--

ID	ABU59111	standard; protein; 720 AA.
----	----------	----------------------------

DE	Novel human secreted or transmembrane protein PRO1344.
----	--

PN	US2002132252-A1.
----	------------------

PD	19-SEP-2002.
----	--------------

PA	(GETH) GENENTECH INC.
----	------------------------

Query Match	100.0%;	Score 720;	DB 6;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 14					
-----------	--	--	--	--	--

ID	ABU82623	standard; protein; 720 AA.
----	----------	----------------------------

DE	Human secreted/transmembrane protein PRO1344.
----	---

PN	US2003032023-A1.
----	------------------

PD	13-FEB-2003.
----	--------------

Query Match	100.0%;	Score 720;	DB 6;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 15					
-----------	--	--	--	--	--

ID	ABU82790	standard; protein; 720 AA.
----	----------	----------------------------

DE	Human PRO polypeptide #85.
----	----------------------------

PN	US2003032113-A1.
----	------------------

PD	13-FEB-2003.
----	--------------

Query Match	100.0%;	Score 720;	DB 6;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 16					
-----------	--	--	--	--	--

ID	ABU89911	standard; protein; 720 AA.
----	----------	----------------------------

DE	Novel human secreted and transmembrane protein PRO1344.
----	---

PN	US2003036147-A1.
----	------------------

PD	20-FEB-2003.
----	--------------

Query Match	100.0%;	Score 720;	DB 6;	Length 720;
-------------	---------	------------	-------	-------------

Best Local Similarity	100.0%;	Pred. No. 0;
-----------------------	---------	--------------

RESULT 17
ID AB68160 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 18
ID AB60542 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 19
ID AB96213 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 20
ID AB92644 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 21
ID AB008721 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 22
ID AB02773 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 23
ID ABR74927 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 24
ID ABR34689 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 25
ID ABU13924 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 26
ID ABUS662 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 27
ID ABU9822 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 28
ID ABU98037 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 29
ID ABU91743 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 30
ID ABU89436 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 31
ID ABU86277 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 32
ID ABU67490 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 33
ID ABU80518 standard; protein; 720 AA.
DE Human PRO protein #85.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 34
ID ABU72509 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US200303531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 35
ID ABU90894 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 36
ID ABO33953 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US200309013-A1.
PD 09-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 37
ID ABR99436 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 38
ID ABR98826 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 39
ID ABO16349 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 40
ID ABR92249 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 41
ID ABO18890 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 42
ID ABR78311 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 43
ID ABUT1970 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 44
ID ABUS5047 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 45
ID ABO00186 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 46
ID ABO11518 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036124-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 47
ID ABO02163 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 48
ID ABUS8737 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 49
ID ABUS3432 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 50
ID ABO06233 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 51
ID ABR59269 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 52
ID ABO09331 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 53
ID ABO19195 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 54
ID ABO11213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 55
ID ABR66831 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 56
ID ABO16044 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 57
ID ABO11518 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036124-A1.
PD 20-FEB-2003.

RESULT 57
ID ABO13750 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 58
ID ABU71524 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 59
ID ABU65653 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, SEQ ID 170.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 60
ID ABO07501 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 61
ID ABO03688 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 62
ID ABR67136 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 63
ID ABO15739 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 64
ID ABUS6020 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, PRO1344.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 65
ID ABU72305 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 66
ID ABUS5348 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 67
ID ABU95293 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 68
ID ABU71196 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 69
ID ABO07806 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 70
ID ABR70047 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 71
ID ABR69380 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 72
ID ABO01521 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 73
ID ABUS1323 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 74
ID ABR60120 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 75
ID ABU90978 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 76
ID ABR67855 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 77
ID ABR65243 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 78
ID ABR68465 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 79
ID ABR71877 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003021335-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 80
ID ABUS9258 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 81
ID ABUS5357 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 82
ID ABUS9047 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 83
ID ABUS3127 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US200302105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 84
ID ABUS94983 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 85
ID ABUS0531 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 86
ID ABUS4042 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 87
ID ABUS3693 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 88
ID ABO25955 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 89
ID ABR64938 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 90
ID ABO27299 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 91
ID ABR68770 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 92
ID ABO06586 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003031625-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 93
ID ABR99131 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 94
ID ABUS7015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 95
ID ABUS9567 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 96
ID ABUS2254 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003031636-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 97
ID ABUS7265 standard; protein; 720 AA.

DE Human PRO polypeptide #85.
PN US2003031638-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 98
ID ABU83737 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 99
ID ABO08111 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 100
ID ABU92494 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 101
ID ABU81822 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 102
ID ABU65986 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US20030316157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 103
ID ABU81164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 104
ID ABR59815 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 105
ID ABU94003 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US20030316155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 106
ID ABU99856 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 107
ID ABR66526 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 108
ID ABR90944 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 109
ID ABO53279 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 110
ID ABU58964 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 111
ID ABU94371 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 112
ID ABU79253 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 113
ID ABU66582 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 114
ID ABU66887 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 115
ID ABU94676 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 116
ID ABO04603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 117
ID ABR70352 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 118
ID ABU92342 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 119
ID ABUS98517 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 120
ID ABR65916 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 121
ID ABR64633 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 122
ID ABUS9407 standard; protein; 720 AA.
DE Novel human secreted or transmembrane protein PRO1109.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 123
ID ABU79558 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 124
ID ABUS2949 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 125
ID ABUS9508 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 126
ID ABUS91128 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 127
ID ABUS90221 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036153-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 128
ID ABO09636 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 129
ID ABO10908 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 130
ID ABR70962 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 131
ID ABUS98281 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 132
ID ABUS7570 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 133
ID ABUS91438 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 134
ID ABUS9286 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 135
ID ABUS4652 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 136
ID ABR69742 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 137
ID ABUS01119 standard; protein; 720 AA.
DE Human PRO protein #85.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 138
ID ABUS01119 standard; protein; 720 AA.
DE Human PRO protein #85.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 138
ID AB062493 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 139
ID AB092173 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 140
ID AB093388 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 141
ID AB009941 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 142
ID AB009026 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 143
ID AB096457 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 144
ID AB010879 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 145
ID AB010594 standard; protein; 720 AA.
DE Human secreted/transmembrane protein #85.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 146
ID AB016131 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 147
ID AB072127 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003023042-A1.

PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 148
ID AB095603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 149
ID AB096812 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 150
ID ABR70657 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 151
ID AB005008 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 152
ID AB008416 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 153
ID AB088570 standard; protein; 720 AA.
DE Human secreted and transmembrane polypeptide PRO1344.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 154
ID AB034084 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 155
ID AB005623 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 156
ID ABR74012 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 157
ID ABR95604 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 158
ID ABR80901 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 159
ID ABR81206 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 160
ID ABM00902 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 161
ID ABR88504 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 162
ID ABM77325 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 163
ID AB028809 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 164
ID AB031554 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 165
ID ABM07971 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 166
ID AB040451 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068682-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 167
ID AB035876 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 168
ID ABO44015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 169
ID ADA77922 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 170
ID ABM24810 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 171
ID ABO03078 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 172
ID ABR90334 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 173
ID ABM17248 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 174
ID ABR94994 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 175
ID ABR95299 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 176
ID ABO40451 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068682-A1.

ID ADB17095 standard; protein; 720 AA.
DE Human transmembrane PRO polypeptide (SeqID 38).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 177
ID ABO21537 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 178
ID ABR97801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 179
ID ABR87589 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 180
ID ABM77630 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 181
ID ABM27860 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 182
ID ABM06141 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 183
ID ABM03647 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 184
ID ABM35098 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 185
ID ABM26335 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 186
ID ABO48117 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 187
ID ABR92859 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 188
ID ABO24620 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 189
ID ADA37742 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 190
ID ABM11631 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 191
ID ABM02732 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 192
ID ABM16028 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 193
ID ABO27589 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 194
ID ABM29080 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068721-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 195
ID ABM07056 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 196
ID ABM21150 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 197
ID ABM09496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 198
ID ABO41366 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 199
ID ABO36181 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 200
ID ABO43710 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 201
ID ABM76410 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 202
ID ABM76106 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 203
ID ABM25725 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 204
ID ABM26030 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 205
ID ADA21428 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 206
ID ABO03383 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 207
ID ABO02468 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 208
ID ABO44257 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 209
ID ABR90639 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 210
ID ABR73707 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 211
ID ABO16959 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 212
ID ABR94384 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 213
ID ABR75891 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;


```
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032134-A1.
PD 13-FEB-2003.
  Query Match
    Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
  RESULT 233
    ID ABL17283 standard; protein; 720 AA.
  DE Human transmembrane PRO polypeptide (seqID 38).
  PN US20030305465-A1.
  PD 13-MAR-2003.
  PA (GETH) GENENTECH INC.
    Query Match
      Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
    RESULT 234
      ID ADA17759 standard; protein; 720 AA.
    DE Human PRO1344 polypeptide.
    PN US200303054987-A1.
    PD 20-MAR-2003.
    PA (GETH) GENENTECH INC.
      Query Match
        Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
      RESULT 235
        ID ABR97191 standard; protein; 720 AA.
      DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
      PN US200303054481-A1.
      PD 20-MAR-2003.
      PA (GETH) GENENTECH INC.
        Query Match
          Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
        RESULT 236
          ID ABR86979 standard; protein; 720 AA.
        DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
        PN US200303049778-A1.
        PD 13-MAR-2003.
        PA (GETH) GENENTECH INC.
          Query Match
            Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
          RESULT 237
            ID ABM11021 standard; protein; 720 AA.
          DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
          PN US200303049782-A1.
          PD 13-MAR-2003.
          PA (GETH) GENENTECH INC.
            Query Match
              Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
            RESULT 238
              ID ABM28165 standard; protein; 720 AA.
            DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
            PN US200303054476-A1.
            PD 20-MAR-2003.
            PA (GETH) GENENTECH INC.
              Query Match
                Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
              RESULT 239
                ID ABO32164 standard; protein; 720 AA.
              DE Human secreted/transmembrane protein (PRO) #85.
              PN US200303068733-A1.
              PD 10-APR-2003.
              PA (GETH) GENENTECH INC.
                Query Match
                  Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
                RESULT 240
                  ID ABM15291 standard; protein; 720 AA.
                DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
                PN US200303068692-A1.
                PD 10-APR-2003.
                PA (GETH) GENENTECH INC.
                  Query Match
                    Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
                    RESULT 241
                      ID ABM06446 standard; protein; 720 AA.
                      DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
                      PN US200303068709-A1.
                      PD 10-APR-2003.
                      PA (GETH) GENENTECH INC.
                        Query Match
                          Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
                          RESULT 242
                            ID ABM04257 standard; protein; 720 AA.
                            DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
                            PN US200303068716-A1.
                            PD 10-APR-2003.
                            PA (GETH) GENENTECH INC.
                              Query Match
                                Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
                                RESULT 243
                                  ID ABM22370 standard; protein; 720 AA.
                                  DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
                                  PN US200303068740-A1.
                                  PD 10-APR-2003.
                                  PA (GETH) GENENTECH INC.
                                    Query Match
                                      Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
                                      RESULT 244
                                        ID ABM07666 standard; protein; 720 AA.
                                        DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
                                        PN US200303068751-A1.
                                        PD 10-APR-2003.
                                        PA (GETH) GENENTECH INC.
                                          Query Match
                                            Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
                                            RESULT 245
                                              ID ABO40756 standard; protein; 720 AA.
                                              DE Human secreted/transmembrane protein (PRO) #85.
                                              PN US200303068684-A1.
                                              PD 10-APR-2003.
                                              PA (GETH) GENENTECH INC.
                                                Query Match
                                                  Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
                                                  RESULT 246
                                                    ID ABM35403 standard; protein; 720 AA.
                                                    DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
                                                    PN US200303073179-A1.
                                                    PD 17-APR-2003.
                                                    PA (GETH) GENENTECH INC.
                                                      Query Match
                                                        Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
                                                        RESULT 247
                                                          ID ABM33166 standard; protein; 720 AA.
                                                          DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
                                                          PN US200303087374-A1.
                                                          PD 08-MAY-2003.
                                                          PA (GETH) GENENTECH INC.
                                                            Query Match
                                                              Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
                                                              RESULT 248
                                                                ID ABO52692 standard; protein; 720 AA.
                                                                DE Human PRO polypeptide #85.
                                                                PN US200303049773-A1.
                                                                PD 13-MAR-2003.
                                                                PA (GETH) GENENTECH INC.
                                                                  Query Match
                                                                    Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
                                                                    RESULT 249
                                                                      ID ABO50252 standard; protein; 720 AA.
                                                                      DE Human secreted/transmembrane protein (PRO) #85.
                                                                      PN US200303049777-A1.
                                                                      PD 13-MAR-2003.
                                                                      PA (GETH) GENENTECH INC.
                                                                        Query Match
                                                                          Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
                                                                          RESULT 250
                                                                            ID ABU9246 standard; protein; 720 AA.
                                                                            DE Human secreted/transmembrane protein (PRO) #85.
                                                                            PN US200303040055-A1.
                                                                            PD 27-FEB-2003.
                                                                            PA (GETH) GENENTECH INC.
                                                                              Query Match
                                                                                Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
```

RESULT 251
ID AB004298 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003036164-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 252
ID AB005928 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003040074-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 253
ID ABM18468 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 254
ID ADA27867 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
FN US2003054359-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 255
ID ABR97496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 256
ID ABR80596 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 257
ID ABM01207 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 258
ID ABR88809 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003073169-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 259
ID ABM13461 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 260
ID ABM20845 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003068711-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 261
ID ABO41976 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 262
ID ABO42586 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 263
ID ABM10106 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 264
ID ABO38621 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 265
ID ABR32861 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 266
ID ABM22675 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003087373-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 267
ID ABM74886 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003096353-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 268
ID ADA79714 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 269
ID ABR96276 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 270
ID ABM02427 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 271
ID ABR66369 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 272
ID ABR86674 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 273
ID ABR16638 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 274
ID ABM29690 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 275
ID ABO29114 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 276
ID ABM23895 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 277
ID ABM23285 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 278
ID ABM22065 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 279
ID ABO37706 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.

PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 280
ID ABM28470 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 281
ID ABM28775 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 282
ID ABM66419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 283
ID ABM75801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 284
ID ABM34081 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 285
ID ABM34386 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 286
ID ABO20317 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 287
ID ABO21332 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;
RESULT 288
ID ABO22147 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PRED. NO. 0;

```
RESULT 289
ID ADA20072 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US200305222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 290
ID ABO34195 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 291
ID ABR96581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 292
ID ADA94447 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 293
ID ABR85759 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 294
ID ABR99741 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 295
ID ABW00597 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 296
ID ABW00292 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 297
ID ABO29724 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 298
ID ABM23590 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 299
ID ABM29385 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 300
ID ABO38316 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 301
ID ABO45616 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 302
ID ABM20540 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 303
ID ADA81441 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 304
ID ABO16654 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 305
ID ABO18280 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 306
ID ABO22707 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 307
ID ABO23012 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
```

RESULT 308
ID ABR92554 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 309
ID ABR81511 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 310
ID ABR7935 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 311
ID ABR89724 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 312
ID ABR26640 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 313
ID ABR13766 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 314
ID ABO28504 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 315
ID ABO30334 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 316
ID ABO7361 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003088702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 317
ID ABO3952 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

FN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 318
ID ABO37096 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 319
ID ABO41671 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 320
ID ABO35266 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
FN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 321
ID ABR25115 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 322
ID ABO47507 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 323
ID ABO47812 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 324
ID ABO48422 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 325
ID ABO51472 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
FN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 326
ID ABO51777 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
FN US2003049767-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 327
ID ABO50557 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 328
ID ABR79681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 329
ID ABM16943 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 330
ID ABO17975 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 331
ID ABO20927 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 332
ID ABR96886 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 333
ID ADA38672 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 334
ID ABM12241 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 335
ID ABM16333 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 336
ID ABM24200 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 337
ID ABM14681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 338
ID ABM04562 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 339
ID ABM06751 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 340
ID ABM09191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 341
ID ABO39231 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 342
ID ABM75496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 343
ID ABM25420 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 344
ID ABM19930 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 345
ID ABO46836 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 346
ID ABO47141 standard; protein; 720 AA.
DE Human secreted polypeptide #85.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 347
ID ADA83239 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 348
ID ABR71572 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 349
ID ABR72182 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 350
ID ABR98521 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 351
ID ABO06891 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 352
ID ABR84844 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 353
ID ABR73402 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 354
ID ABR76496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 355
ID ABR73097 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027270-A1.
PD 06-FEB-2003.

Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 356
ID ABM18163 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 357
ID ABO20622 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 358
ID ABO25365 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 359
ID ABO25670 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 360
ID ABR94079 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 361
ID ADA92793 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 362
ID ABR79986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 363
ID ABM11326 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 364
ID ABO32933 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 365
ID ABO30639 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 366
ID ABO30944 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 367
ID ABM27250 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 368
ID ABM29995 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 369
ID ABM05531 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 370
ID ABM15596 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 371
ID ABM08581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 372
ID ABO42281 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 373
ID ABO38011 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 374
ID ABO45921 standard; protein; 720 AA.
DE Human PRO polypeptide #85.

PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 375
ID ABM66724 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 376
ID ADB20282 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 377
ID ABM19625 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 378
ID ABO49337 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 379
ID ABO49642 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 380
ID ADA78534 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 381
ID ABR88199 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 382
ID ADA00369 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 383
ID ABM26945 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068739-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 384
ID ABO03342 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 385
ID ABO39841 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 386
ID ABO49947 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 387
ID ABO50862 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 388
ID ABO05318 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 389
ID ABR74622 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 390
ID ABR77101 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 391
ID ABM17858 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 392
ID ABR95909 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 393
ID ABO21842 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.

PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 394
ID ABO20012 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 395
ID ABO24315 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 396
ID ABR86064 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 397
ID ABM10716 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 398
ID ABM76715 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 399
ID ABR89419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 400
ID ABM12546 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 401
ID ABM05836 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 402
ID ABO34961 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 403
ID ABW03037 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 404
ID ABM19015 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 405
ID ABM19320 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 406
ID AB046531 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 407
ID AB049032 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 408
ID ABK69075 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 409
ID ABR89114 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 410
ID ABR72487 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 411
ID ABR74317 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 412
ID AB018585 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 413
ID ABR80291 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 414
ID ABM01512 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 415
ID ABM02122 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 416
ID ABR87284 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 417
ID ABM12851 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 418
ID ABM30605 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 419
ID ABM24505 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 420
ID AB029419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 421
ID AB031249 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068710-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 422
ID ABM14376 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003068866-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 423
ID ABM09801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 424
ID ABO38926 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 425
ID ABM34691 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003104538-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 426
ID ABO51167 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 427
ID ABO03993 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003036158-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 428
ID ABO10463 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
FN US2003036151-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 429
ID ABO53170 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
FN US2003044806-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 430
ID ABR77706 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003040067-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 431
ID ABR78916 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003068731-A1.
PD 10-APR-2003.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003054456-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 432
ID ABO24010 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 433
ID ABR93774 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 434
ID ABM01817 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 435
ID ABM78240 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 436
ID ABR90029 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 437
ID ADA22354 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
FN US2003040473-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 438
ID ABM27555 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 439
ID ABM13156 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 440
ID ABO31859 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
FN US2003068731-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 441
ID ABM14071 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 442
ID ABM08276 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 443
ID AB040146 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 444
ID ABM74581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 445
ID ABM33776 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 446
ID ABM20235 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 447
ID AB048727 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 448
ID AB022540 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 449
ID ABR72792 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 450
ID AB015434 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 451
ID ABR85149 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 452
ID AB015129 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 453
ID AB017264 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 454
ID ABM17553 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 455
ID ADA06520 standard; protein; 720 AA.
DE Human secreted/transmembrane PRO polypeptide #65.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 456
ID ADA39213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 457
ID ABR85454 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 458
ID ABM77020 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 459
ID ABO28199 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 460

ID ABM22980 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 461
ID ABM30300 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 462
ID ABM21760 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 463
ID ABM21455 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 464
ID ABM14986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 465
ID ABM31825 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 466
ID ABM31215 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 467
ID ABM316791 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 468
ID ABM75191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 469
ID ABM33471 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 470
ID ABO46226 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 471
ID ADA82605 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 472
ID ADB85611 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 473
ID ADB62339 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 474
ID ABM31825 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 475
ID ABM31215 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 476
ID ADB85913 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 477
ID ABM32130 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 478
ID ABM32435 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068713-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 479
ID AD868290 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 480
ID AD868097 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 481
ID ABM31520 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 482
ID ABM30910 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 483
ID ADB90914 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 484
ID ADC57711 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 485
ID ADC55075 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 486
ID ADC11942 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 487
ID ADC06994 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 488

ID ADC5364 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 489
ID ADC17173 standard; protein; 720 AA.
DE Mammalian PRO polypeptide (SeqID 38).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 490
ID ADC07419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 491
ID ADC11409 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 492
ID ADC14871 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 493
ID ADC52366 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 494
ID ADC14531 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 495
ID ADD08063 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 496
ID ADC81888 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 497
ID ADD07530 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 498
ID ADG82421 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 499
ID ADD05643 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 500
ID ADD08601 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 501
ID ADD06850 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 502
ID ADC83097 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 503
ID ADD55204 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 504
ID .ADD36042 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 505
ID ADD56162 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 506
ID ADD54600 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 507
ID ADE26754 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 508
ID ADE26221 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 509
ID ADF67158 standard; protein; 720 AA.
DE Human PRO1344 amino acid sequence SEQ ID NO:231.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 510
ID ADG01043 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 511
ID ADG08596 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 512
ID ADG02638 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 513
ID ADG01345 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 514
ID ADF95520 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 515
ID ADF95217 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 516
ID ADG12335 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 517
ID ADH24070 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 518
ID ADH34096 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 519
ID ADH29929 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 520
ID ADH23900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 521
ID ADH08995 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 522
ID ADH85304 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 523
ID ADH24580 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 524
ID ADH37436 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 525
ID ADH02025 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 526
ID ADH37606 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.

PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 527
ID ADG85644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 528
ID ADH24240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 529
ID ADH38534 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 530
ID ADG83655 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 531
ID ADH29463 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 532
ID ADH27579 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 533
ID ADH37776 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 534
ID ADH37953 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 535
ID ADH57373 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180920-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 536
ID ADH53515 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 537
ID ADH53685 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 538
ID ADH52021 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 539
ID ADH49876 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 540
ID ADI25386 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 541
ID ADH90179 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 542
ID ADI25556 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 543
ID ADH97730 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 544
ID ADI35412 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003050457-A1.
PD 13-MAR-2003.

Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 545
ID ADI03578 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 546
ID ADI11935 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 547
ID ADH90009 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 548
ID ADH99904 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 549
ID ADH98410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 550
ID ADI11085 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 551
ID ADI11595 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 552
ID ADH98240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 553
ID ADH98580 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
RESULT 554
ID ADI35412 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003050457-A1.
PD 13-MAR-2003.

RESULT 554
ID ADH98070 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 555
ID ADI05058 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 556
ID ADI03408 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 557
ID ADI04803 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 558
ID ADH78257 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 559
ID ADI19601 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 560
ID ADH90349 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 561
ID ADI03068 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 562
ID ADH77917 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 563
ID ADH97900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 564
ID ADI01285 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 565
ID ADI01980 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 566
ID ADI03238 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 567
ID ADI11425 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 568
ID ADI02327 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 569
ID ADI11765 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 570
ID ADI05402 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 571
ID ADH79474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;
Pred. No. 0;
RESULT 572
ID ADI19431 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 573
ID AD105232 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 574
ID ADH79644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 575
ID AD101470 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 576
ID AD101640 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 577
ID AD101810 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 578
ID ADH79814 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 579
ID AD104632 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 580
ID AD107768 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 581
ID ADH78087 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 582
ID AD125726 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 583
ID AD125896 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 584
ID ADK55408 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 585
ID ADH98750 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 586
ID ADH79991 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 587
ID ADL32776 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 588
ID ADM30310 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 589
ID ADL93722 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 590
ID ADC52176 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003130483-A1.

PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 591
ID ADE74307 standard; protein; 720 AA.
DE Human secreted/cransmembrane protein (PRO) #85.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 592
ID ADE74919 standard; protein; 720 AA.
DE Human secreted/cransmembrane protein (PRO) #85.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 593
ID ADF5357 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 594
ID ADG11607 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 595
ID ADP96132 standard; protein; 720 AA.
DE Novel human secreted and cransmembrane protein PRO1344.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 596
ID ADG04403 standard; protein; 720 AA.
DE Novel human secreted and cransmembrane protein PRO1344.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 597
ID ADG00563 standard; protein; 720 AA.
DE Novel human secreted and cransmembrane protein PRO1344.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 598
ID ADH06608 standard; protein; 720 AA.
DE Novel human secreted and cransmembrane protein PRO1344.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 599
ID ADH06438 standard; protein; 720 AA.
DE Novel human secreted and cransmembrane protein PRO1344.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 600

ID ADG68859 standard; protein; 720 AA.
DE Novel human secreted and cransmembrane protein PRO1344.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 601
ID ADH27749 standard; protein; 720 AA.
DE Novel human secreted and cransmembrane protein PRO1344.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 602
ID ADH25090 standard; protein; 720 AA.
DE Novel human secreted and cransmembrane protein PRO1344.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 603
ID ADH33722 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 604
ID ADG82819 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 605
ID ADH02365 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 606
ID ADH07972 standard; protein; 720 AA.
DE Novel human secreted and cransmembrane protein PRO1344.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 607
ID ADG69369 standard; protein; 720 AA.
DE Novel human secreted and cransmembrane protein PRO1344.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 608
ID ADH39190 standard; protein; 720 AA.
DE Novel human secreted and cransmembrane protein PRO1344.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 609
ID ADH26100 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 610
ID ADG83930 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 611
ID ADH19477 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 612
ID ADG85474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 613
ID ADH06268 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 614
ID ADH30098 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 615
ID ADH24410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 616
ID ADH33069 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 617
ID ADG6539 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 618
ID ADH07802 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 619
ID ADG85814 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 620
ID ADH39360 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 621
ID ADH33552 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 622
ID ADH33892 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 623
ID ADH01102 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 624
ID ADG69709 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 625
ID ADH20970 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 626
ID ADH02195 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 627
ID ADG69199 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180847-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 628
ID ADG85984 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 629
ID ADH24920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 630
ID ADH39537 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 631
ID ADH20010 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 632
ID ADH02535 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 633
ID ADG69029 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 634
ID ADH07632 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 635
ID ADG86154 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 636
ID ADH24750 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 637
ID ADH25798 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 638
ID ADH38364 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 639
ID ADH57203 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 640
ID ADH52191 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 641
ID ADH49557 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 642
ID ADH90519 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 643
ID ADI11255 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 644
ID ADH98920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 645
ID ADI02150 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 646
ID ADH9689 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 647
ID ADJ54808 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 648
ID ADJ98564 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 649
ID ADJ98734 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 650
ID ADH7893 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 651
ID ADJ99127 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 652
ID ADJ99297 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 653
ID ADJ99915 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 654
ID ADH79063 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 655
ID ADK00923 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 656
ID ADK1444 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 657
ID ADJ64579 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 658
ID ADM31475 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 659
ID ADM36522 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 660
ID ADM40327 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 661
ID ADM80893 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 662
ID ADN37935 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 663
ID AAB70531 standard; protein; 567 AA.
DE Human PRO1 protein sequence SEQ ID NO:2.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 77.2%; Score 556; DB 4; Length 567;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 664

ID AAY88280 standard; protein; 720 AA.
DE Human TANGO 235 protein.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 71.9%; Score 518; DB 3; Length 720;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 665
ID AAB70532 standard; protein; 720 AA.
DE Human PRO2 protein sequence SEQ ID NO:4.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 71.9%; Score 518; DB 4; Length 720;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 666
ID AAU00401 standard; protein; 720 AA.
DE Human secreted protein, POLY13.
PN WO200119856-A2.
PD 22-MAR-2001.
PA (CURA-) CURAGEN CORP.
Query Match 71.9%; Score 518; DB 4; Length 720;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 667
ID ADH89028 standard; protein; 720 AA.
DE Human POLYX polypeptide #13.
PN US200318958-A1.
PD 23-OCT-2003.
PA (SHIM/) SHIMKETS R. A.
PA (FERN/) FERNANDES E.
PA (HERR/) HERRMANN J L.
PA (LIUX/) LIU X.
PA (YANG/) YANG M.
PA (BOLD/) BOLDOG F L.
PA (SMT/) SMITHSON G.
PA (RAS/) RASTELLI L.
Query Match 71.9%; Score 518; DB 8; Length 720;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 668
ID AAM41706 standard; protein; 499 AA.
DE Human polypeptide SEQ ID NO 6637.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 61.9%; Score 446; DB 4; Length 499;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 669
ID AAB85891 standard; protein; 737 AA.
DE Human serine protease-like protein (hC-PLACE1009992) .
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 61.9%; Score 446; DB 4; Length 737;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 670
ID AAB93670 standard; protein; 737 AA.
DE Human protein sequence SEQ ID NO:13202.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 61.9%; Score 446; DB 4; Length 737;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 671
ID ADJ69990 standard; protein; 737 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1796.
PN WO200308768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 61.9%; Score 446; DB 7; Length 737;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 672
ID ADN04640 standard; protein; 737 AA.

DE Antipsoriatic protein sequence #505.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 61.9%; Score 446; DB 8; Length 737;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 673
ID ADS85034 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SeqID36.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Query Match 61.9%; Score 446; DB 8; Length 737;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 674
ID ADS85022 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SeqID24.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Query Match 61.9%; Score 446; DB 8; Length 737;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 675
ID AAB85893 standard; protein; 762 AA.
DE Human serine protease-like protein (hC-PLACE1009992) .
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 61.9%; Score 446; DB 4; Length 762;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 676
ID ADL06662 standard; protein; 417 AA.
DE Human 3T3 cell conversion promoter FP938.
PN CN1403477-A.
PD 19-MAR-2003.
PA (SHAN-) SHANGHAI XINSHIDIE GENE TECHN DEV CO LTD.
Query Match 53.6%; Score 386; DB 7; Length 417;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 677
ID AAE19180 standard; protein; 649 AA.
DE Human protease, PRTS-17 protein.
PN WO200208396-A2.
PD 31-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 52.1%; Score 375; DB 5; Length 649;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 678
ID AAM39920 standard; protein; 359 AA.
DE Human polypeptide SEQ ID NO 3065.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 49.9%; Score 359; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 679
ID AAM39957 standard; protein; 359 AA.
DE Human polypeptide SEQ ID NO 3102.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 49.9%; Score 359; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 680
ID AAB49533 standard; protein; 570 AA.
DE Clone HPEY75.
PN WO200061774-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 49.3%; Score 355; DB 3; Length 570;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 681

ID AAE20817 standard; protein; 455 AA.
DE Human gene 5 encoded secreted protein HSLGUT5, SEQ ID NO:79.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.5%; Score 277; DB 5; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.5e-261;
RESULT 682
ID ABG64652 standard; protein; 455 AA.
DE Human albumin fusion protein #1327.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.5%; Score 277; DB 5; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.5e-261;
RESULT 683
ID ADL77919 standard; protein; 455 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1401.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 38.5%; Score 277; DB 8; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.5e-261;
RESULT 684
ID ADRA1485 standard; protein; 551 AA.
DE Human CD-like molecule HSKDR41, SEQ ID NO:284.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.5%; Score 277; DB 5; Length 551;
Best Local Similarity 100.0%; Pred. No. 5.4e-261;
RESULT 685
ID AAE20797 standard; protein; 323 AA.
DE Human gene 5 encoded secreted protein HSLGUT5, SEQ ID NO:59.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.3%; Score 276; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 3.2e-260;
RESULT 686
ID ABG64653 standard; protein; 323 AA.
DE Human albumin fusion protein #1328.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.3%; Score 276; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 3.2e-260;
RESULT 687
ID ADL77920 standard; protein; 323 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1402.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 38.3%; Score 276; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 3.2e-260;
RESULT 688
ID AAM24485 standard; protein; 234 AA.
DE Human EST encoded protein SEQ ID NO: 2010.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HSE-) HYSEQ INC.
Query Match 25.4%; Score 183; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-169;
RESULT 689
ID AAM41743 standard; protein; 146 AA.
DE Human polypeptide SEQ ID NO 6674.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HSE-) HYSEQ INC.
Query Match 15.8%; Score 114; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.2e-102;

RESULT 690
ID AAB0927 standard; protein; 719 AA.
DE Murine TANGO 215 protein.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 8.5%; Score 61; DB 3; Length 719;
Best Local Similarity 100.0%; Pred. No. 5.2e-50;
RESULT 691
ID AAB5892 standard; protein; 720 AA.
DE Mouse serine protease-like protein (mc-PLA21009922).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 8.5%; Score 61; DB 4; Length 720;
Best Local Similarity 100.0%; Pred. No. 5.2e-50;
RESULT 692
ID AAY11743 standard; protein; 103 AA.
DE Human 5' EST secreted protein SEQ ID No: 343.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 5.3%; Score 38; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.5e-28;
RESULT 693
ID AAY11763 standard; protein; 34 AA.
DE Human 5' EST secreted protein SEQ ID No: 363.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 2.1%; Score 15; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 694
ID AAB49533 standard; peptide; 12 AA.
DE Clone HPEY75 peptide fragment.
PN WO200061774-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.7%; Score 12; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00086;
RESULT 695
ID AAY72114 standard; peptide; 12 AA.
DE Human serine protease epidermal growth factor (EGF)-like domain.
PN WO200068247-A2.
PD 16-NOV-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.7%; Score 12; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00086;
RESULT 696
ID AAR93594 standard; peptide; 30 AA.
DE UK t-PA hybrid peptide CS14 residues 276-306.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU-) SUMITOMO PHARM CO LTD.
Query Match 1.2%; Score 9; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7;
RESULT 697
ID AAR76945 standard; peptide; 30 AA.
DE UK t-PA hybrid CS13 (residues 276-306).
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU-) SUMITOMO PHARM CO LTD.
Query Match 1.2%; Score 9; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7;
RESULT 698
ID AAR93590 standard; peptide; 30 AA.
DE UK t-PA hybrid peptide CS20 residues 276-306.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU-) SUMITOMO PHARM CO LTD.
Query Match 1.2%; Score 9; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7;
RESULT 699

ID AAR93593 standard; peptide; 30 AA.
DE UK t-PA hybrid peptide CS11 residues 276-306.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SDNU) SDUNITOMO PHARM CO LTD.
Query Match 1.2%; Score 9; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7;
RESULT 700
ID AAR93588 standard; peptide; 30 AA.
DE UK t-PA hybrid peptide CS18 residues 276-306.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SDNU) SDUNITOMO PHARM CO LTD.
Query Match 1.2%; Score 9; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7;
RESULT 701
ID AAY82896 standard; protein; 101 AA.
DE CUB domain from murine BMP-1.
PN WO200009691-A2.
PD 24-FEB-2000.
PA (UROG-) UROGENESYS INC.
PA (APAR/) APAR D E.
PA (HUBE/) HUBERT R S.
PA (LEON/) LEONG K.
PA (RAIT/) RAITANO A B.
PA (SAFF/) SAFFRAN D C.
PA (JAKO/) JAKOBOVITS A.
Query Match 1.2%; Score 9; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 5.1;
RESULT 702
ID AAY27043 standard; protein; 110 AA.
DE Amino acid sequence of human Bmp-1 CUB1 domain.
PN WO9937757-A1.
PD 29-JUL-1999.
PA (TULA) TULANE EDUCATIONAL FUND.
PA (INIM) INST NAT SANTE & RECH MEDICALE.
Query Match 1.2%; Score 9; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.5;
RESULT 703
ID ABM84572 standard; protein; 622 AA.
DE Human diagnostic and therapeutic protease SEQ ID NO:4821.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 1.2%; Score 9; DB 8; Length 622;
Best Local Similarity 100.0%; Pred. No. 27;
RESULT 704
ID ABM80969 standard; protein; 622 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81651, SEQ:2500.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GENTH) GENTECH INC.
Query Match 1.2%; Score 9; DB 8; Length 622;
Best Local Similarity 100.0%; Pred. No. 27;
RESULT 705
ID AAP80618 standard; protein; 730 AA.
DE Human Bone Morphogenic Protein-1 of lambda UZ05-1.
PN WO8800205-A.
PD 14-JAN-1988.
PA (GENV) GENETICS INST INC.
Query Match 1.2%; Score 9; DB 1; Length 730;
Best Local Similarity 100.0%; Pred. No. 31;
RESULT 706
ID AAM13669 standard; protein; 730 AA.
DE C-proteinase encoded by clone pCP-1.
PN WO9706242-A1.
PD 20-FEB-1997.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match 1.2%; Score 9; DB 2; Length 730;
Best Local Similarity 100.0%; Pred. No. 31;
RESULT 707
ID ADP65217 standard; protein; 730 AA.
DE Human bone morphogenetic protein 1, isoform 1, precursor, PCP.

PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 1.2%; Score 9; DB 7; Length 730;
Best Local Similarity 100.0%; Pred. No. 31;
RESULT 708
ID ABM80967 standard; protein; 730 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO3042, SEQ:2496.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GENTH) GENTECH INC.
Query Match 1.2%; Score 9; DB 8; Length 730;
Best Local Similarity 100.0%; Pred. No. 31;
RESULT 709
ID AAW75919 standard; protein; 788 AA.
DE C-proteinase sequence used to cleave procollagens.
PN US5807981-A.
PD 15-SEP-1998.
PA (FIBR-) FIBROGEN INC.
Query Match 1.2%; Score 9; DB 2; Length 788;
Best Local Similarity 100.0%; Pred. No. 33;
RESULT 710
ID ADH41541 standard; protein; 821 AA.
DE Novel human protein NOV8e.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 8; Length 821;
Best Local Similarity 100.0%; Pred. No. 34;
RESULT 711
ID ADH41549 standard; protein; 821 AA.
DE Novel human protein NOV8f.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 8; Length 821;
Best Local Similarity 100.0%; Pred. No. 34;
RESULT 712
ID ADH41533 standard; protein; 821 AA.
DE Novel human protein NOV8a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 8; Length 821;
Best Local Similarity 100.0%; Pred. No. 34;
RESULT 713
ID ADH41543 standard; protein; 821 AA.
DE Novel human protein NOV8f.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 8; Length 821;
Best Local Similarity 100.0%; Pred. No. 34;
RESULT 714
ID ADH41545 standard; protein; 821 AA.
DE Novel human protein NOV8g.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 8; Length 821;
Best Local Similarity 100.0%; Pred. No. 34;
RESULT 715
ID ADH41547 standard; protein; 821 AA.
DE Novel human protein NOV8h.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 8; Length 821;
Best Local Similarity 100.0%; Pred. No. 34;
RESULT 716
ID ADM87216 standard; protein; 823 AA.
DE Human protein SEQ ID NO:309.
PN WO2004009834-A2.

PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match
Best Local Similarity 1.2%; Score 9; DB 8; Length 823;
Pred. No. 34;
RESULT 717
ID ABM80968 standard; protein; 823 AA.
DE Tumour-associated antigenic target (TAT) polypeptide. PRO81650, SEQ:2498.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 1.2%; Score 9; DB 8; Length 823;
Pred. No. 34;
RESULT 718
ID ABG79188 standard; protein; 970 AA.
DE Human colloid-like 2-like protein #2.
PN WO200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 1.2%; Score 9; DB 5; Length 970;
Pred. No. 40;
RESULT 719
ID ADH41539 standard; protein; 970 AA.
DE Novel human protein NOV8d.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 1.2%; Score 9; DB 8; Length 970;
Pred. No. 40;
RESULT 720
ID AAM13670 standard; protein; 986 AA.
DE C-proteinase encoded by clone pcP-2.
PN WO9706242-A1.
PD 20-FEB-1997.
PA (UYU-) UNIV JEFFERSON THOMAS.
Query Match
Best Local Similarity 1.2%; Score 9; DB 2; Length 986;
Pred. No. 41;
RESULT 721
ID ABB90755 standard; protein; 986 AA.
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 242.
PN WO200210217-A2.
PD 07-FEB-2002.
PA (UYU-) UNIV JOHNS HOPKINS.
Query Match
Best Local Similarity 1.2%; Score 9; DB 5; Length 986;
Pred. No. 41;
RESULT 722
ID ABUS4462 standard; protein; 986 AA.
DE Human tumour endothelial marker TEM 25.
PN WO200283874-A2.
PD 24-OCT-2002.
PA (UYU-) UNIV JOHNS HOPKINS.
Query Match
Best Local Similarity 1.2%; Score 9; DB 6; Length 986;
Pred. No. 41;
RESULT 723
ID ADH11578 standard; protein; 986 AA.
DE Human bone morphogenic protein (BMP) polypeptide #6.
PN US2003224501-A1.
PD 04-DEC-2003.
PA (YOUN/) YOUNG P E.
PA (RUBE/) RUBEN S M.
Query Match
Best Local Similarity 1.2%; Score 9; DB 8; Length 986;
Pred. No. 41;
RESULT 724
ID AD018558 standard; protein; 986 AA.
DE Human bovt tissue sarcoma-upregulated protein - SEQ ID 1377.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 1.2%; Score 9; DB 8; Length 986;
Pred. No. 41;
RESULT 725
ID ABG79187 standard; protein; 992 AA.
DE Human colloid-like 2-like protein #1.
PN WO200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 1.2%; Score 9; DB 5; Length 992;
Pred. No. 41;
RESULT 726
ID ADH41535 standard; protein; 992 AA.
DE Novel human protein NOV8b.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 1.2%; Score 9; DB 8; Length 992;
Pred. No. 41;
RESULT 727
ID AAY32240 standard; protein; 1015 AA.
DE Human colloid-like protein mtl1-2.
PN WO9951730-A2.
PD 14-OCT-1999.
PA (WISC-) WISCONSIN ALUMNI RES FOUND.
Query Match
Best Local Similarity 1.2%; Score 9; DB 3; Length 1015;
Pred. No. 42;
RESULT 728
ID ADH41537 standard; protein; 1015 AA.
DE Novel human protein NOV8c.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 1.2%; Score 9; DB 8; Length 1015;
Pred. No. 42;
RESULT 729
ID ABB71111 standard; protein; 1464 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40125.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 1.2%; Score 9; DB 4; Length 1464;
Pred. No. 58;
RESULT 730
ID ABB77068 standard; peptide; 11 AA.
DE ACZ885 antibody light chain hypervariable region CDR1'.
PN WO200216436-A2.
PD 28-FEB-2002.
PA (NOVS-) NOVARTIS AG.
PA (NOVS-) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match
Best Local Similarity 1.1%; Score 8; DB 5; Length 11;
Pred. No. 6.4;
RESULT 731
ID ADH17899 standard; peptide; 11 AA.
DE Human 15H12/19D12 CDR (complementarity determining region)-L1 peptide.
PN WO2003100008-A2.
PD 04-DEC-2003.
PA (SCHE-) SCHERING CORP.
Query Match
Best Local Similarity 1.1%; Score 8; DB 8; Length 11;
Pred. No. 6.4;
RESULT 732
ID ADM41606 standard; peptide; 11 AA.
DE Interleukin-1 receptor type 1 antibody light chain variable region CDR1.
PN WO2004022718-A2.
PD 18-MAR-2004.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 1.1%; Score 8; DB 8; Length 11;
Pred. No. 6.4;
RESULT 733
ID AAE36802 standard; protein; 50 AA.
DE Human epigen BGF-like domain.
PN WO2003014159-A1.
PD 20-FEB-2003.
PA (CSIR-) COMMONWEALTH SCI & IND RES ORG.
PA (BIOW-) BIOMOLECULAR RES INST LTD.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PA (LUDM-) LUDWIG INST CANCER RES.
Query Match
Best Local Similarity 1.1%; Score 8; DB 6; Length 50;
Pred. No. 25;
RESULT 734

ID AAV76087 standard; protein; 51 AA.
DE MUTRI fragment (residues 53-103) mutR1a, SEQ ID NO:342.
PN WO955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 1.1%; Score 8; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 26;
RESULT 735
ID AAB56026 standard; protein; 51 AA.
DE Skin cell protein, SEQ ID NO: 342.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 1.1%; Score 8; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 26;
RESULT 736
ID ABB72226 standard; protein; 51 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 342.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 1.1%; Score 8; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 26;
RESULT 737
ID AAY56653 standard; protein; 88 AA.
DE Partial peptide fragment of chimpanzee V kappa CDNA clone 46-4.
PN WO995369-A1.
PD 04-NOV-1999.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 1.1%; Score 8; DB 3; Length 88;
Best Local Similarity 100.0%; Pred. No. 43;
RESULT 738
ID AAV79331 standard; protein; 94 AA.
DE Human EGF repeat-containing protein EGF-Hy1.
PN WO200017357-A1.
PD 30-MAR-2000.
PA (HYSE-) HYSEQ INC.
Query Match 1.1%; Score 8; DB 3; Length 94;
Best Local Similarity 100.0%; Pred. No. 45;
RESULT 739
ID ABO27159 standard; protein; 95 AA.
DE Human germline light chain variable region gene segment #39.
PN US2003039649-A1.
PD 27-FEB-2003.
PA (FOOT/) FOOT J.
Query Match 1.1%; Score 8; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
RESULT 740
ID ABO27158 standard; protein; 95 AA.
DE Human germline light chain variable region gene segment #38.
PN US2003039649-A1.
PD 27-FEB-2003.
PA (FOOT/) FOOT J.
Query Match 1.1%; Score 8; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
RESULT 741
ID ADF10204 standard; protein; 95 AA.
DE Antibody light chain variable region VLK_6-21.
PN WO2003074679-A2.
PD 12-SEP-2003.
PA (XENC-) XENCOR.
Query Match 1.1%; Score 8; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
RESULT 742
ID ADF10103 standard; protein; 95 AA.
DE VEGF antibody light chain variable region VLK_6D-21.
PN WO2003074679-A2.
PD 12-SEP-2003.
PA (XENC-) XENCOR.
Query Match 1.1%; Score 8; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
RESULT 743
ID ADF10102 standard; protein; 95 AA.

DE VEGF antibody light chain variable region VLK_6-21.
PN WO2003074679-A2.
PD 12-SEP-2003.
PA (XENC-) XENCOR.
Query Match 1.1%; Score 8; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
RESULT 744
ID ADF10000 standard; protein; 95 AA.
DE Antibody light chain variable region VLK_6-21.
PN WO2003074679-A2.
PD 12-SEP-2003.
PA (XENC-) XENCOR.
Query Match 1.1%; Score 8; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
RESULT 745
ID ADF10001 standard; protein; 95 AA.
DE Antibody light chain variable region VLK_6D-21.
PN WO2003074679-A2.
PD 12-SEP-2003.
PA (XENC-) XENCOR.
Query Match 1.1%; Score 8; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
RESULT 746
ID ADF10205 standard; protein; 95 AA.
DE Antibody light chain variable region VLK_6D-21.
PN WO2003074679-A2.
PD 12-SEP-2003.
PA (XENC-) XENCOR.
Query Match 1.1%; Score 8; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
RESULT 747
ID ADF80278 standard; protein; 95 AA.
DE V kappa gene locus antibody amino acid sequence #38.
PN WO2003048321-A2.
PD 12-JUN-2003.
PA (ALEX-) ALEXION PHARM INC.
Query Match 1.1%; Score 8; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
RESULT 748
ID ADF80279 standard; protein; 95 AA.
DE V kappa gene locus antibody amino acid sequence #39.
PN WO2003048321-A2.
PD 12-JUN-2003.
PA (ALEX-) ALEXION PHARM INC.
Query Match 1.1%; Score 8; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
RESULT 749
ID ADO07347 standard; protein; 95 AA.
DE Human antibody A26 light chain variable region.
PN WO2004033658-A2.
PD 22-APR-2004.
PA (INTE-) INTEGRIGEN INC.
Query Match 1.1%; Score 8; DB 8; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
RESULT 750
ID ADO07348 standard; protein; 95 AA.
DE Human antibody A10 light chain variable region.
PN WO2004033658-A2.
PD 22-APR-2004.
PA (INTE-) INTEGRIGEN INC.
Query Match 1.1%; Score 8; DB 8; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
RESULT 751
ID AAR35905 standard; protein; 96 AA.
DE Human A10/A26 antibody light chain germline protein.
PN EP1262193-A1.
PD 04-DEC-2002.
PA (PRIZ) PRIZER PROD INC.
Query Match 1.1%; Score 8; DB 6; Length 96;
Best Local Similarity 100.0%; Pred. No. 46;
RESULT 752
ID ADO07305 standard; protein; 107 AA.
DE Human proteolytic A26-JK1 light chain, used in catalytic antibody.

PN WO2004033658-A2.
PD 22-APR-2004.
PA (INTE-) INTEGRIGEN INC.
Query Match 1.1%; Score 8; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 51;
RESULT 753
ID ADO07307 standard; protein; 107 AA.
DE Human proteolytic A10-JK1 light chain, used in catalytic antibody.
PN WO2004033658-A2.
PD 22-APR-2004.
PA (INTE-) INTEGRIGEN INC.
Query Match 1.1%; Score 8; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 51;
RESULT 754
ID ABB03399 standard; protein; 124 AA.
DE Human musculoskeletal system related polypeptide SEQ ID NO 1346.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.1%; Score 8; DB 4; Length 124;
Best Local Similarity 100.0%; Pred. No. 58;
RESULT 755
ID ABB12693 standard; protein; 124 AA.
DE Novel human musculoskeletal system antigen #313.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.1%; Score 8; DB 6; Length 124;
Best Local Similarity 100.0%; Pred. No. 58;
RESULT 756
ID ADJ28719 standard; protein; 124 AA.
DE Human musculoskeletal system-associated protein - SEQ ID 1346.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.1%; Score 8; DB 8; Length 124;
Best Local Similarity 100.0%; Pred. No. 58;
RESULT 757
ID ABB77064 standard; protein; 126 AA.
DE AC2885 antibody light chain variable region.
PN WO200216436-A2.
PD 28-FEB-2002.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERM GES MBH.
Query Match 1.1%; Score 8; DB 5; Length 126;
Best Local Similarity 100.0%; Pred. No. 59;
RESULT 758
ID ADM41553 standard; protein; 126 AA.
DE Anti-interleukin-1 receptor type 1 antibody kappa chain variable region.
PN WO2004022718-A2.
PD 18-MAR-2004.
PA (AMGE-) AMGEN INC.
Query Match 1.1%; Score 8; DB 8; Length 126;
Best Local Similarity 100.0%; Pred. No. 59;
RESULT 759
ID ABB57370 standard; protein; 127 AA.
DE Anti-TRAIL-R antibody related clone KMTR1 protein SEQ ID NO:35.
PN WO200294880-A1.
PD 28-NOV-2002.
PA (KIRI) KIRIN BEER KK.
Query Match 1.1%; Score 8; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 760
ID AAY56718 standard; protein; 128 AA.
DE Amino acid sequence of chimpanzee Vkapaa cDNA clone 46-4.
PN WO9955369-A1.
PD 04-NOV-1999.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 1.1%; Score 8; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 761

ID ADH17963 standard; protein; 128 AA.
DE Human modified 15H12/19D12 light chain C (LCC) protein.
PN WO2003100008-A2.
PD 04-DEC-2003.
PA (SCHE) SCHERING CORP.
Query Match 1.1%; Score 8; DB 8; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 762
ID ADH17967 standard; protein; 128 AA.
DE Human modified 15H12/19D12 light chain E (LCE) protein.
PN WO2003100008-A2.
PD 04-DEC-2003.
PA (SCHE) SCHERING CORP.
Query Match 1.1%; Score 8; DB 8; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 763
ID ADH17969 standard; protein; 128 AA.
DE Human modified 15H12/19D12 light chain F (LCF) protein.
PN WO2003100008-A2.
PD 04-DEC-2003.
PA (SCHE) SCHERING CORP.
Query Match 1.1%; Score 8; DB 8; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 764
ID ADH17932 standard; protein; 128 AA.
DE Human 15H12/19D12 light chain A (LCA) protein.
PN WO2003100008-A2.
PD 04-DEC-2003.
PA (SCHE) SCHERING CORP.
Query Match 1.1%; Score 8; DB 8; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 765
ID ADH17965 standard; protein; 128 AA.
DE Human modified 15H12/19D12 light chain D (LCD) protein.
PN WO2003100008-A2.
PD 04-DEC-2003.
PA (SCHE) SCHERING CORP.
Query Match 1.1%; Score 8; DB 8; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 766
ID ADH17934 standard; protein; 128 AA.
DE Human 15H12/19D12 light chain B (LCB) protein.
PN WO2003100008-A2.
PD 04-DEC-2003.
PA (SCHE) SCHERING CORP.
Query Match 1.1%; Score 8; DB 8; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 767
ID ADH17893 standard; protein; 128 AA.
DE Human 15H12/19D12 light chain variable region protein.
PN WO2003100008-A2.
PD 04-DEC-2003.
PA (SCHE) SCHERING CORP.
Query Match 1.1%; Score 8; DB 8; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 768
ID AAY7609 standard; protein; 152 AA.
DE Murine TGF-alpha homologue mutRL, SEQ ID 187.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 1.1%; Score 8; DB 3; Length 152;
Best Local Similarity 100.0%; Pred. No. 70;
RESULT 769
ID AAB55948 standard; protein; 152 AA.
DE Skin cell protein, SEQ ID NO: 187.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 1.1%; Score 8; DB 4; Length 152;
Best Local Similarity 100.0%; Pred. No. 70;
RESULT 770
ID ABB72148 standard; protein; 152 AA.

DE Murine protein isolated from skin cells SEQ ID NO: 187.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 1.1%; Score 8; DB 5; Length 152;
Best Local Similarity 100.0%; Pred. No. 70;
RESULT 771
ID AAY93714 standard; protein; 155 AA.
DE The kappa chain of immunoglobulin clone 2.1.3.
PN WO200037504-A2.
PD 29-JUN-2000.
PA (PFIZ-) PFIZER INC.
PA (ABGE-) ABGENIX INC.
Query Match 1.1%; Score 8; DB 3; Length 155;
Best Local Similarity 100.0%; Pred. No. 71;
RESULT 772
ID AAE35906 standard; protein; 155 AA.
DE Human 2.1.3 anti-CTLA-4 antibody kappa chain.
PN EP1262193-A1.
PD 04-DEC-2002.
PA (PFIZ-) PFIZER PROD INC.
Query Match 1.1%; Score 8; DB 6; Length 155;
Best Local Similarity 100.0%; Pred. No. 71;
RESULT 773
ID ADK52330 standard; protein; 157 AA.
DE Human anti-MCP-1 variable region light chain #9.
PN WO2004016769-A2.
PD 26-FEB-2004.
PA (ABGE-) ABGENIX INC.
Query Match 1.1%; Score 8; DB 8; Length 157;
Best Local Similarity 100.0%; Pred. No. 72;
RESULT 774
ID AAM41575 standard; protein; 233 AA.
DE Anti-interleukin-1 receptor type 1 antibody light chain.
PN WO2004022718-A2.
PD 18-MAR-2004.
PA (AMGE-) AMGEN INC.
Query Match 1.1%; Score 8; DB 8; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
RESULT 775
ID ABU70774 standard; protein; 235 AA.
DE Human adipocyte Selected Interacting domain, STD, #405.
PN WO200286122-A2.
PD 31-OCT-2002.
PA (HYBR-) HYBRGENICS.
Query Match 1.1%; Score 8; DB 6; Length 235;
Best Local Similarity 100.0%; Pred. No. 1e+02;
RESULT 776
ID ADN24003 standard; protein; 302 AA.
DE Bacterial polypeptide #6656.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 1.1%; Score 8; DB 8; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
RESULT 777
ID AAY93332 standard; protein; 467 AA.
DE Human EGF repeat-containing protein EGF-Hy1.
PN WO200017357-A1.
PD 30-MAR-2000.
PA (HYSE-) HYSEQ INC.
Query Match 1.1%; Score 8; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
RESULT 778
ID ABH22131 standard; protein; 596 AA.
DE Protein encoded by Prokaryotic essential gene #7658.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match 1.1%; Score 8; DB 6; Length 596;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 779
ID ADG93413 standard; protein; 807 AA.
DE Maize lipoxygenase (LOX) polypeptide #22.
PN US2003166855-A1.
PD 04-SEP-2003.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 1.1%; Score 8; DB 7; Length 807;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
RESULT 780
ID ADG93411 standard; protein; 807 AA.
DE Maize lipoxygenase (LOX) polypeptide #21.
PN US2003166855-A1.
PD 04-SEP-2003.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 1.1%; Score 8; DB 7; Length 807;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
RESULT 781
ID ABP68935 standard; protein; 859 AA.
DE Human polypeptide SEQ ID NO 982.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 1.1%; Score 8; DB 5; Length 859;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
RESULT 782
ID AAM43394 standard; protein; 1019 AA.
DE Singapore horseshoe crab factor C proenzyme (CrFC 21).
PN SG42456-A1.
PD 15-AUG-1997.
PA (UVSI-) UNIV SINGAPORE NAT.
Query Match 1.1%; Score 8; DB 2; Length 1019;
Best Local Similarity 100.0%; Pred. No. 4e+02;
RESULT 783
ID AAY05750 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN WO9915676-A1.
PD 01-APR-1999.
PA (UVSI-) UNIV SINGAPORE NAT.
Query Match 1.1%; Score 8; DB 2; Length 1019;
Best Local Similarity 100.0%; Pred. No. 4e+02;
RESULT 784
ID AAM94302 standard; protein; 1019 AA.
DE Horseshoe crab Factor C protein #2.
PN US5858706-A.
PD 12-JAN-1999.
PA (UVSI-) UNIV SINGAPORE NAT.
Query Match 1.1%; Score 8; DB 2; Length 1019;
Best Local Similarity 100.0%; Pred. No. 4e+02;
RESULT 785
ID AAY42490 standard; protein; 1019 AA.
DE Recombinant N-terminally truncated Horseshoe crab Factor C protein.
PN US5985590-A.
PD 16-NOV-1999.
PA (UVSI-) UNIV SINGAPORE NAT.
Query Match 1.1%; Score 8; DB 3; Length 1019;
Best Local Similarity 100.0%; Pred. No. 4e+02;
RESULT 786
ID AAB60935 standard; protein; 1019 AA.
DE Horseshoe crab recombinant Factor C #2.
PN WO200127289-A2.
PD 19-APR-2001.
PA (UVSI-) UNIV SINGAPORE NAT.
Query Match 1.1%; Score 8; DB 4; Length 1019;
Best Local Similarity 100.0%; Pred. No. 4e+02;
RESULT 787
ID ABP72332 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN WO2003002976-A2.
PD 09-JAN-2003.
PA (WHIK-) BIOWHITTAKER INC.
Query Match 1.1%; Score 8; DB 6; Length 1019;

Best Local Similarity 100.0%; Pred. No. 4e+02;
RESULT 788
ID ABR72334 standard; protein; 1019 AA.
DE Horsehoe crab Factor C.
PN W02003002976-A2.
PD 09-JAN-2003.
PA (WHIK) B10WHITTAKER INC.
Query Match 1.1%; Score 8; DB 6; Length 1019;
Best Local Similarity 100.0%; Pred. No. 4e+02;
RESULT 789
ID AAW43393 standard; protein; 1083 AA.
DE Singapore horsehoe crab factor C proenzyme (CrFC 26).
PN SG42456-A1.
PD 15-AUG-1997.
PA (YYSI-) UNIV SINGAPORE NAT.
Query Match 1.1%; Score 8; DB 2; Length 1083;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 790
ID AAY05749 standard; protein; 1083 AA.
DE Horsehoe crab Factor C.
PN W09915676-A1.
PD 01-APR-1999.
PA (YYSI-) UNIV SINGAPORE NAT.
Query Match 1.1%; Score 8; DB 2; Length 1083;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 791
ID AAW94301 standard; protein; 1083 AA.
DE Horsehoe crab Factor C protein #1.
PN US5858706-A.
PD 12-JAN-1999.
PA (YYSI-) UNIV SINGAPORE NAT.
Query Match 1.1%; Score 8; DB 2; Length 1083;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 792
ID AAY42489 standard; protein; 1083 AA.
DE Horsehoe crab recombinant Factor C protein.
PN US5985590-A.
PD 16-NOV-1999.
PA (YYSI-) UNIV SINGAPORE NAT.
Query Match 1.1%; Score 8; DB 3; Length 1083;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 793
ID AAB60934 standard; protein; 1083 AA.
DE Horsehoe crab recombinant Factor C #1.
PN W0200127289-A2.
PD 19-APR-2001.
PA (YYSI-) UNIV SINGAPORE NAT.
Query Match 1.1%; Score 8; DB 4; Length 1083;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 794
ID ABR72333 standard; protein; 1083 AA.
DE Horsehoe crab Factor C.
PN W02003002976-A2.
PD 09-JAN-2003.
PA (WHIK) B10WHITTAKER INC.
Query Match 1.1%; Score 8; DB 6; Length 1083;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 795
ID AAB62022 standard; protein; 1238 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12858.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PB CORP NY.
Query Match 1.1%; Score 8; DB 4; Length 1238;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
RESULT 796
ID AAB94754 standard; protein; 1316 AA.
DE Human protein sequence SEQ ID NO:15811.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 1.1%; Score 8; DB 4; Length 1316;
Best Local Similarity 100.0%; Pred. No. 5e+02;
RESULT 797
ID ADF28695 standard; protein; 1484 AA.
DE Neurological therapy-related protein - SED ID 605.
PN W02003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 1.1%; Score 8; DB 7; Length 1484;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
RESULT 798
ID ADF28692 standard; protein; 1487 AA.
DE Human peroxidase-like protein - SED ID 602.
PN W02003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 1.1%; Score 8; DB 7; Length 1487;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
RESULT 799
ID ADS10671 standard; protein; 1507 AA.
DE Human therapeutic protein - SEQ ID 908.
PN W02004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 1.1%; Score 8; DB 8; Length 1507;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 800
ID ADF28708 standard; protein; 1538 AA.
DE Peroxidase-like protein - SED ID 618.
PN W02003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 1.1%; Score 8; DB 7; Length 1538;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 801
ID ADS10672 standard; protein; 1538 AA.
DE Human therapeutic protein - SEQ ID 909.
PN W02004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 1.1%; Score 8; DB 8; Length 1538;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 802
ID ADN39112 standard; protein; 3557 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:430.
PN W02003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 1.1%; Score 8; DB 7; Length 3557;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 803
ID ADN39979 standard; protein; 3557 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C349.
PN W02003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 1.1%; Score 8; DB 7; Length 3557;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 804
ID AAB37944 standard; protein; 3570 AA.
DE Human CGPD-33 protein.
PN W02003050253-A2.
PD 19-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.1%; Score 8; DB 7; Length 3570;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 805
ID AAE20146 standard; protein; 3571 AA.
DE Human CB/Cab complement receptor-like protein.
PN W0200210388-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 1.1%; Score 8; DB 5; Length 3571;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 806

```
ID ADL22512 standard; protein; 3571 AA.
DE Human CNGH0004 antibody protein.
PN WO2004003147-A2.
PD 08-JAN-2004.
PA (CENZ ) CENTOCOR INC.
Query Match
  Best Local Similarity 1.1%; Score 8; DB 8; Length 3571;
  Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 807
ID ADO75791 standard; peptide; 10 AA.
DE Human 213P1F11 HLA motif bearing epitope #9890.
PN US2004019915-A1.
PD 29-JAN-2004.
PA (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 8; Length 10;
  Best Local Similarity 100.0%; Pred. No. 56;
RESULT 808
ID ADO77622 standard; peptide; 15 AA.
DE Human 213P1F11 HLA motif bearing epitope #11721.
PN US2004019915-A1.
PD 29-JAN-2004.
PA (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 8; Length 15;
  Best Local Similarity 100.0%; Pred. No. 81;
RESULT 809
ID AAR71665 standard; peptide; 30 AA.
DE Modified urinary plasminogen activator residues 159-188.
PN UP07039374-A.
PD 10-FEB-1995.
PA (SUMV ) SUMITOMO SEIYAKU KK.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 2; Length 30;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
RESULT 810
ID ABB78761 standard; protein; 43 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 4052.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 6; Length 43;
  Best Local Similarity 100.0%; Pred. No. 2.1e+02;
RESULT 811
ID AAM23655 standard; protein; 49 AA.
DE Human EST encoded protein SEQ ID NO: 1380.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 4; Length 49;
  Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 812
ID AOC3379 standard; protein; 49 AA.
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:3361.
PN WO2003028271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 7; Length 49;
  Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 813
ID AAM06451 standard; protein; 50 AA.
DE Human foetal protein, SEQ ID NO: 182.
PN WO200155339-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 4; Length 50;
  Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 814
ID AAG91460 standard; protein; 54 AA.
DE C glutamincum protein fragment SEQ ID NO: 5214.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW ) KYOWA HAKKO KOGYO KK.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 4; Length 54;
  Best Local Similarity 100.0%; Pred. No. 2.6e+02;
RESULT 815
ID AAY02522 standard; protein; 56 AA.
DE Clone selected after panning a NNK library of the invention.
PN WO9920749-A1.
PD 29-APR-1999.
PA (MED-) MEDICAL RES COUNCIL.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 2; Length 56;
  Best Local Similarity 100.0%; Pred. No. 2.7e+02;
RESULT 816
ID ABM71426 standard; protein; 59 AA.
DE Staphylococcus aureus protein #666.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 6; Length 59;
  Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 817
ID AAU48293 standard; protein; 62 AA.
DE Propionibacterium acnes immunogenic protein #9189.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 4; Length 62;
  Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 818
ID AAM4812 standard; protein; 62 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9488.
PN WO200303515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 6; Length 62;
  Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 819
ID ABB42063 standard; peptide; 63 AA.
DE Peptide #9569 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 4; Length 63;
  Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 820
ID AAM75756 standard; protein; 63 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 36062.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 4; Length 63;
  Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 821
ID AAM62944 standard; protein; 63 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 35049.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 4; Length 63;
  Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 822
ID ABG57494 standard; peptide; 63 AA.
DE Human liver peptide, SEQ ID NO 36142.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
  Best Local Similarity 1.0%; Score 7; DB 4; Length 63;
  Best Local Similarity 100.0%; Pred. No. 3e+02;
```


Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 823
ID AAB35189 standard; protein; 74 AA.
DE Human deaminase-like ORF4162 protein, SEQ ID NO:8324.
PN W0200190366-A2.
PD 29-NOV-2001.
PA (CURA-) CURAGEN CORP.
Query Match 1.0%; Score 7; DB 5; Length 74;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
RESULT 824
ID AAV66472 standard; protein; 76 AA.
DE Propionibacterium acnes immunogenic protein #27368.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
RESULT 825
ID AAV67610 standard; protein; 76 AA.
DE Propionibacterium acnes immunogenic protein #28506.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
RESULT 826
ID AAB62991 standard; protein; 76 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #27667.
PN W0200303515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
RESULT 827
ID AAB64129 standard; protein; 76 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #28805.
PN W0200303515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
RESULT 828
ID AAB20816 standard; protein; 79 AA.
DE Human gene 5 encoded secreted protein HSLG75, SEQ ID NO:78.
PN W0200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 5; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 829
ID AAB64651 standard; protein; 79 AA.
DE Human albumin fusion protein #1326.
PN W0200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 5; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 830
ID AAV77918 standard; protein; 79 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1400.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
Query Match 1.0%; Score 7; DB 8; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 831
ID AAB64695 standard; protein; 81 AA.
DE Propionibacterium acnes immunogenic polypeptide #29371.
PN W0200303515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 6; Length 81;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 832
ID ADF05104 standard; protein; 83 AA.
DE Bacterial polypeptide #1217.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 83;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
RESULT 833
ID AAG03800 standard; protein; 103 AA.
DE Human secreted protein, SEQ ID NO: 7881.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GERT-) GENSET.
Query Match 1.0%; Score 7; DB 3; Length 103;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
RESULT 834
ID AAY64590 standard; peptide; 105 AA.
DE Nonclassical cadherin extracellular domain SEQ ID NO:18.
PN W09957149-A2.
PD 11-NOV-1999.
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
Query Match 1.0%; Score 7; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
RESULT 835
ID AAB06753 standard; protein; 107 AA.
DE Human ORFX protein sequence SEQ ID NO:13488.
PN W0200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 1.0%; Score 7; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
RESULT 836
ID AAU27656 standard; protein; 108 AA.
DE Human protein AFP548753.
PN W020016748-A2.
PD 13-SEP-2001.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match 1.0%; Score 7; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
RESULT 837
ID AAD32136 standard; protein; 108 AA.
DE Mutant B licheniformis secreted polypeptide Seqid 106.
PN W02003093453-A2.
PD 13-NOV-2003.
PA (NOVO-) NOVOTYMS AS.
Query Match 1.0%; Score 7; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
RESULT 838
ID AAM99113 standard; protein; 111 AA.
DE Bovine zeta 2 prethrombin 2.
PN W09855130-A1.
PD 10-DEC-1998.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 5e+02;
RESULT 839
ID ABO74597 standard; protein; 111 AA.
DE Pseudomonas aeruginosa polypeptide #6772.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 111;
Best Local Similarity 100.0%; Pred. No. 5e+02;
RESULT 840
ID AAM99115 standard; protein; 116 AA.
DE Human zeta 2 prethrombin 2.
PN W09855130-A1.
PD 10-DEC-1998.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;

RESULT 841
ID AAG26792 standard; protein: 117 AA.
DE Zea mays protein fragment SEQ ID NO: 31379.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.2e+02; Length 117;
RESULT 842
ID AAG51373 standard; protein: 121 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65194.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e+02; Length 121;
RESULT 843
ID AAG26791 standard; protein: 121 AA.
DE Zea mays protein fragment SEQ ID NO: 31378.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e+02; Length 121;
RESULT 844
ID ABO73690 standard; protein: 121 AA.
DE Pseudomonas aeruginosa polypeptide #5865.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e+02; Length 121;
RESULT 845
ID AAG11631 standard; protein: 128 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 10420.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.7e+02; Length 128;
RESULT 846
ID AAG51372 standard; protein: 128 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65193.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.7e+02; Length 128;
RESULT 847
ID AAG26790 standard; protein: 142 AA.
DE Zea mays protein fragment SEQ ID NO: 31377.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Length 142;
RESULT 848
ID ABO63944 standard; protein: 142 AA.
DE Klebsiella pneumoniae polypeptide seqid 10461.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Length 142;
RESULT 849
ID AAW41967 standard; protein: 144 AA.
DE Flea serine protease SEQ ID NO: 81.
PN WO9740058-A1.
PD 30-OCT-1997.
PA (HESK-) HESKA CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Length 144;
RESULT 850
ID AAB50629 standard; protein: 144 AA.
DE Flea serine protease PFSPP3-144 protein sequence #153.
PN US6150125-A.
PD 21-NOV-2000.
PA (HESK-) HESKA CORP.
Query Match
1.0%; Score 7; DB 2; Length 144;
1.0%; Score 7; DB 4; Length 144;

Best Local Similarity 100.0%; Pred. No. 6.3e+02; Length 144;
RESULT 851
ID AAF64494 standard; protein: 148 AA.
DE Propionibacterium acnes immunogenic protein #25390.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 6.5e+02; Length 148;
RESULT 852
ID AAM61013 standard; protein: 148 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #25689.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 6.5e+02; Length 148;
RESULT 853
ID AAG51371 standard; protein: 151 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65192.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 100.0%; Pred. No. 6.6e+02; Length 151;
RESULT 854
ID AD145291 standard; protein: 164 AA.
DE Rice isoprenoid biosynthesis-associated protein #111.
PN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG/) LANGE B M.
PA (GHAS/) GHASSEMILAN M.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKER D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.1e+02; Length 164;
RESULT 855
ID AAY34950 standard; protein: 172 AA.
DE Amino acid sequence of a Chlamydia pneumoniae protein.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e+02; Length 172;
RESULT 856
ID ABO39246 standard; protein: 172 AA.
DE Protein encoded by Prokaryotic essential gene #24773.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e+02; Length 172;
RESULT 857
ID AAG51370 standard; protein: 184 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65190.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.9e+02; Length 184;
RESULT 858
ID ADC97109 standard; protein: 187 AA.
DE E. faecium protein sequence SEQ ID 6736.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
1.0%; Score 7; DB 7; Length 187;
1.0%; Score 7; DB 7; Length 187;

```

Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 859
ID AAU25597 standard; protein: 194 AA.
DE Human G Protein-Coupled Receptor (GPCR) polypeptide #44.
PN W0200162797-A2.
PD 30-AUG-2001.
PA (PHAA ) PHARMACIA & UPJOHN CO.
Query Match 1.0%; Score 7; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
RESULT 860
ID AAU29491 standard; protein: 200 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #112.
PN W0200168858-A2.
PD 20-SEP-2001.
PA (PHAA ) PHARMACIA & UPJOHN CO.
Query Match 1.0%; Score 7; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
RESULT 861
ID ABG60779 standard; protein: 200 AA.
DE Novel G protein coupled receptor (nGCPR-X) #112.
PN US2002058306-A1.
PD 16-MAY-2002.
PA (VOGE/) VOGELI G.
Query Match 1.0%; Score 7; DB 5; Length 200;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
RESULT 862
ID ABB65610 standard; protein: 202 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23622.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (BEKE ) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 202;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
RESULT 863
ID ABR09068 standard; protein: 202 AA.
DE Human protein useful for treating neurological disease Seq 2574.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.0%; Score 7; DB 8; Length 202;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
RESULT 864
ID AAU45202 standard; protein: 209 AA.
DE Propionibacterium acnes immunogenic protein #6098.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (COR1-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 865
ID ABM41721 standard; protein: 209 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #6397.
PN W02003033515-A1.
PD 24-APR-2003.
PA (COR1-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 6; Length 209;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 866
ID AAY35451 standard; protein: 210 AA.
DE Chlamydia pneumoniae transmembrane protein sequence.
PN W09927105-A2.
PD 03-JUN-1999.
PA (GEBT ) GENSET.
Query Match 1.0%; Score 7; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 867
ID ABU27599 standard; protein: 210 AA.
DE Protein encoded by Prokaryotic essential gene #13126.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 210;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 868
ID ADS41665 standard; protein: 210 AA.
DE Bacterial polypeptide #20095.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 1.0%; Score 7; DB 8; Length 210;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 869
ID ABU49962 standard; protein: 211 AA.
DE Protein encoded by Prokaryotic essential gene #35489.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 211;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 870
ID AAU34556 standard; protein: 212 AA.
DE E. coli cellular proliferation protein #137.
PN W0200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 871
ID ABU31486 standard; protein: 212 AA.
DE Protein encoded by Prokaryotic essential gene #17013.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 872
ID ABU48063 standard; protein: 212 AA.
DE Protein encoded by Prokaryotic essential gene #33590.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 873
ID ABU15066 standard; protein: 212 AA.
DE Protein encoded by Prokaryotic essential gene #593.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 874
ID ABU45471 standard; protein: 212 AA.
DE Protein encoded by Prokaryotic essential gene #30998.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 875
ID ABB54972 standard; protein: 213 AA.
DE Lactococcus lactis protein kdga.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
Query Match 1.0%; Score 7; DB 5; Length 213;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 876
ID ABU40559 standard; protein: 213 AA.
DE Protein encoded by Prokaryotic essential gene #26086.
PN W0200277183-A2.
PD 03-OCT-2002.

```

PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 213;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 877
ID ADF04315 standard; protein; 214 AA.
DE Bacterial polypeptide #428.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 214;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
RESULT 878
ID AAB65059 standard; protein; 221 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21969.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 221;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
RESULT 879
ID ADR49443 standard; protein; 221 AA.
DE Drosophila small endoplasmic reticulum resident protein 3 (smerp3).
PN EPI447412-A1.
PD 18-AUG-2004.
PA (UYUR-) UNIV UTRECHT HOLDING BV.
Query Match 1.0%; Score 7; DB 8; Length 221;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
RESULT 880
ID ABO61145 standard; protein; 226 AA.
DE Klebsiella pneumoniae polypeptide seqid 7662.
PN US610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 226;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
RESULT 881
ID AAG51369 standard; protein; 227 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65189.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
RESULT 882
ID AAB92525 standard; protein; 227 AA.
DE Human protein sequence SEQ ID NO:10677.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 1.0%; Score 7; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
RESULT 883
ID ABU40124 standard; protein; 227 AA.
DE Protein encoded by Prokaryotic essential gene #25651.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
RESULT 884
ID AAG15809 standard; protein; 228 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16207.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 228;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
RESULT 885
ID ABA1513 standard; protein; 228 AA.
DE Protein encoded by Prokaryotic essential gene #27040.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
RESULT 886
ID AAG33373 standard; protein; 230 AA.
DE Zea mays protein fragment SEQ ID NO: 40426.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 230;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
RESULT 887
ID ABU27062 standard; protein; 231 AA.
DE Protein encoded by Prokaryotic essential gene #12589.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 231;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
RESULT 888
ID AAU33655 standard; protein; 232 AA.
DE Pseudomonas aeruginosa cellular proliferation protein #99.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
RESULT 889
ID ABU15506 standard; protein; 232 AA.
DE Protein encoded by Prokaryotic essential gene #1033.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
RESULT 890
ID AAM41957 standard; protein; 233 AA.
DE Plea serine protease SEQ ID NO:27.
PN WO9740058-A1.
PD 30-OCT-1997.
PA (HESK-) HESKA CORP.
Query Match 1.0%; Score 7; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
RESULT 891
ID AAG51368 standard; protein; 234 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65188.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 234;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
RESULT 892
ID AAG15808 standard; protein; 235 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16206.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
RESULT 893
ID AAG33372 standard; protein; 237 AA.
DE Zea mays protein fragment SEQ ID NO: 40425.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 237;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 894
ID ABU49459 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #34986.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 239;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 895
ID AAG33371 standard; protein; 241 AA.
DE Zea mays protein fragment SEQ ID NO: 40424.
PN EPI033405-A2.
PD 06-SEP-2000.

Query Match 1.0%; Score 7; DB 3; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 RESULT 896
 ID ABO77745 standard; protein; 245 AA.
 DE Pseudomonas aeruginosa polypeptide #9920.
 PN US651795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 1.0%; Score 7; DB 7; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 RESULT 897
 ID ADC73285 standard; protein; 254 AA.
 DE Human 187H H protein - SEQ ID 11.
 PN WO2003060765-A1.
 PD 24-JUL-2003.
 PA (AJIN) AJINOMOTO CO INC.
 PA (UMEX/) UMEYAMA H.
 Query Match 1.0%; Score 7; DB 7; Length 254;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 898
 ID ADK17097 standard; protein; 254 AA.
 DE Nonoarchaeum equitans cancer-associated (CA) protein #524.
 PN WO2003093434-A2.
 PD 13-NOV-2003.
 PA (DIVE-) DIVERSA CORP.
 Query Match 1.0%; Score 7; DB 8; Length 254;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 899
 ID ADL05143 standard; protein; 255 AA.
 DE M. catarrhalis protein #909.
 PN US6673910-B1.
 PD 06-JAN-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 1.0%; Score 7; DB 8; Length 255;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 900
 ID AAU38252 standard; protein; 257 AA.
 DE Salmonella typhi cellular proliferation protein #143.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 1.0%; Score 7; DB 4; Length 257;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 901
 ID ADA35762 standard; protein; 257 AA.
 DE Actinobacter baumannii protein #2923.
 PN US6562958-B1.
 PD 13-MAY-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 1.0%; Score 7; DB 6; Length 257;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 902
 ID AAG15807 standard; protein; 258 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 16205.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.0%; Score 7; DB 3; Length 258;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 903
 ID AAM11545 standard; protein; 259 AA.
 DE Human thrombin Asn99 mutant.
 PN WO9641868-A2.
 PD 27-DEC-1996.
 PA (IMMO) IMMONO AG.
 Query Match 1.0%; Score 7; DB 2; Length 259;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 904
 ID ABP60565 standard; protein; 259 AA.
 DE Human thrombin variant W215A/E217A B-chain.
 PN WO2002100337-A2.
 PD 19-DEC-2002.
 PA (UYEM-) UNIV EMORY.
 Query Match 1.0%; Score 7; DB 6; Length 259;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 905
 ID ABP60563 standard; protein; 259 AA.
 DE Human thrombin variant W215A B-chain.
 PN WO2002100337-A2.
 PD 19-DEC-2002.
 PA (UYEM-) UNIV EMORY.
 Query Match 1.0%; Score 7; DB 6; Length 259;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 906
 ID AAW72891 standard; protein; 265 AA.
 DE Mycobacterium tuberculosis antigen CFP29.
 PN WO9844119-A1.
 PD 08-OCT-1998.
 PA (STAT-) STATENS SERUM INST.
 Query Match 1.0%; Score 7; DB 2; Length 265;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 907
 ID AAY21908 standard; protein; 265 AA.
 DE Amino acid sequence of antigen CFP29.
 PN WO9924577-A1.
 PD 20-MAY-1999.
 PA (STAT-) STATENS SERUM INST.
 Query Match 1.0%; Score 7; DB 2; Length 265;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 908
 ID AAM41956 standard; protein; 266 AA.
 DE Flea serine protease SEQ ID NO:24.
 PN WO9740058-A1.
 PD 30-OCT-1997.
 PA (HESK-) HESKA CORP.
 Query Match 1.0%; Score 7; DB 2; Length 266;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 909
 ID AAO17669 standard; protein; 266 AA.
 DE B tropicalis allergen B1oc 3 protein SEQ ID NO: 4.
 PN WO200230968-A1.
 PD 18-APR-2002.
 PA (UYST-) UNIV SINGAPORE NAT.
 Query Match 1.0%; Score 7; DB 5; Length 266;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 910
 ID AAO17668 standard; protein; 266 AA.
 DE B tropicalis allergen B1oc 3 protein SEQ ID NO: 2.
 PN WO200230968-A1.
 PD 18-APR-2002.
 PA (UYST-) UNIV SINGAPORE NAT.
 Query Match 1.0%; Score 7; DB 5; Length 266;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 911
 ID AAB62510 standard; protein; 268 AA.
 DE Flea serine protease P1SP32_268.
 PN US6204010-B1.
 PD 20-MAR-2001.
 PA (HESK-) HESKA CORP.
 Query Match 1.0%; Score 7; DB 4; Length 268;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 912
 ID ADJ69394 standard; protein; 271 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID1200.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match 1.0%; Score 7; DB 7; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 913
 ID ADQ21743 standard; protein; 271 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4563.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 1.0%; Score 7; DB 8; Length 271;

RESULT 923	ID AAR76035 standard; protein; 295 AA.	
DE Mutant thrombin R233D.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 924	ID AAR74775 standard; protein; 295 AA.	
DE Wild-type thrombin.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 925	ID AAR74780 standard; protein; 295 AA.	
DE Mutant thrombin E229W.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 926	ID AAR76036 standard; protein; 295 AA.	
DE Mutant thrombin R233F.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 927	ID AAR74777 standard; protein; 295 AA.	
DE Mutant thrombin E229D.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 928	ID AAR76034 standard; protein; 295 AA.	
DE Mutant thrombin R233N.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 929	ID AAR76040 standard; protein; 295 AA.	
DE Mutant thrombin W50K.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 930	ID AAR76037 standard; protein; 295 AA.	
DE Mutant thrombin W50C.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 931	ID AAR2892 standard; protein; 295 AA.	
DE Human mature thrombin mutant Gly274Ala.		
PN DE19605126-A1.		
PD 14-AUG-1997.		
PA (BADI) BASF AG.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 932	ID AAR76035 standard; protein; 295 AA.	
DE Mutant thrombin R233D.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 933	ID AAR76036 standard; protein; 295 AA.	
DE Mutant thrombin R233F.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 934	ID AAR76037 standard; protein; 295 AA.	
DE Mutant thrombin W50C.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 935	ID AAR76034 standard; protein; 295 AA.	
DE Mutant thrombin R233N.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 936	ID AAR76036 standard; protein; 295 AA.	
DE Mutant thrombin R233F.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 937	ID AAR76037 standard; protein; 295 AA.	
DE Mutant thrombin W50C.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 938	ID AAR76034 standard; protein; 295 AA.	
DE Mutant thrombin R233N.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 939	ID AAR76037 standard; protein; 295 AA.	
DE Mutant thrombin W50C.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 940	ID AAR76037 standard; protein; 295 AA.	
DE Mutant thrombin W50C.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCI.		
Query Match	1.0%; Score 7; DB 2; Length 295;	
Best Local Similarity	100.0%; Pred. No. 1.2e+03;	
RESULT 941	ID AAR76037 standard; protein; 295 AA.	
DE Mutant thrombin W50C.		

ID AAB08633 standard; protein; 295 AA.
DE Amino acid sequence of a wild type human thrombin.
PN US6110721-A.
PD 29-AUG-2000.
PA (GILE-) GILEAD SCI INC.
Query Match 1.0%; Score 7; DB 3; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 933
ID AAB60562 standard; protein; 295 AA.
DE Human thrombin variant W215A.
PN WO2002100337-A2.
PD 19-DEC-2002.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 6; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 934
ID AAB60564 standard; protein; 295 AA.
DE Human thrombin variant W215A/E217A.
PN WO2002100337-A2.
PD 19-DEC-2002.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 6; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 935
ID ADS11062 standard; protein; 295 AA.
DE Human therapeutic protein - SEQ ID 1299.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 1.0%; Score 7; DB 8; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 936
ID AAO17678 standard; protein; 296 AA.
DE B tropicalis allergen Bloc 3 polymorphic variant protein SEQ ID NO: 40.
PN WO200230968-A1.
PD 18-APR-2002.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 1.0%; Score 7; DB 5; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 937
ID AAO17676 standard; protein; 296 AA.
DE B tropicalis allergen Bloc 3 polymorphic variant protein SEQ ID NO: 38.
PN WO200230968-A1.
PD 18-APR-2002.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 1.0%; Score 7; DB 5; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 938
ID AAO17677 standard; protein; 296 AA.
DE B tropicalis allergen Bloc 3 polymorphic variant protein SEQ ID NO: 39.
PN WO200230968-A1.
PD 18-APR-2002.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 1.0%; Score 7; DB 5; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 939
ID AAW99107 standard; protein; 308 AA.
DE Bovine prethrombin 2.
PN WO9855130-A1.
PD 10-DEC-1998.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 940
ID AAW99109 standard; protein; 308 AA.
DE Human prethrombin 2.
PN WO9855130-A1.
PD 10-DEC-1998.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 941
ID AAB87820 standard; protein; 308 AA.

DE Mouse T2R26 amino acid sequence SEQ ID NO:155.
PN WO200118050-A2.
PD 15-MAR-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 1.0%; Score 7; DB 4; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 942
ID ADR29216 standard; protein; 308 AA.
DE Taste receptor modulation-related mouse T2R26 protein sequence SeqID155.
PN WO2004069191-A2.
PD 19-AUG-2004.
PA (SENO-) SENOMYX INC.
Query Match 1.0%; Score 7; DB 8; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 943
ID ADC94558 standard; protein; 310 AA.
DE E. faecium protein sequence SEQ ID 4185.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 944
ID ABR52886 standard; protein; 312 AA.
DE Epi258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 1.0%; Score 7; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 945
ID ADK62400 standard; protein; 312 AA.
DE Disease treating protein complex-derived protein #326.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 1.0%; Score 7; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 946
ID ADC73300 standard; protein; 313 AA.
DE Stereosestructure-related IBTH protein.
PN WO2003060765-A1.
PD 24-JUL-2003.
PA (AJIN) AJINOMOTO CO INC.
Query Match 1.0%; Score 7; DB 7; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 947
ID AAB72885 standard; protein; 314 AA.
DE Murine ztrypl.
PN WO200112788-A2.
PD 22-FEB-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 1.0%; Score 7; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 948
ID ABU62253 standard; protein; 314 AA.
DE Mouse tryptase-like polypeptide Ztryp-1.
PN US6514741-B1.
PD 04-FEB-2003.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 1.0%; Score 7; DB 6; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 949
ID ABR62454 standard; protein; 314 AA.
DE Bovine recombinant prethrombin-2, expressed in Escherichia coli.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIT) LILLY & CO ELI.
Query Match 1.0%; Score 7; DB 7; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 950

```
ID ABR62456 standard; protein; 314 AA.  
DE Bovine Factor Xa activated recombinant prethrombin-2.  
PN WO2003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 951  
ID ABR62453 standard; protein; 314 AA.  
DE Bovine thrombin.  
PN WO2003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 952  
ID ABR62450 standard; protein; 314 AA.  
DE Bovine recombinant prethrombin-2, expressed in Escherichia coli.  
PN WO2003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 953  
ID ADC17377 standard; protein; 314 AA.  
DE Mouse serine protease ztrypl.  
PN US2003119035-A1.  
PD 26-JUN-2003.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 1.0%; Score 7; DB 7; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 954  
ID ABP41695 standard; protein; 324 AA.  
DE Human ovarian antigen HNTB23, SEQ ID NO:2827.  
PN WO20020677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 5; Length 324;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 955  
ID ADS27176 standard; protein; 330 AA.  
DE Bacterial polypeptide #16209.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 330;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 956  
ID ADS26796 standard; protein; 330 AA.  
DE Bacterial polypeptide #15829.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 330;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 957  
ID AAB87793 standard; protein; 332 AA.  
DE Rat T2R13 amino acid sequence SEQ ID NO:101.  
PN WO200118050-A2.  
PD 15-MAR-2001.  
PA (PRGC ) UNIV CALIFORNIA  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 1.0%; Score 7; DB 4; Length 332;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 958  
ID ADR29162 standard; protein; 332 AA.  
DE Taste receptor modulation-related rat T2R13 protein sequence SeqID101.  
PN WO2004069191-A2.  
PD 19-AUG-2004.  
PA (SENO-) SENOMYX INC.  
Query Match 1.0%; Score 7; DB 8; Length 332;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 959  
ID ADS26428 standard; protein; 332 AA.  
DE Bacterial polypeptide #15461.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 332;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 960  
ID ADJ49544 standard; protein; 336 AA.  
DE O11-associated gene related protein #1044.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match 1.0%; Score 7; DB 8; Length 336;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 961  
ID ADJ49561 standard; protein; 338 AA.  
DE O11-associated gene related protein #1061.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match 1.0%; Score 7; DB 8; Length 338;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 962  
ID ADC31358 standard; protein; 357 AA.  
DE Human novel polypeptide sequence, SEQ ID NO:1440.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.0%; Score 7; DB 7; Length 357;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 963  
ID ADR09339 standard; protein; 357 AA.  
DE Human protein useful for treating neurological disease Seq 2845.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 1.0%; Score 7; DB 8; Length 357;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 964  
ID ABR62452 standard; protein; 362 AA.  
DE Bovine recombinant prethrombin-2, expressed in CHO cells.  
PN WO2003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 362;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 965  
ID AAY38815 standard; protein; 375 AA.  
DE Neisseria meningitidis strain A antigen encoded by ORF146.  
PN WO9924578-A2.  
PD 20-MAY-1999.  
PA (CHIR-) CHIRON SPA.
```


Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 375;
PA (CREA/) CREA R.
RESULT 966
ID AAY38814 standard; protein; 375 AA.
DE Neisseria meningitidis antigen encoded by ORF146.
PN W09924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 375;
RESULT 967
ID AAY38817 standard; protein; 375 AA.
DE Neisseria gonorrhoeae antigenic protein encoded by ORF146.
PN W09924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 375;
RESULT 968
ID AAY75445 standard; protein; 375 AA.
DE Neisseria gonorrhoeae ORF 706 protein sequence SEQ ID NO:2364.
PN W09957280-A2.
PD 11-NOV-1999.
PA (CHIR-) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 375;
RESULT 969
ID AAY75446 standard; protein; 375 AA.
DE Neisseria meningitidis ORF 706 protein sequence SEQ ID NO:2366.
PN W09957280-A2.
PD 11-NOV-1999.
PA (CHIR-) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 375;
RESULT 970
ID AAY75447 standard; protein; 375 AA.
DE Neisseria meningitidis ORF 706 protein sequence SEQ ID NO:2368.
PN W09957280-A2.
PD 11-NOV-1999.
PA (CHIR-) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 375;
RESULT 971
ID AAY72957 standard; protein; 375 AA.
DE Neisseria meningitidis virulence protein #47.
PN W0200185772-A2.
PD 15-NOV-2001.
PA (MICR-) MICROSCIENCE LTD.
Query Match
Best Local Similarity 100.0%; Score 7; DB 5; Length 375;
RESULT 972
ID AAR41797 standard; protein; 376 AA.
DE CD4/thrombin fusion protein.
PN W09318162-A1.
PD 16-SEP-1993.
PA (CREA-) CREGEN INC.
Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 376;
RESULT 973
ID AAY42789 standard; protein; 376 AA.
DE Human CD4/thrombin fusion protein.
PN US5961973-A.
PD 05-OCT-1999.
PA (CREA/) CREA R.
Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 376;
RESULT 974
ID AAU10703 standard; protein; 376 AA.
DE Human CD4-thrombin fusion protein.
PN US6287561-B1.
PD 11-SEP-2001.
PA (CREA/) CREA R.
Query Match
Best Local Similarity 100.0%; Score 7; DB 5; Length 376;
RESULT 975
ID AAG21667 standard; protein; 398 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24304.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 398;
RESULT 976
ID AB080228 standard; protein; 399 AA.
DE Pseudomonas aeruginosa polypeptide #12403.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 100.0%; Score 7; DB 7; Length 399;
RESULT 977
ID AAY38816 standard; protein; 409 AA.
DE Neisseria gonorrhoeae antigen encoded by partial ORF146.
PN W09924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 409;
RESULT 978
ID ABP80460 standard; protein; 409 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 7450.
PN W0200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 100.0%; Score 7; DB 6; Length 409;
RESULT 979
ID ABP79601 standard; protein; 409 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 5732.
PN W0200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 100.0%; Score 7; DB 6; Length 409;
RESULT 980
ID ABP37254 standard; protein; 409 AA.
DE Protein encoded by prokaryotic essential gene #22781.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 100.0%; Score 7; DB 6; Length 409;
RESULT 981
ID ADD15316 standard; protein; 420 AA.
DE Fruitfly odourant receptor protein (Seqid 68).
PN W02003020913-A2.
PD 13-MAR-2003.
PA (SENT-) SENTIGEN CORP.
Query Match
Best Local Similarity 100.0%; Score 7; DB 7; Length 420;
RESULT 982
ID AB065926 standard; protein; 422 AA.
DE Klebsiella pneumoniae polypeptide seqid 12443.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 100.0%; Score 7; DB 7; Length 422;
RESULT 983
ID AAB03444 standard; protein; 426 AA.
DE Candida albicans essential growth protein #2.
PN W0200034481-A2.
PD 15-JUN-2000.
PA (JANC) JANSSEN PHARM NV.

```
Query Match
Best Local Similarity 1.0%; Score 7; DB 3; Length 426;
RESULT 984
ID ABO61095 standard; protein; 437 AA.
DE Klebsiella pneumoniae polypeptide seqid 7612.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENC-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 1.0%; Score 7; DB 7; Length 437;
RESULT 985
ID ABU34680 standard; protein; 443 AA.
DE Protein encoded by Prokaryotic essential gene #20207.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 443;
RESULT 986
ID ABU17062 standard; protein; 444 AA.
DE Protein encoded by Prokaryotic essential gene #2589.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 444;
RESULT 987
ID ADA34407 standard; protein; 448 AA.
DE Acinetobacter baumannii protein #1568.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENC-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 448;
RESULT 988
ID AAG21666 standard; protein; 452 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24303.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 1.0%; Score 7; DB 3; Length 452;
RESULT 989
ID AAB26435 standard; protein; 456 AA.
DE Drosophila melanogaster odorant receptor DOR28.
PN W020050566-A2.
PD 31-AUG-2000.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match
Best Local Similarity 1.0%; Score 7; DB 3; Length 456;
RESULT 990
ID ABB64797 standard; protein; 456 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21183.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 1.0%; Score 7; DB 4; Length 456;
RESULT 991
ID ADJ32828 standard; protein; 459 AA.
DE Human prethrombin protein.
PN US200323414-A1.
PD 18-DEC-2003.
PA (MOOR/) MOORE M D.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 459;
RESULT 992
ID ABG33733 standard; protein; 461 AA.
DE Protein encoded by Prokaryotic essential gene #19260.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 461;
RESULT 993
ID ABU36990 standard; protein; 461 AA.
DE Protein encoded by Prokaryotic essential gene #22517.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 461;
RESULT 994
ID AAB60460 standard; protein; 463 AA.
DE Human cell cycle and proliferation protein CCYPR-8, SEQ ID NO:8.
PN W0200107471-A2.
PD 01-FEB-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 4; Length 463;
RESULT 995
ID ADP23764 standard; protein; 463 AA.
DE PRO polypeptide SEQ ID NO:942.
PN W02004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 463;
RESULT 996
ID ABW73357 standard; protein; 465 AA.
DE Staphylococcus aureus protein #2597.
PN W0200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 465;
RESULT 997
ID ADJ50012 standard; protein; 465 AA.
DE Oil-associated gene related protein #1512.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDERUX J R.
PA (ROGE/) ROGERS J A.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 465;
RESULT 998
ID ADN21085 standard; protein; 467 AA.
DE Bacterial polypeptide #3738.
PN US2003234675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 467;
RESULT 999
ID AAG21665 standard; protein; 469 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24302.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 1.0%; Score 7; DB 3; Length 469;
RESULT 1000
ID ABW72219 standard; protein; 469 AA.
DE Staphylococcus aureus protein #1459.
PN W0200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 469;
RESULT 1001
ID ADK41715 standard; protein; 470 AA.
```

DE Soybean amino acid transporter protein.
 PN MO2003066879-A2.
 PD 14-AUG-2003.
 PA (MONS) MONSENTO TECHNOLOGY LLC.
 Query Match 1.0%; Score 7; DB 7; Length 470;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 RESULT 1002
 ID AAY20047 standard; protein; 481 AA.
 DE B. burgdorferi antigenic protein, t352.aa.
 PN MO9859071-A1.
 PD 30-DEC-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 (MEDI-) MEDIMMUNE INC.
 Query Match 1.0%; Score 7; DB 2; Length 481;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 RESULT 1003
 ID AAM68866 standard; protein; 492 AA.
 DE Photophadus lumniscens protein sequence #1963.
 PN MO200294867-A2.
 PD 28-NOV-2002.
 PA (INSP) INST PASTEUR.
 (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 1.0%; Score 7; DB 6; Length 492;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 RESULT 1004
 ID ABO84661 standard; protein; 494 AA.
 DE Mouse cancer-associated protein MP20-004.1.
 PN MO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 1.0%; Score 7; DB 8; Length 494;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 RESULT 1005
 ID AAM72030 standard; protein; 497 AA.
 DE HSV-2 strain SBS Contig ID 103 ORF#8 protein.
 PN MO9820016-A1.
 PD 14-MAY-1998.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 Query Match 1.0%; Score 7; DB 2; Length 497;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1006
 ID AAM72132 standard; protein; 497 AA.
 DE HSV-2 strain SBS Contig ID 16 ORF#8 protein.
 PN MO9820016-A1.
 PD 14-MAY-1998.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 Query Match 1.0%; Score 7; DB 2; Length 497;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1007
 ID AAY20046 standard; protein; 497 AA.
 DE B. burgdorferi antigenic protein, f352.aa.
 PN MO9859071-A1.
 PD 30-DEC-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 (MEDI-) MEDIMMUNE INC.
 Query Match 1.0%; Score 7; DB 2; Length 497;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1008
 ID ABP27287 standard; protein; 497 AA.
 DE Streptococcus polypeptide SEQ ID NO 3750.
 PN MO200234771-A2.
 PD 02-MAY-2002.
 PA (CHIR-) CHIRON SPA.
 (GENO-) INST GENOMIC RES.
 Query Match 1.0%; Score 7; DB 5; Length 497;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1009
 ID ABO23531 standard; protein; 497 AA.
 DE Borrelia burgdorferi outlier protein #1.
 PN US200303963-A1.
 PD 27-FEB-2003.
 PA (BRAH/) BRAHMACHARI S K.
 (RAMA/) RAMACHANDRAN S.

PA (NAND/) NANDI T.
 (BHIM/) BHIMARAO C.
 Query Match 1.0%; Score 7; DB 7; Length 497;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1010
 ID AAU16169 standard; protein; 498 AA.
 DE Human novel secreted protein, Seq ID 1122.
 PN MO200155322-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.0%; Score 7; DB 4; Length 498;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1011
 ID ABUS5238 standard; protein; 498 AA.
 DE Human novel polypeptide #325.
 PN US2002132753-A1.
 PD 19-SEP-2002.
 PA (ROSE/) ROSEN C A.
 (RUBE/) RUBEN S M.
 (BARA/) BARASH S C.
 Query Match 1.0%; Score 7; DB 6; Length 498;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1012
 ID ADS41994 standard; protein; 500 AA.
 DE Bacterial polypeptide #20424.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 (HINK/) HINKLE G J.
 (SLAT/) SLATER S C.
 (CHEN/) CHEN X.
 (GOLD/) GOLDMAN B S.
 Query Match 1.0%; Score 7; DB 8; Length 500;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1013
 ID ABU01365 standard; protein; 502 AA.
 DE S. pneumoniae type 4 strain protein from coding region #940.
 PN MO200277021-A2.
 PD 03-OCT-2002.
 PA (CHIR-) CHIRON SPA.
 (GENO-) INST GENOMIC RES.
 Query Match 1.0%; Score 7; DB 6; Length 502;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1014
 ID ABB81378 standard; protein; 502 AA.
 DE Streptococcus pneumoniae polypeptide SEQ ID NO 295.
 PN MO200283855-A2.
 PD 24-OCT-2002.
 PA (AMCY) AMERICAN CYANAMID CO.
 Query Match 1.0%; Score 7; DB 6; Length 502;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1015
 ID AAY00189 standard; protein; 503 AA.
 DE Enterococcus faecalis antigenic polypeptide fragment EF094.
 PN MO9850554-A2.
 PD 12-NOV-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.0%; Score 7; DB 2; Length 503;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1016
 ID ABP43408 standard; protein; 503 AA.
 DE B. faecalis EF094 antigenic fragment.
 PN US2002045737-A1.
 PD 18-APR-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.0%; Score 7; DB 5; Length 503;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1017
 ID ABB88436 standard; protein; 503 AA.
 DE E. faecalis novel protein #180.
 PN US2003017495-A1.
 PD 23-JAN-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.

```
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 503;
PA (GENO-) GENOME THERAPEUTICS CORP.
RESULT 1018
ID ABU13687 standard; protein; 503 AA.
DE Enterococcus faecalis EF040 polypeptide #180.
PN US6448043-B1.
PD 10-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 503;
RESULT 1019
ID AAB68138 standard; protein; 504 AA.
DE Amino acid sequence of a partial murine SPG4 polypeptide.
PN FR278818-A1.
PD 09-MAR-2001.
PA (CNRS ) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 1.0%; Score 7; DB 4; Length 504;
RESULT 1020
ID AAG29530 standard; protein; 508 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35152.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 1.0%; Score 7; DB 3; Length 508;
RESULT 1021
ID AAU54588 standard; protein; 509 AA.
DE Human NOVX polypeptide #47.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 509;
RESULT 1022
ID ADS22207 standard; protein; 513 AA.
DE Bacterial polypeptide #11240.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 513;
RESULT 1023
ID AAE20968 standard; protein; 517 AA.
DE Staphylococcus aureus von Willebrand factor binding protein (vmb).
PN WO200228892-A1.
PD 11-APR-2002.
PA (BIOS-) BIOSAPPRO AB.
Query Match
Best Local Similarity 1.0%; Score 7; DB 5; Length 517;
RESULT 1024
ID ABUS5877 standard; protein; 518 AA.
DE Mouse notch ligand jagged 2 protein.
PN WO20027204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 518;
RESULT 1025
ID AAE34033 standard; protein; 518 AA.
DE Murine notch ligand jagged 2 protein.
PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 518;
RESULT 1026
ID ABO75124 standard; protein; 525 AA.
DE Pseudomonas aeruginosa polypeptide #7299.
PN US6551795-B1.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 525;
PA (GENO-) GENOME THERAPEUTICS CORP.
RESULT 1027
ID ADO26850 standard; protein; 525 AA.
DE Human receptors and membrane-associated protein, REMAP-40.
PN WO2004044159-A2.
PD 27-MAY-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 525;
RESULT 1028
ID ABB58809 standard; protein; 542 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3219.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 1.0%; Score 7; DB 4; Length 542;
RESULT 1029
ID ADN21059 standard; protein; 543 AA.
DE Bacterial polypeptide #3712.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 543;
RESULT 1030
ID AAU37798 standard; protein; 553 AA.
DE Streptococcus pneumoniae cellular proliferation protein #227.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 4; Length 553;
RESULT 1031
ID AAM01018 standard; protein; 553 AA.
DE CFE 17 protein sequence.
PN WO200149721-A2.
PD 12-JUL-2001.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 1.0%; Score 7; DB 4; Length 553;
RESULT 1032
ID ABU00989 standard; protein; 553 AA.
DE S. pneumoniae type 4 strain protein from coding region #558.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 553;
RESULT 1033
ID ABU45930 standard; protein; 553 AA.
DE Protein encoded by prokaryotic essential gene #31457.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 553;
RESULT 1034
ID ADK48791 standard; protein; 553 AA.
DE Streptococcus pneumoniae protein, Seq ID NO 5306.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 553;
PA (GENO-) GENOME THERAPEUTICS CORP.
RESULT 1035
ID ABO75124 standard; protein; 525 AA.
DE Pseudomonas aeruginosa polypeptide #7299.
PN US6551795-B1.
```

RESULT 1035
ID AAG29529 standard; protein; 555 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35151.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 555;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1036
ID AAU08803 standard; protein; 556 AA.
DE Human phosphatidyl glycerol phosphate (PGP) synthase.
PN W0200164895-A2.
PD 07-SEP-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.0%; Score 7; DB 4; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1037
ID ADC14217 standard; protein; 556 AA.
DE Human enzyme ENZM-23.
PN W02003042357-A2.
PD 22-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.0%; Score 7; DB 7; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1038
ID ADJ57901 standard; protein; 556 AA.
DE Human 27411 GGP synthase protein.
PN US2004009553-A1.
PD 15-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.0%; Score 7; DB 8; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1039
ID ABP61060 standard; protein; 557 AA.
DE Lactobacillus rhamnosus HN001 polypeptide SEQ ID NO 120.
PN W0200244383-A1.
PD 06-JUN-2002.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (VIAL-) VIALACTIA BIOSCIENCE NZ LTD.
Query Match 1.0%; Score 7; DB 5; Length 557;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1040
ID ADR55837 standard; protein; 558 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 4472.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 8; Length 558;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1041
ID ABP75529 standard; protein; 563 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 713.
PN W0200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.0%; Score 7; DB 6; Length 563;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1042
ID ABU18645 standard; protein; 573 AA.
DE Protein encoded by prokaryotic essential gene #4172.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 573;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1043
ID AAR35763 standard; protein; 579 AA.
DE Prothrombin (PT).
PN W09309804-A1.
PD 27-MAY-1993.
PA (SCRI) SCRIPPS RES INST.
Query Match 1.0%; Score 7; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1044
ID AAW11544 standard; protein; 579 AA.
DE Human prothrombin Aen419 mutant.
PN W09641868-A2.
PD 27-DEC-1996.
PA (IMMO) IMMUNO AG.
Query Match 1.0%; Score 7; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1045
ID AAW11546 standard; protein; 579 AA.
DE Human prothrombin mutant (generic sequence).
PN W09641868-A2.
PD 27-DEC-1996.
PA (IMMO) IMMUNO AG.
Query Match 1.0%; Score 7; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1046
ID AAW99108 standard; protein; 579 AA.
DE Human prothrombin.
PN W09855130-A1.
PD 10-DEC-1998.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1047
ID ADI33974 standard; protein; 579 AA.
DE Human meizothrombin analogue mature protein.
PN W02004007714-A1.
PD 22-JAN-2004.
PA (ASAH) ASAH KASEI KK.
Query Match 1.0%; Score 7; DB 8; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1048
ID AAW99106 standard; protein; 582 AA.
DE Bovine prothrombin.
PN W09855130-A1.
PD 10-DEC-1998.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1049
ID AAG29528 standard; protein; 582 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35150.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 582;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1050
ID ABR62449 standard; protein; 583 AA.
DE Bovine recombinant prothrombin, expressed in Escherichia coli.
PN W02003052059-A2.
PD 26-JUN-2003.
PA (ELIT) LILLY & CO ELI.
Query Match 1.0%; Score 7; DB 7; Length 583;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1051
ID ADS28808 standard; protein; 588 AA.
DE Bacterial polypeptide #17841.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 1.0%; Score 7; DB 8; Length 588;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1052
ID ABB66001 standard; protein; 603 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24795.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 603;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1053
ID AAR38741 standard; protein; 615 AA.
DE Human prothrombin.
PN WO9313208-A1.
PD 08-JUL-1993.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 1.0%; Score 7; DB 2; Length 615;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1054
ID AAR90377 standard; protein; 615 AA.
DE Human prothrombin.
PN US5476777-A.
PD 19-DEC-1995.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 1.0%; Score 7; DB 2; Length 615;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1055
ID AAR96216 standard; protein; 615 AA.
DE Human prothrombin.
PN US5502034-A.
PD 26-MAR-1996.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 1.0%; Score 7; DB 2; Length 615;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1056
ID AAB68137 standard; protein; 616 AA.
DE Amino acid sequence of the human SPG4 polypeptide.
PN FR2798138-A1.
PD 09-MAR-2001.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 1.0%; Score 7; DB 4; Length 616;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1057
ID AAM1543 standard; protein; 622 AA.
DE Human prothrombin (wild-type).
PN WO9641868-A2.
PD 27-DEC-1996.
PA (IMMO) IMMO AG.
Query Match 1.0%; Score 7; DB 2; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1058
ID AAY4956 standard; protein; 622 AA.
DE Platelet membrane glycoprotein IIb beta subunit protein sequence.
PN WO9950454-A2.
PD 07-OCT-1999.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 1.0%; Score 7; DB 2; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1059
ID AAG74671 standard; protein; 622 AA.
DE Human F2 protein.
PN WO2003016494-A2.
PD 27-FEB-2003.
PA (VITI) VITIVITY INC.
Query Match 1.0%; Score 7; DB 6; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1060
ID ADB88551 standard; protein; 622 AA.
DE Human Factor 2, F2, protein, SEQ ID 2.
PN WO2003029493-A1.
PD 10-APR-2003.
PA (VITI) VITIVITY INC.
Query Match 1.0%; Score 7; DB 7; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1061
ID ADI18196 standard; protein; 622 AA.
DE Human coagulation factor II protein SEQ ID NO:116.
PN WO2003014381-A1.
PD 20-FEB-2003.
PA (AARA) AARAM BIOSYSTEMS INC.
Query Match 1.0%; Score 7; DB 7; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;

RESULT 1062
ID ADI33975 standard; protein; 622 AA.
DE Human meizothrombin analogue full-length protein.
PN WO2004007714-A1.
PD 22-JAN-2004.
PA (ASAH) ASAH KASEI KK.
Query Match 1.0%; Score 7; DB 8; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1063
ID ADQ30580 standard; protein; 622 AA.
DE Pancreas cancer marker - prothrombin precursor.
PN WO2004055519-A2.
PD 01-JUL-2004.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (SINO) SINGENOMAX CO LTD CHINESE NAT HUMAN GEN.
Query Match 1.0%; Score 7; DB 8; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1064
ID ABR62455 standard; protein; 625 AA.
DE Bovine prothrombin.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 1.0%; Score 7; DB 7; Length 625;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1065
ID ABR62451 standard; protein; 635 AA.
DE Bovine recombinant prothrombin, expressed in CHO cells.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 1.0%; Score 7; DB 7; Length 635;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1066
ID ADI27332 standard; peptide; 638 AA.
DE Amino acid sequence of prothrombin (G4S)3scFvalphaHA.
PN WO2004019878-A2.
PD 11-MAR-2004.
PA (COMP) COMPOUND THERAPEUTICS INC.
PA (AFEV) AFEV N B.
Query Match 1.0%; Score 7; DB 8; Length 638;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1067
ID ADI27333 standard; peptide; 638 AA.
DE Amino acid sequence of scHA(G4S)3prethrombin.
PN WO2004019878-A2.
PD 11-MAR-2004.
PA (COMP) COMPOUND THERAPEUTICS INC.
PA (AFEV) AFEV N B.
Query Match 1.0%; Score 7; DB 8; Length 638;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1068
ID ABB93056 standard; protein; 658 AA.
DE Herbicidally active polypeptide SEQ ID NO 2267.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 1.0%; Score 7; DB 5; Length 658;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1069
ID ABB58511 standard; protein; 683 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2325.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 683;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
RESULT 1070
ID AAG30915 standard; protein; 684 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37042.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 684;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Query Match
RESULT 1071
ID ABB03731 standard; protein: 696 AA.
DE Novel human diagnostic protein #3722.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e+03; Length 696;
RESULT 1072
ID ABB22196 standard; protein: 713 AA.
DE Protein encoded by Prokaryotic essential gene #7723.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 100.0%; Score 7; DB 6; Length 713;
RESULT 1073
ID ABB68587 standard; protein: 716 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 32553.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 716;
RESULT 1074
ID AAB70937 standard; protein: 763 AA.
DE S. pombe potassium transporter Ttkp protein.
PN DE19941768-A1.
PD 15-MAR-2001.
PA (LICH-) LICHTENBERG-FRATE H.
Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 763;
RESULT 1075
ID ABB70253 standard; protein: 776 AA.
DE C. neoformans amino acid sequence SEQ ID NO:3297.
PN W02003052076-A2.
PD 26-JUN-2003.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 100.0%; Score 7; DB 7; Length 776;
RESULT 1076
ID ADS1498 standard; protein: 783 AA.
DE Pseudomonas aeruginosa quorum sensing controlled protein, SEQ ID 553.
PN W02004083385-A2.
PD 30-SEP-2004.
PA (IOWA) UNIV IOWA RES FOUND.
Query Match
Best Local Similarity 100.0%; Score 7; DB 8; Length 783;
RESULT 1077
ID ADI45247 standard; protein: 784 AA.
DE Rice isoprenoid biosynthesis-associated protein #89.
PN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG/) LANGE B M.
PA (GHAS/) GHASSEMIAN M.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUT/) MOUTHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKES D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 100.0%; Score 7; DB 8; Length 784;
RESULT 1078
ID ABB58512 standard; protein: 787 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2328.
PN W0200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 787;
RESULT 1079
ID AAG90377 standard; protein: 799 AA.
DE C glutamicum protein fragment SEQ ID NO: 4131.
PN EPI108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 799;
RESULT 1080
ID ADL65785 standard; protein: 799 AA.
DE C. glutamicum RXA-associated protein #71.
PN DE10154177-A1.
PD 08-MAY-2003.
PA (BADT) BASF AG.
Query Match
Best Local Similarity 100.0%; Score 7; DB 7; Length 799;
RESULT 1081
ID ABO69076 standard; protein: 805 AA.
DE Pseudomonas aeruginosa polypeptide #1251.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 100.0%; Score 7; DB 7; Length 805;
RESULT 1082
ID AAB47019 standard; protein: 808 AA.
DE A. thaliana DGD1.
PN CA2307960-A1.
PD 06-NOV-2000.
PA (UNMS) UNIV MICHIGAN STATE.
Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 808;
RESULT 1083
ID ABB92279 standard; protein: 808 AA.
DE Herbicidially active polypeptide SEQ ID NO 1490.
PN W0200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 100.0%; Score 7; DB 5; Length 808;
RESULT 1084
ID ADB95044 standard; protein: 808 AA.
DE A. thaliana protein 21878 #SEQ ID 42.
PN W0200308440-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 100.0%; Score 7; DB 7; Length 808;
RESULT 1085
ID ADU63822 standard; protein: 808 AA.
DE Plant lipid metabolism protein PK239 SEQ ID NO:24.
PN W02004013304-A2.
PD 12-FEB-2004.
PA (BADT) BASF PLANT SCI GMBH.
Query Match
Best Local Similarity 100.0%; Score 7; DB 8; Length 808;
RESULT 1086
ID AAM07872 standard; protein: 859 AA.
DE Aluminium resistance gene ALR1.
PN W09634959-A1.
PD 07-NOV-1996.
PA (AUCC-) AUCCLAND UNISERVICES LTD.
Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 859;
RESULT 1087
ID ADB08613 standard; protein: 892 AA.
DE Novel protein (useful for identifying genetic disorders) #768.
PN W02003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.

Query Match 1.0%; Score 7; DB 7; Length 892;
PA Best Local Similarity 100.0%; Pred. No. 3.3e+03;
RESULT 1088
ID ADE31112 standard; protein; 912 AA.
DE Human diagnostic and therapeutic polypeptide (DITHP), SEQ ID NO 244.
PN WO2003062376-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.0%; Score 7; DB 7; Length 912;
PA Best Local Similarity 100.0%; Pred. No. 3.4e+03;
RESULT 1089
ID ABB65063 standard; protein; 921 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21981.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 921;
PA Best Local Similarity 100.0%; Pred. No. 3.4e+03;
RESULT 1090
ID ABB62769 standard; protein; 984 AA.
DE Protein fragment #6 of S. roseosporus biosynthetic gene cluster.
PN WO200259322-A2.
PD 01-AUG-2002.
PA (MIAO/) MIAO V P W.
PA (BRIA/) BRIAN P.
PA (BALU/) BALUTZ R H.
PA (SILV/) SILVA C J.
Query Match 1.0%; Score 7; DB 5; Length 984;
PA Best Local Similarity 100.0%; Pred. No. 3.6e+03;
RESULT 1091
ID AD772180 standard; protein; 984 AA.
DE Streptomyces roseosporus daptomycin biosynthesis gene cluster protein #6.
PN WO2003014297-A2.
PD 20-FEB-2003.
PA (CUBI-) CUBIST PHARM INC.
Query Match 1.0%; Score 7; DB 7; Length 984;
PA Best Local Similarity 100.0%; Pred. No. 3.6e+03;
RESULT 1092
ID AM57327 standard; protein; 995 AA.
DE Recombinant protein production method related polypeptide SEQ ID NO: 8.
PN WO2004027067-A2.
PD 01-APR-2004.
PA (CYMO-) CYMP AS.
Query Match 1.0%; Score 7; DB 8; Length 995;
PA Best Local Similarity 100.0%; Pred. No. 3.7e+03;
RESULT 1093
ID ABB93966 standard; protein; 1047 AA.
DE Herbicidally active polypeptide SEQ ID NO 3177.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB-) BAYER AG.
Query Match 1.0%; Score 7; DB 5; Length 1047;
PA Best Local Similarity 100.0%; Pred. No. 3.8e+03;
RESULT 1094
ID ABM83005 standard; protein; 1061 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3254.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 1.0%; Score 7; DB 8; Length 1061;
PA Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1095
ID AAY0188 standard; protein; 1074 AA.
DE Enterococcus faecalis protein EF094.
PN WO9850554-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 2; Length 1074;
PA Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1096
ID AAY0206 standard; protein; 1074 AA.
DE Enterococcus faecalis protein EF102.
PN WO9850554-A2.

PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 2; Length 1074;
PA Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1097
ID ABB43425 standard; protein; 1074 AA.
DE E faecalis EF102 protein.
PN US2002045737-A1.
PD 18-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 5; Length 1074;
PA Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1098
ID ABB43407 standard; protein; 1074 AA.
DE E faecalis EF094 protein.
PN US2002045737-A1.
PD 18-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 5; Length 1074;
PA Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1099
ID ABB88435 standard; protein; 1074 AA.
DE E. faecalis novel protein #179.
PN US2003017495-A1.
PD 23-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 6; Length 1074;
PA Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1100
ID ABB88453 standard; protein; 1074 AA.
DE E. faecalis novel protein #197.
PN US2003017495-A1.
PD 23-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 6; Length 1074;
PA Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1101
ID ABU13686 standard; protein; 1074 AA.
DE Enterococcus faecalis EF040 polypeptide #179.
PN US6448043-B1.
PD 10-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 6; Length 1074;
PA Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1102
ID ABU13704 standard; protein; 1074 AA.
DE Enterococcus faecalis EF040 polypeptide #197.
PN US6448043-B1.
PD 10-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 6; Length 1074;
PA Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1103
ID ADH87879 standard; protein; 1096 AA.
DE Enterococcus faecalis polypeptide #2359.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 1.0%; Score 7; DB 7; Length 1096;
PA Best Local Similarity 100.0%; Pred. No. 4e+03;
RESULT 1104
ID AAE37912 standard; protein; 1104 AA.
DE Human CGPD-1 protein.
PN WO2003050253-A2.
PD 19-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.0%; Score 7; DB 7; Length 1104;
PA Best Local Similarity 100.0%; Pred. No. 4e+03;
RESULT 1105
ID AAY9613 standard; protein; 1140 AA.
DE Streptococcus pneumoniae UvrA-like protein.
PN GB2345288-A.

PD 05-JUL-2000.
PA (GLAXO) GLAXO GROUP LTD.
Query Match 1.0%; Score 7; DB 3; Length 1140;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
RESULT 1106
ID ADR88899 standard; protein; 1158 AA.
DE Anopheles chloester-containing protein (TEP) 16 sequence.
PN EPI452184-A1.
PD 01-SEP-2004.
PA (EMBL-) EMBL.
Query Match 1.0%; Score 7; DB 8; Length 1158;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
RESULT 1107
ID ABB66758 standard; protein; 1240 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 27056.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 1240;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
RESULT 1108
ID ADR88898 standard; protein; 1340 AA.
DE Anopheles chloester-containing protein (TEP) 1 sequence.
PN EPI452184-A1.
PD 01-SEP-2004.
PA (EMBL-) EMBL.
Query Match 1.0%; Score 7; DB 8; Length 1340;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1109
ID AAY77195 standard; protein; 1346 AA.
DE S. venezuelae macrolide biosynthetic enzyme PIKAIY, SEQ ID NO:37.
PN W020000620-A2.
PD 06-JAN-2000.
PA (MINT) UNIV MINNESOTA.
Query Match 1.0%; Score 7; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1110
ID AAY77203 standard; protein; 1346 AA.
DE S. venezuelae pik (macrolide biosynthesis) gene cluster protein #4.
PN W020000620-A2.
PD 06-JAN-2000.
PA (MINT) UNIV MINNESOTA.
Query Match 1.0%; Score 7; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1111
ID AAB18640 standard; protein; 1346 AA.
DE Amino acid sequence of narbonolide synthase subunit 4 (PICAIY).
PN US6117659-A.
PD 12-SEP-2000.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 1.0%; Score 7; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1112
ID AAY67204 standard; protein; 1346 AA.
DE Narbonolide synthase subunit 4 (PICAIY) protein sequence.
PN W09961599-A2.
PD 02-DEC-1999.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 1.0%; Score 7; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1113
ID ABG71664 standard; protein; 1346 AA.
DE S. venezuelae narbonolide synthase subunit 4, PICAIY.
PN W0200297062-A2.
PD 05-DEC-2002.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 1.0%; Score 7; DB 6; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1114
ID ADA09403 standard; protein; 1346 AA.
DE S. venezuelae narbonolide synthase subunit 4 (PICAIY).
PN US6509455-B1.
PD 21-JAN-2003.

PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 1.0%; Score 7; DB 6; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1115
ID ADH53447 standard; protein; 1346 AA.
DE Streptomyces venezuelae narbonolide synthase subunit 4 protein, PICAIY.
PN US2003162262-A1.
PD 28-AUG-2003.
PA (ASHL) ASHLEY G.
PA (BETL) BETLACH M. C.
PA (BETL) BETLACH M.
PA (MCDA) MCDANIEL R.
PA (TANG) TANG L.
Query Match 1.0%; Score 7; DB 7; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1116
ID ADL91922 standard; protein; 1346 AA.
DE Streptomyces macrolide biosynthetic protein - PIKIV.
PN US2003194784-A1.
PD 16-OCT-2003.
PA (SHER) SHERMAN D H.
PA (LIUH) LIU H.
PA (XUEY) XUE Y.
PA (ZHAO) ZHAO L.
Query Match 1.0%; Score 7; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1117
ID ABR53267 standard; protein; 1522 AA.
DE Protein sequence #SEQ ID 1399.
PN EPI258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 1.0%; Score 7; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
RESULT 1118
ID ADK63630 standard; protein; 1522 AA.
DE Disease treating protein complex-derived protein #838.
PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 1.0%; Score 7; DB 7; Length 1522;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
RESULT 1119
ID ADM35845 standard; protein; 1522 AA.
DE Yeast Okazaki fragment endonuclease Dna2.
PN KR2002072712-A.
PD 18-SEP-2002.
PA (SEOV) SEO Y S.
Query Match 1.0%; Score 7; DB 7; Length 1522;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
RESULT 1120
ID ADS43628 standard; protein; 1522 AA.
DE Bacterial polypeptide #22058.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 1.0%; Score 7; DB 8; Length 1522;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
RESULT 1121
ID ABB28343 standard; protein; 1631 AA.
DE Streptococcus polypeptide SEQ ID NO 5862.
PN W0200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 1.0%; Score 7; DB 5; Length 1631;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
RESULT 1122
ID ADG71666 standard; protein; 1666 AA.

DE Chlamydomonas reinhardtii PRB1 protein, SEQ ID NO:1.
PN JP2003255186-A.
PD 24-SEP-2003.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (UYTY) UNIV TOKYO.
Query Match 1.0%; Score 7; DB 7; Length 1666;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
RESULT 1123
ID ABM65038 standard; protein; 1862 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:5287.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 1.0%; Score 7; DB 8; Length 1862;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
RESULT 1124
ID ABB62819 standard; protein; 1963 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15249.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 1963;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
RESULT 1125
ID ADO59382 standard; protein; 2910 AA.
DE Human cancer-associated (CA) protein sequence SEQ ID NO:18.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.0%; Score 7; DB 8; Length 2910;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
RESULT 1126
ID AEU56630 standard; protein; 2911 AA.
DE Lung cancer-associated polypeptide #223.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 1.0%; Score 7; DB 6; Length 2911;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
RESULT 1127
ID ABO07259 standard; protein; 2911 AA.
DE Human p53 modifying protein, SEQ ID 219.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 1.0%; Score 7; DB 6; Length 2911;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
RESULT 1128
ID ADJ68615 standard; protein; 2911 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID421.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 1.0%; Score 7; DB 7; Length 2911;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
RESULT 1129
ID ADJ38844 standard; protein; 2911 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:162.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (BOSB-) BOS BIOTECHNOLOGY INC.
Query Match 1.0%; Score 7; DB 7; Length 2911;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
RESULT 1130
ID ADQ18204 standard; protein; 2911 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1021.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 1.0%; Score 7; DB 8; Length 2911;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
RESULT 1131
ID AEG06402 standard; protein; 2912 AA.
DE Novel human diagnostic protein #6393.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.0%; Score 7; DB 4; Length 2912;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
RESULT 1132
ID AAE20788 standard; protein; 3095 AA.
DE Rat C3b/C4b complement receptor like protein.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 1.0%; Score 7; DB 5; Length 3095;
Best Local Similarity 100.0%; Pred. No. 1e+04;
RESULT 1133
ID AAB23749 standard; protein; 3972 AA.
DE S. avermitilis avermectin aglycon synthase protein SEQ ID NO:3.
PN WO200050605-A1.
PD 31-AUG-2000.
PA (KITA) KITASATO INST.
Query Match 1.0%; Score 7; DB 3; Length 3972;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
RESULT 1134
ID AAG65264 standard; protein; 3972 AA.
DE Streptomyces avermitilis protein SEQ ID NO: 4.
PN WO200162939-A1.
PD 30-AUG-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (KITA) KITASATO INST.
Query Match 1.0%; Score 7; DB 4; Length 3972;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
RESULT 1135
ID AAG65268 standard; protein; 3972 AA.
DE Streptomyces avermitilis protein derivative SEQ ID NO: 8.
PN WO200162939-A1.
PD 30-AUG-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (KITA) KITASATO INST.
Query Match 1.0%; Score 7; DB 4; Length 3972;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
RESULT 1136
ID ABB59051 standard; protein; 4547 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3945.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 4547;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
RESULT 1137
ID ABB65885 standard; protein; 4899 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24447.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 4899;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
RESULT 1138
ID ADJ91934 standard; protein; 11877 AA.
DE Streptomyces venezuelae pik gene cluster protein.
PN US2003194784-A1.
PD 16-OCT-2003.
PA (SHER/) SHERMAN D H.
PA (LITU/) LIU H.
PA (XUEY/) XUE Y.
PA (ZHAO/) ZHAO L.
Query Match 1.0%; Score 7; DB 8; Length 11877;
Best Local Similarity 100.0%; Pred. No. 3.5e+04;
RESULT 1139
ID AAY77180 standard; protein; 12199 AA.
DE S. venezuelae pik gene cluster-encoded protein, SEQ ID NO:6.
PN WO200000620-A2.
PD 06-JAN-2000.

PA (MINU) UNIV MINNESOTA.
Query Match
Best Local Similarity 1.0%; Score 7; DB 3; Length 12199;
RESULT 1140
ID AAR74921 standard; peptide; 8 AA.
DE Human 193P1E1B protein activator residues 173-180.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match
Best Local Similarity 0.8%; Score 6; DB 2; Length 8;
RESULT 1141
ID ADD9639 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2631.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1142
ID ADD97076 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 70.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1143
ID ADD99119 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2111.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1144
ID ADD99105 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2097.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1145
ID ADD99567 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2559.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1146
ID ADD9832 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 1524.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1147
ID ADD99106 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2098.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1148
ID ADD97325 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 319.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.

Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1149
ID ADD99783 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2775.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1150
ID ADD9689 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2681.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1151
ID ADD98760 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 1752.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1152
ID ADD99217 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2209.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1153
ID ADD97053 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 47.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1154
ID ADD98456 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 1448.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1155
ID ADD99266 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2258.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1156
ID ADD97623 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 617.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1157
ID ADD97659 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 653.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.

Query Match
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;
RESULT 1158
ID ADD97659 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 653.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.

```
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1158
ID ADD99515 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 2507.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1159
ID ADD9936 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 2928.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1160
ID ADD97875 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 869.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1161
ID ADD9933 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 2227.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1162
ID ADD9455 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 2447.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1163
ID ADD98169 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 1161.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1164
ID ADD99017 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 2009.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1165
ID ADO73283 standard; peptide: 9 AA.
DE Human 213P1F11 HLA motif bearing epitope #7382.
PN US2004019915-A1.
PD 29-JAN-2004.
PA (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARI S.
PA (HUBERT/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1166
ID ADO73127 standard; peptide: 9 AA.
DE Human 213P1F11 HLA motif bearing epitope #7226.
PN US2004019915-A1.
PD 29-JAN-2004.
PA (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARI S.
PA (HUBERT/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1167
ID ADP51254 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #1448.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S.
PA (HUBERT/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1168
ID ADP5203 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #2227.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S.
PA (HUBERT/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1169
ID ADP52487 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #2561.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S.
PA (HUBERT/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1170
ID ADP49875 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #70.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S.
PA (HUBERT/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1171
ID ADP50967 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #1161.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S.
PA (HUBERT/) HUBERT R S.
```

PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1172
ID ADP52437 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #2631.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1173
ID ADP51917 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #2111.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1174
ID ADP52734 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #2928.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1175
ID ADP52064 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #2258.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1176
ID ADP52313 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #2507.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1177
ID ADP50125 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #319.
PN US2004102407-A1.

PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1178
ID ADP51815 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #2009.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1179
ID ADP51903 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #2097.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1180
ID ADP51330 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #1524.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1181
ID ADP52581 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #2775.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1182
ID ADP52015 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #2209.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1183
ID ADP50125 standard; peptide: 9 AA.
DE Human 193P1E1B epitope #319.
PN US2004102407-A1.

```
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1183
ID ADP50423 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #617.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1184
ID ADP50675 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #869.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1185
ID ADP52365 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2559.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1186
ID ADP51558 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #1752.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1187
ID ADP52253 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2447.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1188
ID ADP49653 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #47.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1189
ID ADP50459 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #653.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1190
ID ADP51904 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2098.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1191
ID AAR59476 standard; peptide; 10 AA.
DE Neuropeptide for controlling muscle contraction.
PN JP06100590-A.
PD 12-APR-1994.
PA (SUNR ) SUNTORY LTD.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1192
ID ADP97214 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 208.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Length 10;
RESULT 1193
ID ADP98893 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 1885.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Length 10;
RESULT 1194
ID ADE00146 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 3137.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Length 10;
RESULT 1195
ID ADP97235 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 229.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Length 10;
RESULT 1196
ID ADP97235 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 229.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Length 10;
```

ID ADE00128 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 3119.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1197
ID ADE00321 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 3312.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1198
ID ADE98389 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 1381.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1199
ID ADE00477 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 3468.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1200
ID ADE00419 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 3410.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1201
ID ADE00260 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 3251.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1202
ID ADE97458 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 452.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1203
ID ADE97779 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 773.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1204
ID ADE97789 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 783.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1205
ID ADE00572 standard; peptide; 10 AA.

DE Human 193P1E1B protein peptide fragment 3563.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1206
ID ADE98579 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 1571.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1207
ID ADE98038 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 1030.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1208
ID ADE00277 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 3268.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1209
ID ADE00419 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 3410.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1210
ID ADE00145 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 3136.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1211
ID ADE97471 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 465.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1212
ID ADE98312 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 1304.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1213
ID ADE00322 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 3313.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1214
ID ADE97241 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 235.

PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1215
ID ADD97805 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 799.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1216
ID ADD97809 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 803.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1217
ID ADN14200 standard; peptide; 10 AA.
DE HIV B cell epitope #58.
PN US2003049253-A1.
PD 13-MAR-2003.
PA (UIFO/) LI P Q.
PA (CHUY/) CHU Y.
PA (QITU/) QIU J.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1218
ID ADP53057 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3251.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1219
ID ADP53216 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3410.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1220
ID ADP52943 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3137.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1221
ID ADP53074 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3268.

PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1222
ID ADP53118 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3312.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1223
ID ADP50605 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #799.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1224
ID ADP52942 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3136.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1225
ID ADP50579 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #773.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1226
ID ADP52925 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3119.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.

Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1227
ID ADP50014 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #208.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1228
ID ADP51691 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #1885.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1229
ID ADP50035 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #229.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1230
ID ADP53274 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3468.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1231
ID ADP50589 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #783.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1232
ID ADP50609 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #803.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.

PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1233
ID ADP53369 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3563.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1234
ID ADP50836 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #1030.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1235
ID ADP51110 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #1304.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1236
ID ADP50271 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #465.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1237
ID ADP51377 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #1571.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1238
ID ADP50271 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #1571.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1239
ID ADP50271 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #1571.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.

```
ID ADP53119 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #313.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1239
ID ADP50041 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #235.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1240
ID ADP50258 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #452.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1241
ID ADP51187 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #1381.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1242
ID ADP50844 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #1038.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1243
ID AAR74926 standard; peptide; 11 AA.
DE Urea plasminogen activator residues 173-182.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1244
ID AAR74924 standard; peptide; 11 AA.
DE Urea plasminogen activator residues 173-183.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1245
ID AAB68774 standard; peptide; 11 AA.
DE Saccharopolyspora polyspora module 1 PKS peptide #1.
PN WO200104274-A2.
PD 18-JAN-2001.
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1246
ID AAB68770 standard; peptide; 11 AA.
DE Rat FAS peptide #1.
PN WO200104274-A2.
PD 18-JAN-2001.
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1247
ID AAB68775 standard; peptide; 11 AA.
DE Streptomyces venezuelae module 1 PKS peptide #1.
PN WO200104274-A2.
PD 18-JAN-2001.
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1248
ID AAB68771 standard; peptide; 11 AA.
DE Human FAS peptide #1.
PN WO200104274-A2.
PD 18-JAN-2001.
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1249
ID AAB68772 standard; peptide; 11 AA.
DE Caenorhabditis elegans FAS peptide #1.
PN WO200104274-A2.
PD 18-JAN-2001.
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1250
ID AAR10873 standard; peptide; 11 AA.
DE Bovine uroplakin II protein fragment (1-11 amino acids).
PN US6290959-B1.
PD 18-SEP-2001.
PA (UTNY) UNIV NEW YORK STATE.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1251
ID AAR74922 standard; peptide; 12 AA.
DE Urea plasminogen activator residues 173-183.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1252
ID AAW88589 standard; protein; 12 AA.
DE Secreted protein encoded by gene 56 clone HE20F09.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1253
ID ABB50356 standard; protein; 12 AA.
```

DE Human secreted protein encoded by gene 56 SEQ ID NO:304.
PN WC0200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
ID ABR38980 standard; peptide: 12 AA.
DE Human topoisomerase II alpha inhibitory protein fragment #SEQ ID 6.
PN WC0200300237-A1.
PD 03-JAN-2003.
PA (RIKE) RIKEN KK.
Query Match 0.8%; Score 6; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
ID ABO44613 standard; protein: 12 AA.
DE Novel human secreted protein #56.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
ID ABO26093 standard; protein: 12 AA.
DE Human protein from novel secreted protein gene 56.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
ID AAB01945 standard; peptide: 13 AA.
DE Human Endothelinase 2 repetitive peptide sequence.
PN WC200136604-A2.
PD 25-MAY-2001.
PA (CORV-) CORVAS INT INC.
Query Match 0.8%; Score 6; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
ID MAG98215 standard; peptide: 14 AA.
DE Human SNP associated peptide SEQ ID NO. 857.
PN WC0200148245-A2.
PD 05-JUL-2001.
PA (CURA-) CURAGEN CORP.
Query Match 0.8%; Score 6; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
ID AAB56899 standard; peptide: 14 AA.
DE Human SNP related amino acid sequence SEQ ID NO:1464.
PN WC0200138586-A2.
PD 31-MAY-2001.
PA (CURA-) CURAGEN CORP.
Query Match 0.8%; Score 6; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
ID ABB67423 standard; peptide: 14 AA.
DE Human ADP1 tryptic digest peptide #132.
PN WC0200246767-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Query Match 0.8%; Score 6; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
ID ADA23531 standard; peptide: 14 AA.
DE Alzheimer's disease-associated protein isoform tryptic peptide #140.
PN US2003064411-A1.
PD 03-APR-2003.
PA (HERA-) HERATH H M A C.
PA (PARE-) PAREKH R B.
PA (ROHL-) ROHLFF C.
Query Match 0.8%; Score 6; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 1262

ID ADN14199 standard; peptide: 14 AA.
DE HIV B cell epitope #57.
PN US2003049253-A1.
PD 13-MAR-2003.
PA (LIFQ/) LI F Q.
PA (CHUY/) CHU Y.
PA (QIUJ/) QIU J.
Query Match 0.8%; Score 6; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
ID ADO34385 standard; peptide: 14 AA.
DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 162.
PN WC02004043403-A2.
PD 27-MAY-2004.
PA (UABR-) UAB RES FOUND.
Query Match 0.8%; Score 6; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
ID ADO34421 standard; peptide: 14 AA.
DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 198.
PN WC02004043403-A2.
PD 27-MAY-2004.
PA (UABR-) UAB RES FOUND.
Query Match 0.8%; Score 6; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
ID AAG78745 standard; peptide: 15 AA.
DE Human ribose phosphate glycine amide synthetase 12 N-terminus.
PN WC0200173065-A1.
PD 04-OCT-2001.
PA (SHAN-) SHANGHAI BLOWDOWN GENE DEV INC.
Query Match 0.8%; Score 6; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
ID ADE00866 standard; peptide: 15 AA.
DE Human 193P1B1B protein peptide fragment 3857.
PN WC02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
ID ADE00911 standard; peptide: 15 AA.
DE Human 193P1B1B protein peptide fragment 3902.
PN WC02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
ID ADE01040 standard; peptide: 15 AA.
DE Human 193P1B1B protein peptide fragment 4031.
PN WC02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
ID ADE00912 standard; peptide: 15 AA.
DE Human 193P1B1B protein peptide fragment 3903.
PN WC02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
ID ADE00664 standard; peptide: 15 AA.
DE Human 193P1B1B protein peptide fragment 3655.
PN WC02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1263

```
RESULT 1271
ID ADE00810 standard; peptide; 15 AA.
DE Human 193P1E1B protein peptide fragment 3801.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1272
ID ADE00966 standard; peptide; 15 AA.
DE Human 193P1E1B protein peptide fragment 3957.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1273
ID ADE01108 standard; peptide; 15 AA.
DE Human 193P1E1B protein peptide fragment 4099.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1274
ID ADE01070 standard; peptide; 15 AA.
DE Human 193P1E1B protein peptide fragment 4061.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1275
ID ADE00825 standard; peptide; 15 AA.
DE Human 193P1E1B protein peptide fragment 3816.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1276
ID ADP53709 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #3903.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1277
ID ADP53622 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #3816.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1278
ID ADP53837 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #4031.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1279
ID ADP53663 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #3857.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1280
ID ADP53763 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #3957.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1281
ID ADP53461 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #3655.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1282
ID ADP53505 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #4099.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1283
ID ADP53867 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #4061.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1284
ID ADP53607 standard; peptide; 15 AA.
```

DE Human 193PIE1B epitope #3801.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1285
ID ADP53708 standard; peptide; 15 AA.
DE Human 193PIE1B epitope #3902.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1286
ID AAR83658 standard; peptide; 17 AA.
DE Insect haemolymph antibacterial polypeptide #8.
PN WO9523513-A1.
PD 08-SEP-1995.
PA (SLOK/) SLOAN KETTERING INST CANCER RES.
Query Match 0.8%; Score 6; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
RESULT 1287
ID AAR74918 standard; peptide; 18 AA.
DE Urea plasmidogen activator residues 163-180.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMO/) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 1288
ID AAR99573 standard; peptide; 18 AA.
DE Wasp venom BrTx-1 subunit (b) N-terminal peptide.
PN WO9616171-A1.
PD 30-MAY-1996.
PA (ZENE/) ZENECA LTD.
PA (CSIR/) COMMONWEALTH SCI & IND RES ORG.
Query Match 0.8%; Score 6; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 1289
ID ADI29454 standard; peptide; 19 AA.
DE ErbB ligand HB-EGF CCF/F motif peptide.
PN WO2004005320-A2.
PD 15-JAN-2004.
PA (UMOR/) UNIV MISSOURI.
Query Match 0.8%; Score 6; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
RESULT 1290
ID AAR83657 standard; peptide; 20 AA.
DE Insect haemolymph antibacterial polypeptide #7.
PN WO9523513-A1.
PD 08-SEP-1995.
PA (SLOK/) SLOAN KETTERING INST CANCER RES.
Query Match 0.8%; Score 6; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
RESULT 1291
ID ABU08144 standard; peptide; 20 AA.
DE Human IL-1 RI signal peptide.
PN GB2375604-A.
PD 20-NOV-2002.
PA (WARN/) WARNER LAMBERT CO.
Query Match 0.8%; Score 6; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;

RESULT 1292
ID ADG17865 standard; peptide; 20 AA.
DE Binding affinity measurement-related peptide Segid67.
PN WO2003089662-A1.
PD 30-OCT-2003.
PA (REGC/) UNIV CALIFORNIA.
Query Match 0.8%; Score 6; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
RESULT 1293
ID ADK52540 standard; peptide; 20 AA.
DE Fungal mycotoxin biosynthetic protein consensus sequence #2.
PN EPI329521-A1.
PD 23-JUL-2003.
PA (EVIA/) EVIALIS T.
Query Match 0.8%; Score 6; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
RESULT 1294
ID ADN14077 standard; peptide; 20 AA.
DE HIV helper T cell epitope #44.
PN US2003049253-A1.
PD 13-MAR-2003.
PA (LIFO/) LI F O.
PA (CHUY/) CHU Y.
PA (QIUJ/) QIU J.
Query Match 0.8%; Score 6; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
RESULT 1295
ID ADN14201 standard; peptide; 20 AA.
DE HIV B cell epitope #59.
PN US2003049253-A1.
PD 13-MAR-2003.
PA (LIFO/) LI F O.
PA (CHUY/) CHU Y.
PA (QIUJ/) QIU J.
Query Match 0.8%; Score 6; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
RESULT 1296
ID AAB89179 standard; peptide; 21 AA.
DE HIV gp120 protein binding peptide #272.
PN WO200116182-A2.
PD 08-MAR-2001.
PA (USSH/) US DEPT HEALTH & HUMAN SERVICES.
Query Match 0.8%; Score 6; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1297
ID AAB89181 standard; peptide; 21 AA.
DE HIV gp120 protein binding peptide #274.
PN WO200116182-A2.
PD 08-MAR-2001.
PA (USSH/) US DEPT HEALTH & HUMAN SERVICES.
Query Match 0.8%; Score 6; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1298
ID AAB89180 standard; peptide; 21 AA.
DE HIV gp120 protein binding peptide #273.
PN WO200116182-A2.
PD 08-MAR-2001.
PA (USSH/) US DEPT HEALTH & HUMAN SERVICES.
Query Match 0.8%; Score 6; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1299
ID AAU89796 standard; peptide; 21 AA.
DE Insulin/insulin-like growth factor receptor-binding peptide #1752.
PN WO200172771-A2.
PD 04-OCT-2001.
PA (DGI-) DGI BIOTECHNOLOGIES LLC.
PA (NOVO/) NOVO NORDISK AS.
Query Match 0.8%; Score 6; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1300
ID AAU89556 standard; peptide; 21 AA.
DE Insulin/insulin-like growth factor receptor-binding peptide #1512.
PN WO200172771-A2.

PD 04-OCT-2001.
PA (DGB-) DGI BIOTECHNOLOGIES LLC.
PA (NOVO) NOVO NORDISK AS.
Query Match 0.8%; Score 6; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1301
ID AAM18205 standard; protein; 22 AA.
DE Peptide #4639 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1302
ID AAM47407 standard; peptide; 22 AA.
DE Peptide #37 for illustrating method of anticipating protein interaction.
PN WO200167299-A1.
PD 13-SEP-2001.
PA (DAUC) DAICHI PHARM CO LTD.
PA (PUT) FUJITSU LTD.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1303
ID ABB31987 standard; peptide; 22 AA.
DE Peptide #4638 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1304
ID ABB22530 standard; protein; 22 AA.
DE Protein #4529 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1305
ID AAM70365 standard; protein; 22 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30671.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1306
ID AAM57939 standard; protein; 22 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 30044.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1307
ID ABB52060 standard; peptide; 22 AA.
DE Human liver peptide; SEQ ID NO 30708.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1308
ID AAM05822 standard; protein; 22 AA.
DE Peptide #4504 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1309
ID ABB28549 standard; protein; 22 AA.
DE Novel human diagnostic protein #28540.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1310
ID ABB40009 standard; peptide; 22 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29674.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1311
ID AAO20901 standard; peptide; 22 AA.
DE Swine fever envelope protein E2 fragment #5.
PN WO20032453-A1.
PD 25-APR-2002.
PA (UYOI) UNIV QINGHUA.
PA (BEID-) BEIJING FEIKAI BIOTECH CO LTD.
Query Match 0.8%; Score 6; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1312
ID AAM19926 standard; protein; 23 AA.
DE Peptide #6360 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1313
ID ABB39934 standard; peptide; 23 AA.
DE Peptide #7440 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1314
ID AAM33553 standard; protein; 23 AA.
DE Peptide #7590 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1315
ID ABB24479 standard; protein; 23 AA.
DE Protein #6478 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1316
ID AAM73351 standard; protein; 23 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 33657.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1317
ID AAM60679 standard; protein; 23 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32784.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1318
ID ABB55067 standard; peptide; 23 AA.
DE Human liver peptide; SEQ ID NO 33715.

PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1319
ID ABG433204 standard; peptide; 23 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 32869.
PN W0200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1320
ID AAP93093 standard; peptide; 25 AA.
DE CD4 anti-receptor peptide.
PN W08909782-A.
PD 19-OCT-1989.
PA (USDC) US SEC OF COMMERCE.
Query Match 0.8%; Score 6; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 1321
ID AAR74927 standard; peptide; 25 AA.
DE Urea plasmidogen activator residues 163-186.
PN W05009908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 1322
ID AAR71493 standard; peptide; 25 AA.
DE *Escherichia chaffeensis* P28 protein N-terminal signal peptide.
PN W0200032745-A2.
PD 08-JUN-2000.
PA (RRRE-) RES DEV FOUND.
Query Match 0.8%; Score 6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 1323
ID AAR96113 standard; peptide; 25 AA.
DE *Escherichia chaffeensis* P28 N-terminal signal peptide.
PN W0200222782-A2.
PD 21-MAR-2002.
PA (RRRE-) RES DEV FOUND.
Query Match 0.8%; Score 6; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 1324
ID ADR84080 standard; peptide; 26 AA.
DE *S. pyogenes* hyperimmune system reactive antigen SP00287.4.
PN W02004078907-A2.
PD 16-SEP-2004.
PA (INTE-) INTERCELL AG.
Query Match 0.8%; Score 6; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1325
ID AAR11853 standard; peptide; 27 AA.
DE Eel natrictic peptide.
PN JP03074400-A.
PD 28-MAR-1991.
PA (SMIB-) SMI BRYSTOL KK.
PA (SUMU) SUMITOMO METAL IND LTD.
Query Match 0.8%; Score 6; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1326
ID AAB91306 standard; peptide; 27 AA.
DE Atrial-natriuretic peptide (ANP) SEQ ID NO:482.
PN W0200069900-A2.
PD 23-NOV-2000.
PA (CONU-) CONUTCHEM INC.
Query Match 0.8%; Score 6; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1327
ID AAB91315 standard; peptide; 27 AA.
DE Atrial-natriuretic peptide (ANP) SEQ ID NO:491.

PN W0200069900-A2.
PD 23-NOV-2000.
PA (CONU-) CONUTCHEM INC.
Query Match 0.8%; Score 6; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1328
ID AAB91325 standard; peptide; 27 AA.
DE Atrial-natriuretic peptide (ANP) SEQ ID NO:501.
PN W0200069900-A2.
PD 23-NOV-2000.
PA (CONU-) CONUTCHEM INC.
Query Match 0.8%; Score 6; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1329
ID AAR26346 standard; peptide; 28 AA.
DE Spacer oligopeptide D28.
PN JP04190791-A.
PD 09-JUL-1992.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1330
ID AAR71663 standard; peptide; 29 AA.
DE Modified urinary plasmidogen activator residues 159-188.
PN JP07039374-A.
PD 10-FEB-1995.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1331
ID AAR26347 standard; peptide; 30 AA.
DE Spacer oligopeptide D30.
PN JP04190791-A.
PD 09-JUL-1992.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1332
ID AAR42811 standard; peptide; 30 AA.
DE U-PA (159-188).
PN W09320194-A1.
PD 14-OCT-1993.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1333
ID AAR72872 standard; peptide; 30 AA.
DE Urokinase peptide fragment from amino acids 159-188.
PN JP07075580-A.
PD 20-MAR-1995.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1334
ID AAR93589 standard; peptide; 30 AA.
DE UK t-PA hybrid peptide CS19 residues 276-306.
PN W09509908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1335
ID AAR93591 standard; peptide; 30 AA.
DE UK t-PA hybrid peptide CS21 residues 276-306.
PN W09509908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1336
ID AAR76947 standard; peptide; 30 AA.
DE UK t-PA hybrid peptide CS16 residues 276-306.
PN W09509908-A1.

```
PD 13-APR-1995.
PA (SUMU ) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1337
ID AAR76946 standard; peptide; 30 AA.
DE UK t-PA hybrid peptide CS15 residues 276-306.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU ) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1338
ID AAR93592 standard; peptide; 30 AA.
DE UK t-PA hybrid peptide CS12 residues 276-306.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU ) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1339
ID AAR71666 standard; peptide; 30 AA.
DE Modified urinary plasminogen activator residues 159-188.
PN JF07039374-A.
PD 10-FEB-1995.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1340
ID AAR72874 standard; peptide; 31 AA.
DE t-PA peptide fragment from amino acids 276-306.
PN JF07075580-A.
PD 20-MAR-1995.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1341
ID AAR71904 standard; peptide; 31 AA.
DE Wild type tissue plasminogen activator residues 276-306.
PN JF07039374-A.
PD 10-FEB-1995.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1342
ID AAM05988 standard; protein; 31 AA.
DE Peptide #4670 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1343
ID AAR24949 standard; peptide; 32 AA.
DE Urokinase fragment.
PN JF04144682-A.
PD 19-MAY-1992.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1344
ID AAM16011 standard; protein; 33 AA.
DE Peptide #2445 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1345
ID ABB35004 standard; peptide; 33 AA.
DE Peptide #2510 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1346
ID AAM28512 standard; protein; 33 AA.
DE Peptide #2549 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1347
ID ABB20416 standard; protein; 33 AA.
DE Protein #2415 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1348
ID AAM68189 standard; protein; 33 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28495.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1349
ID AAO00415 standard; protein; 33 AA.
DE Human polypeptide SEQ ID NO 14307.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1350
ID AAM55815 standard; protein; 33 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27920.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1351
ID ABG49840 standard; peptide; 33 AA.
DE Human liver peptide, SEQ ID NO 28488.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1352
ID AAM03745 standard; protein; 33 AA.
DE Peptide #2427 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1353
ID ABB72759 standard; peptide; 33 AA.
DE Anticancer peptide derived from human thrombin.
PN WO2003013569-A2.
PD 20-FEB-2003.
PA (TEXA ) UNIV TEXAS SYSTEM.
Query Match 0.8%; Score 6; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1354
ID ABB72759 standard; peptide; 33 AA.
DE Anticancer peptide derived from human thrombin.
PN WO2003013569-A2.
PD 20-FEB-2003.
PA (TEXA ) UNIV TEXAS SYSTEM.
```



```
Query Match          0.8%; Score 6; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1355
ID AAR74068 standard; peptide; 35 AA.
DE Superantigen peptide HIV Nef(31-65).
PN WO9511975-A2.
PD 04-MAY-1995.
PA (UYFL ) UNIV FLORIDA.
Query Match          0.8%; Score 6; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1356
ID AAY39987 standard; peptide; 35 AA.
DE HIV Negative factor (Nef) protein residues 31-65.
PN US5968514-A.
PD 19-OCT-1999.
PA (UYFL ) UNIV FLORIDA.
Query Match          0.8%; Score 6; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1357
ID ABU61264 standard; peptide; 35 AA.
DE Human A domain from APOBR2 #7.
PN WO200288171-A2.
PD 07-NOV-2002.
PA (MAXY-) MAXYGEN INC.
Query Match          0.8%; Score 6; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1358
ID ADP21486 standard; peptide; 35 AA.
DE Human LDL receptor A domain peptide SeqID 62.
PN WO2004044011-A2.
PD 27-MAY-2004.
PA (AVID-) AVIDIA RES INST.
Query Match          0.8%; Score 6; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1359
ID AAO02449 standard; protein; 36 AA.
DE Human polypeptide SEQ ID NO 16341.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match          0.8%; Score 6; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1360
ID AAR97691 standard; protein; 37 AA.
DE Rat PB65 WW domain-1.
PN WO9617061-A1.
PD 06-JUN-1996.
PA (UYRQ ) UNIV ROCKEFELLER.
DE (DELB-) DELBRUECK CENT MOLECULAR MEDICINE MAX.
Query Match          0.8%; Score 6; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1361
ID AAM21577 standard; protein; 37 AA.
DE Alzheimer's disease protein encoded by DNA from plasmid pGCS1243.
PN WO9721807-A1.
PD 19-JUN-1997.
PA (KYOM ) KYOMA HAKKO KOGYO KK.
Query Match          0.8%; Score 6; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1362
ID AAY48444 standard; protein; 37 AA.
DE Human prostate cancer-associated protein 141.
PN DE19811194-A1.
PD 16-SEP-1999.
PA (MSTA-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match          0.8%; Score 6; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1363
ID AAB21981 standard; peptide; 37 AA.
DE F865/rat peptide containing a WW-domain #2.
PN WO200048621-A2.
PD 24-AUG-2000.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

Query Match          0.8%; Score 6; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1364
ID AAR83566 standard; protein; 37 AA.
DE Colicin N 40-76 amino acid sequence SEQ ID NO:33.
PN WO2003057708-A2.
PD 17-JUL-2003.
PA (UYNE-) UNIV NEWCASTLE VENTURES LTD.
Query Match          0.8%; Score 6; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1365
ID AAR74067 standard; peptide; 38 AA.
DE Superantigen peptide HIV Nef(1-38).
PN WO9511975-A2.
PD 04-MAY-1995.
PA (UYFL ) UNIV FLORIDA.
Query Match          0.8%; Score 6; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1366
ID AAY39972 standard; peptide; 38 AA.
DE HIV Negative factor (Nef) protein residues 1-38.
PN US5968514-A.
PD 19-OCT-1999.
PA (UYFL ) UNIV FLORIDA.
Query Match          0.8%; Score 6; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1367
ID AAB70442 standard; peptide; 38 AA.
DE L. lactis signal peptide Sp310 mutant amino acid sequence SEQ:55.
PN WO200111060-A2.
PD 15-FEB-2001.
PA (BIOT-) BIOTEKNOLOGISK INST.
Query Match          0.8%; Score 6; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1368
ID ABO58270 standard; protein; 38 AA.
DE Human genome derived single exon protein #4504.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match          0.8%; Score 6; DB 8; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1369
ID AAR64211 standard; peptide; 39 AA.
DE Urinary plasminogen activator residues 150-188.
PN JP06327473-A.
PD 29-NOV-1994.
PA (SUMU ) SUMITOMO SRIYAKU KK.
Query Match          0.8%; Score 6; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1370
ID AAO11683 standard; protein; 39 AA.
DE Human polypeptide SEQ ID NO 25575.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match          0.8%; Score 6; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1371
ID AAE32936 standard; peptide; 39 AA.
DE Human albumin-CD4 fusion protein junction peptide.
PN WO200279232-A2.
PD 10-OCT-2002.
PA (LEXI-) LEXIGEN PHARM CORP.
Query Match          0.8%; Score 6; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1372
ID AAE32648 standard; peptide; 39 AA.
DE Albumin-CD4 fusion protein junction peptide.
PN WO200279415-A2.
PD 10-OCT-2002.
```

PA (LEXI-) LEXIGEN PHARM CORP.
Query Match 0.8%; Score 6; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1373
ID ADF75022 standard; peptide; 39 AA.
DE Human serum albumin-CD4 fusion protein junction sequence.
PN US2003166877-A1.
PD 04-SEP-2003.
PA (LEXI-) LEXIGEN PHARM CORP.
Query Match 0.8%; Score 6; DB 7; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1374
ID AAP71494 standard; protein; 40 AA.
DE Antigenic peptide cross-reactive with HTLV-III env protein 3'ORF.
PN W08702988-A1.
PD 21-MAY-1987.
PA (HARD) HARVARD COLLEGE.
Query Match 0.8%; Score 6; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
RESULT 1375
ID AAY48263 standard; protein; 40 AA.
DE Human prostate cancer-associated protein 49.
PN DE1981193-A1.
PD 16-SEP-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 0.8%; Score 6; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
RESULT 1376
ID AAB09340 standard; protein; 40 AA.
DE Hepatitis GB virus protein sequence SEQ ID NO:467.
PN US6051374-A.
PD 18-APR-2000.
PA (ABBO) ABBOTT LAB.
Query Match 0.8%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
RESULT 1377
ID AAE23150 standard; peptide; 40 AA.
DE Influenza A virus subtype 16 haemagglutinin (HA) protein fragment #14.
PN W0200224734-A2.
PD 28-MAR-2002.
PA (CHIR-) CHIRON SPA.
Query Match 0.8%; Score 6; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
RESULT 1378
ID AAB07101 standard; protein; 41 AA.
DE Melanocyte-stimulating hormone inhibitor #6.
PN EP389950-A.
PD 03-OCT-1990.
PA (LLOY) LION CORP.
Query Match 0.8%; Score 6; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
RESULT 1379
ID AAM24782 standard; peptide; 42 AA.
DE Adhesin Pctr44 N-terminal peptide.
PN W09716542-A1.
PD 09-MAY-1997.
PA (UYME) UNIV MELBOURNE.
Query Match 0.8%; Score 6; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
RESULT 1380
ID AAO02438 standard; protein; 42 AA.
DE Human polypeptide SEQ ID NO 16330.
PN W0200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
RESULT 1381
ID ABO60596 standard; protein; 42 AA.
DE Human genome derived single exon protein #6830.
PN US2003194704-A1.
PD 16-OCT-2003.

PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 0.8%; Score 6; DB 8; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
RESULT 1382
ID AAR58896 standard; protein; 43 AA.
DE Human-223 cadherin-related molecule.
PN W09414960-A2.
PD 07-JUL-1994.
PA (DOHE-) DOHENY EYE INST.
Query Match 0.8%; Score 6; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+03;
RESULT 1383
ID AAR87135 standard; peptide; 43 AA.
DE Protocadherin clone HUMAN-223.
PN W09600289-A1.
PD 04-JAN-1996.
PA (DOHE-) DOHENY EYE INST.
Query Match 0.8%; Score 6; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+03;
RESULT 1384
ID AAY21020 standard; protein; 43 AA.
DE Human glial fibrillary acidic protein GFAP mutant fragment 29.
PN W09845322-A2.
PD 15-OCT-1998.
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
PA (UYUT-) RIJKSUNIV UTRECHT.
Query Match 0.8%; Score 6; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+03;
RESULT 1385
ID AAY32350 standard; peptide; 43 AA.
DE Human C1gRP EGF-2 peptide.
PN W09355838-A1.
PD 04-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 0.8%; Score 6; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+03;
RESULT 1386
ID ABG77431 standard; protein; 43 AA.
DE Selected Interacting Domain (SID) polypeptide #242.
PN W0200259255-A2.
PD 01-AUG-2002.
PA (HYBR-) HYBRGENICS.
Query Match 0.8%; Score 6; DB 5; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+03;
RESULT 1387
ID AAE30226 standard; peptide; 43 AA.
DE Human LP288 YMTD Island 2 repeat peptide #1.
PN W0200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 0.8%; Score 6; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+03;
RESULT 1388
ID ADR51552 standard; protein; 43 AA.
DE DT-binding receptor region of HB-EGF from humans.
PN W02004069870-A2.
PD 19-AUG-2004.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 0.8%; Score 6; DB 8; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+03;
RESULT 1389
ID ADR51550 standard; protein; 43 AA.
DE DT-binding receptor region of HB-EGF from pigs.
PN W02004069870-A2.
PD 19-AUG-2004.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 0.8%; Score 6; DB 8; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+03;
RESULT 1390
ID AAO01303 standard; protein; 44 AA.

DE Human polypeptide SEQ ID NO 15195.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 2e+03;
RESULT 1391
ID ADR51549 standard; protein; 44 AA.
DE DT-binding receptor region of HB-EGF from rabbits.
PN WO2004069870-A2.
PD 13-AUG-2004.
PA (VYLR-) RIJKSUNIV LEIDEN.
Query Match 0.8%; Score 6; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 2e+03;
RESULT 1392
ID ADR51551 standard; protein; 44 AA.
DE DT-binding receptor region of HB-EGF from monkeys.
PN WO2004069870-A2.
PD 13-AUG-2004.
PA (VYLR-) RIJKSUNIV LEIDEN.
Query Match 0.8%; Score 6; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 2e+03;
RESULT 1393
ID AAR64212 standard; peptide; 45 AA.
DE Urinary plasminogen activator residues 159-203.
PN JP06327473-A.
PD 28-NOV-1994.
PA (SUMU-) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1394
ID AAY08546 standard; protein; 45 AA.
DE C-terminal alpha-CTD protein fragment FTSH_HELPY.
PN WO9925733-A2.
PD 27-MAY-1999.
PA (YISS-) YISSUM RES & DEV CO.
Query Match 0.8%; Score 6; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1395
ID AAG21119 standard; protein; 45 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23559.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1396
ID AAM14231 standard; protein; 45 AA.
DE Peptide #665 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1397
ID ABB31178 standard; peptide; 45 AA.
DE Peptide #684 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 03-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1398
ID AAM26641 standard; protein; 45 AA.
DE Peptide #678 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 02-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1399
ID AAB28006 standard; peptide; 45 AA.
DE Human peptide #657 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.

PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1400
ID ABB18643 standard; protein; 45 AA.
DE Protein #642 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1401
ID AAM66362 standard; protein; 45 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26668.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1402
ID AAM53974 standard; protein; 45 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26079.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1403
ID ABB48028 standard; peptide; 45 AA.
DE Human liver peptide, SEQ ID No 26676.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1404
ID AAM01963 standard; protein; 45 AA.
DE Peptide #645 encoded by probe for measuring human breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1405
ID ABB36010 standard; peptide; 45 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 25675.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 5; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1406
ID ADN05538 standard; protein; 45 AA.
DE Antipsoaric protein sequence #935.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GERTH-) GENENTECH INC.
Query Match 0.8%; Score 6; DB 8; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1407
ID ABB03327 standard; protein; 46 AA.
DE Human musculoskeletal system related polypeptide SEQ ID NO 1274.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1408
ID AAO01399 standard; protein; 46 AA.
DE Human polypeptide SEQ ID NO 15291.
PN WO200164835-A2.
PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1409
ID AAO08005 standard; protein; 46 AA.
DE Human polypeptide SEQ ID NO 21897.
PN W0200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1410
ID ADH32592 standard; protein; 46 AA.
DE Yeast smorf387-encoded polypeptide, SEQ ID NO:10550.
PN W0200268693-A2.
PD 06-SEP-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 0.8%; Score 6; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1411
ID AAD12621 standard; protein; 46 AA.
DE Novel human musculoskeletal system antigen #241.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 0.8%; Score 6; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1412
ID ADJ28647 standard; protein; 46 AA.
DE Human musculoskeletal system-associated protein - SEQ ID 1274.
PN US2004009486-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 8; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1413
ID ADS07325 standard; protein; 46 AA.
DE Staphylococcus epidermis polypeptide seqid 6620.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match 0.8%; Score 6; DB 8; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1414
ID AAM28321 standard; protein; 47 AA.
DE Staphylococcus aureus protein of unknown function.
PN W09730070-A1.
PD 21-AUG-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 0.8%; Score 6; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1415
ID AAG18782 standard; protein; 47 AA.
DE Zea mays protein fragment SEQ ID NO: 20328.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1416
ID AAM47202 standard; peptide; 47 AA.
DE Modular enzyme system related ACP-domain N-terminal peptide AYBAI_3.
PN W0200181564-A2.
PD 01-NOV-2001.
PA (ACTI-) ACTINODRUG PHARM GMBH.
Query Match 0.8%; Score 6; DB 5; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1417
ID ADD96929 standard; protein; 47 AA.
DE Human 1931E1B protein variant 1 fragment #2.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1418
ID ADP49728 standard; peptide; 47 AA.
DE Human 1931E1Bv.1.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-ELD P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1419
ID AAB33113 standard; protein; 48 AA.
DE Pinus radiata transcription factor protein sequence #240.
PN W0200053724-A2.
PD 14-SEP-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 0.8%; Score 6; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1420
ID ABP43712 standard; protein; 48 AA.
DE PRO566 protein.
PN W0200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1421
ID AAE36818 standard; protein; 48 AA.
DE Human HB-EGF domain.
PN W02003014159-A1.
PD 20-FEB-2003.
PA (GSTR) COMMONWEALTH SCI & IND RES ORG.
PA (BIOM-) BIOMOLECULAR RES INST LTD.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 0.8%; Score 6; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1422
ID ADN48881 standard; peptide; 48 AA.
DE Heparin-binding epidermal-growth factor (HB-EGF) peptide.
PN US6727077-B1.
PD 27-APR-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (GEOU) UNIV GEORGETOWN MEDICAL CENT.
Query Match 0.8%; Score 6; DB 8; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1423
ID ABB38598 standard; peptide; 49 AA.
DE Peptide #6104 encoded by human foetal liver single exon probe.
PN W0200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1424
ID AAM32054 standard; protein; 49 AA.
DE Peptide #6091 encoded by probe for measuring placental gene expression.
PN W0200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1425
ID AAM71762 standard; protein; 49 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32068.

PN W0200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1426
ID AAM59226 standard; protein; 49 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31331.
PN W0200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1427
ID AAG53447 standard; peptide; 49 AA.
DE Human liver peptide, SEQ ID No 32095.
PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1428
ID AAG41576 standard; peptide; 49 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 31241.
PN W0200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1429
ID ADK14940 standard; protein; 49 AA.
DE Urinary specific protein #46.
PN W02003057839-A2.
PD 17-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1430
ID AAG04489 standard; protein; 50 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 535.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1431
ID AAG37508 standard; protein; 50 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 46130.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1432
ID AAB22229 standard; protein; 50 AA.
DE Protein #4228 encoded by probe for measuring heart cell gene expression.
PN W0200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1433
ID AAM70055 standard; protein; 50 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30361.
PN W0200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1434
ID AAM40213 standard; protein; 50 AA.
DE Propionibacterium acnes immunogenic protein #1109.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.

Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1435
ID AAM57648 standard; protein; 50 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29753.
PN W0200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1436
ID AAG51748 standard; peptide; 50 AA.
DE Human liver peptide, SEQ ID No 30396.
PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1437
ID AAM05532 standard; protein; 50 AA.
DE Peptide #4214 encoded by probe for measuring breast gene expression.
PN W0200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1438
ID AAG39686 standard; peptide; 50 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29351.
PN W0200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1439
ID AAB36732 standard; protein; 50 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #1408.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1440
ID AAB36799 standard; protein; 50 AA.
DE Human HB-EGF protein BGF-like domain.
PN W02003014159-A1.
PD 20-FEB-2003.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (BIOM-) BIOMOLECULAR RES INST LTD.
PA (HALT-) HALT INST MEDICAL RES WALTER & ELIZA.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1441
ID AAM67925 standard; protein; 51 AA.
DE Fragment of human secreted protein encoded by gene 3.
PN W09842738-A1.
PD 01-OCT-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1442
ID AAG04488 standard; protein; 51 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 534.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1443
ID AAG37507 standard; protein; 51 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 46129.
PN EP1033405-A2.
PD 06-SEP-2000.

Best Local Similarity	100.0%;	Pred. No. 2.5e+03;
RESULT 1453		
ID AAU39328 standard; protein; 54 AA.		
DE Propionibacterium acnes immunogenic protein #224.		
PN WO200181581-A2.		
PD 01-NOV-2001.		
PA (CORI-) CORIXA CORP.		
Query Match	0.8%;	Score 6; DB 4; Length 54;
Best Local Similarity	100.0%;	Pred. No. 2.5e+03;
RESULT 1454		
ID ABU02285 standard; protein; 54 AA.		
DE S. pneumoniae type 4 strain protein from coding region #1863.		
PN WO200277021-A2.		
PD 03-OCT-2002.		
PA (CHIR-) CHIRON SPA.		
PA (GENO-) INST GENOMIC RES.		
Query Match	0.8%;	Score 6; DB 6; Length 54;
Best Local Similarity	100.0%;	Pred. No. 2.5e+03;
RESULT 1455		
ID ABM42757 standard; protein; 54 AA.		
DE Propionibacterium acnes predicted ORF-encoded polypeptide #7433		
PN WO2003033515-A1.		
PD 24-APR-2003.		
PA (CORI-) CORIXA CORP.		
Query Match	0.8%;	Score 6; DB 6; Length 54;
Best Local Similarity	100.0%;	Pred. No. 2.5e+03;
RESULT 1456		
ID ABM35447 standard; protein; 54 AA.		
DE Propionibacterium acnes predicted ORF-encoded polypeptide #523.		
PN WO2003033515-A1.		
PD 24-APR-2003.		
PA (CORI-) CORIXA CORP.		
Query Match	0.8%;	Score 6; DB 6; Length 54;
Best Local Similarity	100.0%;	Pred. No. 2.5e+03;
RESULT 1457		
ID AAR45145 standard; protein; 55 AA.		
DE Plasmid pCDM6-D09 - D44 fragment D11.		
PN WO9324624-A1.		
PD 09-DEC-1993.		
PA (SUMU) SUMITOMO PHARM CO LTD.		
Query Match	0.8%;	Score 6; DB 2; Length 55;
Best Local Similarity	100.0%;	Pred. No. 2.5e+03;
RESULT 1458		
ID AAR45146 standard; protein; 56 AA.		
DE Plasmid pCDM6-D09 - D44 Fragment D(1+11).		
PN WO9324624-A1.		
PD 09-DEC-1993.		
PA (SUMU) SUMITOMO PHARM CO LTD.		
Query Match	0.8%;	Score 6; DB 2; Length 56;
Best Local Similarity	100.0%;	Pred. No. 2.5e+03;
RESULT 1459		
ID AAR64210 standard; peptide; 56 AA.		
DE Tissue plasminogen activator residues 266-321.		
PN JP06327473-A.		
PD 29-NOV-1994.		
PA (SUMU) SUMITOMO SEIYAKU KK.		
Query Match	0.8%;	Score 6; DB 2; Length 56;
Best Local Similarity	100.0%;	Pred. No. 2.5e+03;
RESULT 1460		
ID AAG2118 standard; protein; 56 AA.		
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23558.		
PN EP1033405-A2.		
PD 06-SEP-2000.		
Query Match	0.8%;	Score 6; DB 3; Length 56;
Best Local Similarity	100.0%;	Pred. No. 2.5e+03;
RESULT 1461		
ID AAG55284 standard; protein; 56 AA.		
DE Arabidopsis thaliana protein fragment SEQ ID NO: 70861.		
PN EP1033405-A2.		
PD 06-SEP-2000.		
Query Match	0.8%;	Score 6; DB 3; Length 56;
Best Local Similarity	100.0%;	Pred. No. 2.5e+03;
RESULT 1462		

ID AAM14482 standard; protein; 56 AA.
DE Peptide #916 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1463
ID ABB33430 standard; peptide; 56 AA.
DE Peptide #936 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1464
ID AAM26895 standard; protein; 56 AA.
DE Peptide #932 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1465
ID ABB28255 standard; peptide; 56 AA.
DE Human peptide #906 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1466
ID ABB18889 standard; protein; 56 AA.
DE Protein #888 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1467
ID AAM66609 standard; protein; 56 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26915.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1468
ID AAM54215 standard; protein; 56 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26320.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1469
ID ABB44827 standard; peptide; 56 AA.
DE Human liver peptide; SEQ ID NO 26925.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1470
ID AAM02209 standard; protein; 56 AA.
DE Peptide #891 encoded by probe for measuring human breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1471
ID ABB05146 standard; protein; 56 AA.

DE Human ORFX protein sequence SEQ ID NO:10274.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 0.8%; Score 6; DB 5; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1472
ID ABB09848 standard; protein; 56 AA.
DE Human ORFX protein sequence SEQ ID NO:19678.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 0.8%; Score 6; DB 5; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1473
ID ABB36261 standard; peptide; 56 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 25926.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 5; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1474
ID ABB05586 standard; protein; 56 AA.
DE M. tuberculosis and M. leprae marker protein #237.
PN WO200274903-A2.
PD 26-SEP-2002.
PA (INSP-) INST PASTEUR.
Query Match 0.8%; Score 6; DB 5; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1475
ID ABB47344 standard; protein; 56 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1222.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 0.8%; Score 6; DB 8; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1476
ID AAG10655 standard; protein; 57 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9063.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 3; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
RESULT 1477
ID AAR45147 standard; protein; 58 AA.
DE Plasmid pCDM8-D09 - D44 fragment D(14).
PN WO9324624-A1.
PD 09-DEC-1993.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
RESULT 1478
ID AAO1116 standard; protein; 58 AA.
DE Human polypeptide SEQ ID NO 25008.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
RESULT 1479
ID AAO02406 standard; protein; 58 AA.
DE Human polypeptide SEQ ID NO 16238.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
RESULT 1480
ID AAB41904 standard; protein; 59 AA.
DE Human ORFX ORF1668 polypeptide sequence SEQ ID NO:3336.
PN WO200058473-A2.

PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 0.8%; Score 6; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1481
ID AAB90620 standard; protein; 59 AA.
DE Human secreted protein, SEQ ID NO: 163.
PN W0200121658-A1.
PD 29-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1482
ID AAG99892 standard; peptide; 59 AA.
DE ERA binding domain polypeptide SEQ ID NO 334.
PN W0200153458-A2.
PD 26-JUL-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1483
ID AAM96307 standard; protein; 59 AA.
DE Human reproductive system related antigen SEQ ID NO: 4965.
PN W0200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1484
ID AAO11933 standard; protein; 59 AA.
DE Human polypeptide SEQ ID NO 25825.
PN W0200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1485
ID AAU64191 standard; protein; 59 AA.
DE Propionibacterium acnes immunogenic protein #25087.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1486
ID AAU43121 standard; protein; 59 AA.
DE Propionibacterium acnes immunogenic protein #4017.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1487
ID AAU65216 standard; protein; 59 AA.
DE Propionibacterium acnes immunogenic protein #26112.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1488
ID AAM61735 standard; protein; 59 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #26411.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1489
ID AAM39640 standard; protein; 59 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4316.
PD W02003033515-A1.

PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1490
ID AAM60710 standard; protein; 59 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #25386.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1491
ID AAB70853 standard; protein; 60 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39351.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1492
ID AAB41719 standard; peptide; 60 AA.
DE Peptide #9225 encoded by human foetal liver single exon probe.
PN W0200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1493
ID AAM35515 standard; protein; 60 AA.
DE Peptide #9552 encoded by probe for measuring placental gene expression.
PN W0200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1494
ID AAM75403 standard; protein; 60 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 35709.
PN W0200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1495
ID AAU52361 standard; protein; 60 AA.
DE Propionibacterium acnes immunogenic protein #13257.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1496
ID AAU63335 standard; protein; 60 AA.
DE Propionibacterium acnes immunogenic protein #24231.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1497
ID AAU61570 standard; protein; 60 AA.
DE Propionibacterium acnes immunogenic protein #22466.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1498
ID AAM62593 standard; protein; 60 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 34698.
PN W0200157275-A2.
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1499
ID ABG57158 standard; peptide; 60 AA.
DE Human liver peptide; SEQ ID No 35806.
PN WO200157273-A2.
PD 09-AUG-2001.
PR (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1500
ID ABG44990 standard; peptide; 60 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 34655.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 5; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 8, 2005, 16:06:48 ; Search time 18 Seconds
(without alignments)
3848.671 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 720

Sequence: 1 MEIGCWTVQLFPLQLLIS.....LSTAFKVLPEFKDIERNMK 720

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1500 summaries

Database :

1: p1r79:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	178	24.7	181	2 T08805	hypothetical prote
2	9	1.2	232	2 E70372	hypothetical prote
3	9	1.2	276	2 T29125	ketocacyl reductase
4	9	1.2	730	1 BMH01	procollagen C-endo
5	9	1.2	823	1 A58788	procollagen C-endo
6	9	1.2	986	1 B58788	procollagen C-endo
7	9	1.2	991	2 I49540	procollagen C-endo
8	9	1.2	1464	2 S58984	development protei
9	9	1.2	2531	2 T31070	notch homolog - se
10	9	1.1	114	2 S00996	Ig kappa chain pre
11	8	1.1	158	2 G70323	conserved hypochet
12	8	1.1	235	2 D42696	thrombin (EC 3.4.2
13	8	1.1	235	2 H42696	thrombin (EC 3.4.2
14	8	1.1	236	2 C42696	thrombin (EC 3.4.2
15	8	1.1	240	2 AB0338	probable membrane
16	8	1.1	302	2 T25020	hypothetical prote
17	8	1.1	395	2 A82283	vibriolectin-spect
18	8	1.1	407	1 KFB07	coagulation factor
19	8	1.1	486	2 T38174	probable GCS1/GLO3
20	8	1.1	737	2 AG2156	hypothetical prote
21	8	1.1	1019	2 A38738	coagulation factor
22	8	1.1	1070	2 T31069	collid-BMP-1 like
23	7	1.0	59	2 B89983	hypothetical prote
24	7	1.0	75	2 AB6487	unknown protein [i
25	7	1.0	91	2 E96528	protein F27015.6 [i
26	7	1.0	114	2 D72600	hypothetical prote
27	7	1.0	143	2 A85072	hypothetical prote
28	7	1.0	167	2 S05364	hypothetical prote
29	7	1.0	168	2 D86534	CT066 hypothetical

30	7	1.0	168	2 D72089	ct066 hypothetical
31	7	1.0	171	2 E81580	conserved hypochet
32	7	1.0	173	2 T45501	hypothetical prote
33	7	1.0	178	2 F86271	protein F16A14.6 [i
34	7	1.0	191	2 G75299	cellulium resistan
35	7	1.0	193	2 G64241	hypothetical prote
36	7	1.0	196	2 JC4257	beta A4-crystallin
37	7	1.0	201	2 S16262	auxin-binding prot
38	7	1.0	209	2 S27494	nods protein - Bra
39	7	1.0	211	2 AC0268	probable exported
40	7	1.0	212	2 AE0652	probable outer mem
41	7	1.0	212	2 S07797	ycid protein precu
42	7	1.0	212	2 C85706	probable outer mem
43	7	1.0	212	2 D90848	hypothetical prote
44	7	1.0	213	2 B86828	hypothetical prote
45	7	1.0	215	2 T50589	probable TetR-fami
46	7	1.0	227	2 D69296	conserved hypochet
47	7	1.0	231	2 A86592	low calcium respon
48	7	1.0	231	2 H72031	type III secretion
49	7	1.0	232	2 C83139	outer membrane pro
50	7	1.0	235	2 E42696	thrombin (EC 3.4.2
51	7	1.0	236	2 F84273	hypothetical prote
52	7	1.0	239	2 G42696	thrombin (EC 3.4.2
53	7	1.0	239	2 B82123	chemotaxis protein
54	7	1.0	243	2 A56338	venom proteinase (
55	7	1.0	247	2 G86011	glycerophosphodies
56	7	1.0	247	2 G91165	glycerophosphodies
57	7	1.0	250	2 A10206	probable chaperone
58	7	1.0	255	2 S07553	hypothetical prote
59	7	1.0	259	2 A12835	N-acetylmutamoyl-L
60	7	1.0	259	2 D97613	hypothetical prote
61	7	1.0	260	2 A36402	corticotropin / li
62	7	1.0	263	2 S05433	corticotropin / li
63	7	1.0	265	2 E70520	hypothetical prote
64	7	1.0	270	2 S04380	opacity protein P.
65	7	1.0	271	2 S05620	hypothetical prote
66	7	1.0	307	2 B82343	D-isomer specific
67	7	1.0	312	2 S67052	hypothetical prote
68	7	1.0	315	2 A87249	conserved hypochet
69	7	1.0	333	2 A84055	transcription regu
70	7	1.0	336	2 G87202	probable membrane
71	7	1.0	337	2 D72690	hypothetical prote
72	7	1.0	339	2 AG2041	queuine tRNA-ribos
73	7	1.0	349	2 C72630	probable threonine
74	7	1.0	350	2 T25172	hypothetical prote
75	7	1.0	351	2 S67649	MSS2 protein - yea
76	7	1.0	355	2 T13831	NADH2 dehydrogenas
77	7	1.0	355	2 T13830	NADH2 dehydrogenas
78	7	1.0	355	2 T14016	NADH2 dehydrogenas
79	7	1.0	355	2 T11734	NADH2 dehydrogenas
80	7	1.0	355	2 T14009	NADH2 dehydrogenas
81	7	1.0	355	2 T14012	NADH2 dehydrogenas
82	7	1.0	355	2 T14011	NADH2 dehydrogenas
83	7	1.0	355	2 T11737	NADH2 dehydrogenas
84	7	1.0	355	2 T13989	NADH2 dehydrogenas
85	7	1.0	355	2 T14010	NADH2 dehydrogenas
86	7	1.0	355	2 T11752	NADH2 dehydrogenas
87	7	1.0	355	2 T11760	NADH2 dehydrogenas
88	7	1.0	355	2 T14013	NADH2 dehydrogenas
89	7	1.0	355	2 T11733	NADH2 dehydrogenas
90	7	1.0	355	2 T11762	NADH2 dehydrogenas
91	7	1.0	355	2 T14014	NADH2 dehydrogenas
92	7	1.0	355	2 T11754	NADH2 dehydrogenas
93	7	1.0	355	2 T13988	NADH2 dehydrogenas
94	7	1.0	355	2 T14008	NADH2 dehydrogenas
95	7	1.0	355	2 T11739	NADH2 dehydrogenas
96	7	1.0	355	2 T13977	NADH2 dehydrogenas
97	7	1.0	355	2 T13894	NADH2 dehydrogenas
98	7	1.0	355	2 T12118	NADH2 dehydrogenas
99	7	1.0	355	2 T14028	NADH2 dehydrogenas
100	7	1.0	355	2 T14048	NADH2 dehydrogenas
101	7	1.0	355	2 T11603	NADH2 dehydrogenas
102	7	1.0	355	2 T11604	NADH2 dehydrogenas

ct066 hypothetical
conserved hypochet
hypothetical prote
protein F16A14.6 [i
cellulium resistan
hypothetical prote
beta A4-crystallin
auxin-binding prot
nods protein - Bra
probable exported
probable outer mem
ycid protein precu
probable outer mem
hypothetical prote
probable TetR-fami
conserved hypochet
low calcium respon
type III secretion
outer membrane pro
thrombin (EC 3.4.2
hypothetical prote
thrombin (EC 3.4.2
chemotaxis protein
venom proteinase (

103	7	1.0	355	2	T11602	NADH2 dehydrogenas	176	6	0.8	27	2	A33431	atrial natriuretic
104	7	1.0	355	2	T11601	NADH2 dehydrogenas	177	6	0.8	35	2	D82224	hypothetical prote
105	7	1.0	355	2	T12109	NADH2 dehydrogenas	178	6	0.8	40	2	E82433	hypothetical prote
106	7	1.0	355	2	T12107	NADH2 dehydrogenas	179	6	0.8	48	2	G81543	hypothetical prote
107	7	1.0	355	2	T12119	NADH2 dehydrogenas	180	6	0.8	53	2	G82813	hypothetical prote
108	7	1.0	355	2	A48358	ORF355 - Bradyrhiz	181	6	0.8	54	2	A95210	conserved hypochet
109	7	1.0	359	2	A28700	mandelate racemase	182	6	0.8	54	2	H81814	probable small sec
110	7	1.0	372	2	A83260	hypothetical prote	183	6	0.8	55	1	FECLCU	ferredoxin 2[Fe-4
111	7	1.0	375	2	A81237	conserved hypochet	184	6	0.8	55	2	T07197	hypothetical prote
112	7	1.0	375	2	F81599	probable integral	185	6	0.8	56	2	E87173	conserved hypochet
113	7	1.0	387	1	S75050	IMP dehydrogenase	186	6	0.8	57	2	S66318	protein kinase AK5
114	7	1.0	387	2	AC1813	IMP dehydrogenase	187	6	0.8	57	2	S66316	protein kinase AK3
115	7	1.0	398	2	E83438	probable transpor	188	6	0.8	59	2	A83209	hypothetical prote
116	7	1.0	413	2	F69383	coenzyme F390 synt	189	6	0.8	62	2	G59147	conotoxin Im5.1 pr
117	7	1.0	437	2	TS0237	hypothetical 48k p	190	6	0.8	64	2	T08457	ferredoxin PA83048
118	7	1.0	439	2	T49289	kinesin heavy chai	191	6	0.8	64	2	H75204	degenerate transpo
119	7	1.0	459	2	T08594	probable sulfate a	192	6	0.8	67	2	D98068	hypothetical prote
120	7	1.0	461	2	D70561	hypothetical prote	193	6	0.8	68	2	T00189	hypothetical prote
121	7	1.0	472	2	T27755	hypothetical prote	194	6	0.8	68	2	A95993	hypothetical prote
122	7	1.0	479	2	H90042	hypothetical prote	195	6	0.8	69	2	AE2949	hypothetical prote
123	7	1.0	489	2	S69027	ammonium transport	196	6	0.8	70	1	R5EC31	ribosomal protein
124	7	1.0	492	2	T23349	hypothetical prote	197	6	0.8	70	2	G91236	50S ribosomal subu
125	7	1.0	492	2	S46225	ammonium transport	198	6	0.8	70	2	G82588	50S ribosomal subu
126	7	1.0	493	2	A33809	cartilage matrix p	199	6	0.8	70	2	G82588	hypothetical prote
127	7	1.0	494	1	A29079	lymphocyte surface	200	6	0.8	71	2	160082	CD4 receptor - hum
128	7	1.0	497	2	S43609	rofa protein - Str	201	6	0.8	71	2	H86751	prophage p12 prote
129	7	1.0	497	2	H70168	hypothetical prote	202	6	0.8	73	2	H83204	conserved hypochet
130	7	1.0	505	2	C90869	hypothetical prote	203	6	0.8	73	2	F97136	hypothetical prote
131	7	1.0	529	2	T18595	hypothetical prote	204	6	0.8	75	2	UQ1429	hypothetical 8.1K
132	7	1.0	532	2	A72694	hypothetical prote	205	6	0.8	75	2	D82592	hypothetical prote
133	7	1.0	544	2	S06602	modulo antigen - f	206	6	0.8	77	2	T06954	hypothetical prote
134	7	1.0	553	2	D95071	metallo-beta-lacta	207	6	0.8	77	2	AC2101	lipoprotein limpor
135	7	1.0	556	2	B97939	conserved hypochet	208	6	0.8	78	2	A42506	F-ORF-B protein -
136	7	1.0	566	2	S02154	NADH2 dehydrogenas	209	6	0.8	79	2	D69309	conserved hypochet
137	7	1.0	561	2	C75543	6-aminohexanoate-c	210	6	0.8	80	2	E97949	hypothetical prote
138	7	1.0	580	2	D84772	probable sugar tra	211	6	0.8	80	2	S27162	heparin-binding ep
139	7	1.0	581	2	T38864	probable regulator	212	6	0.8	84	2	G64217	ribosomal protein
140	7	1.0	582	2	F71411	hypothetical prote	213	6	0.8	85	2	T12211	auxin-induced prot
141	7	1.0	583	2	T25690	hypothetical prote	214	6	0.8	85	2	T02494	hypothetical prote
142	7	1.0	585	2	T18736	hypothetical prote	215	6	0.8	86	2	E90660	damage-inducible p
143	7	1.0	617	2	S10511	thrombin (BC 3.4.2	216	6	0.8	86	2	C85511	DNA-damage-inducib
144	7	1.0	617	2	D90467	maltoase ABC transp	217	6	0.8	86	2	G64747	hypothetical prote
145	7	1.0	618	2	A35827	thrombin (BC 3.4.2	218	6	0.8	87	2	T10462	hypothetical prote
146	7	1.0	622	1	T8HU	thrombin (BC 3.4.2	219	6	0.8	87	2	T50008	hypothetical prote
147	7	1.0	625	1	T8BO	thrombin (BC 3.4.2	220	6	0.8	88	2	B82860	hypothetical prote
148	7	1.0	658	2	T04831	probable serine/th	221	6	0.8	88	2	C97251	probable membrane
149	7	1.0	678	2	D87607	hypothetical prote	222	6	0.8	88	2	AB1901	hypothetical prote
150	7	1.0	684	2	H96646	hypothetical prote	223	6	0.8	88	2	C81922	hypothetical prote
151	7	1.0	684	2	T02149	hypothetical prote	224	6	0.8	91	2	AE0710	conserved hypochet
152	7	1.0	707	2	JC2218	procollagen C-endo	225	6	0.8	92	2	F36905	conserved hypochet
153	7	1.0	709	2	T43109	cytolysin B transp	226	6	0.8	94	2	T44732	hypothetical prote
154	7	1.0	746	2	C95110	competence protein	227	6	0.8	95	2	C83517	hypothetical prote
155	7	1.0	783	2	B83232	conserved hypochet	228	6	0.8	95	2	B82463	hypothetical prote
156	7	1.0	790	2	G02678	cadherin-14 - huma	229	6	0.8	98	2	T44883	hypothetical prote
157	7	1.0	791	2	H96839	hypothetical prote	230	6	0.8	98	2	S03386	antigen (clone 22)
158	7	1.0	825	2	T06036	hypothetical prote	231	6	0.8	99	2	S44658	ZK353.2 protein -
159	7	1.0	833	2	S50225	potassium transpor	232	6	0.8	100	2	C71012	hypothetical prote
160	7	1.0	841	2	T38703	hypothetical prote	233	6	0.8	102	2	D84024	transcription regu
161	7	1.0	856	2	T16543	hypothetical prote	234	6	0.8	104	2	I40195	transposase - Bact
162	7	1.0	859	2	S66827	aluminum resistan	235	6	0.8	104	2	F45681	orf 61.2 - phage T
163	7	1.0	903	2	B88221	protein T0133.2 [i	236	6	0.8	104	2	C69068	divalent cation to
164	7	1.0	980	2	T24336	hypothetical prote	237	6	0.8	105	2	D90392	conserved hypochet
165	7	1.0	995	2	AB8483	protein C05D1.1 [238	6	0.8	106	2	G71517	probable L21 ribos
166	7	1.0	1048	2	T31653	hypothetical prote	239	6	0.8	107	2	G84532	similar to gibbere
167	7	1.0	1100	2	JC8033	leukocyte formin p	240	6	0.8	108	2	A28667	hypothetical prote
168	7	1.0	1240	2	T04833	hypothetical prote	241	6	0.8	109	2	B53291	tetracenomycin-bio
169	7	1.0	1346	2	T17412	polyketide synthas	242	6	0.8	109	2	T47985	hypothetical prote
170	7	1.0	1522	2	S48904	probable purine nu	243	6	0.8	109	2	T44129	hypothetical prote
171	7	1.0	1742	2	T49451	kinesin-like prote	244	6	0.8	109	2	T45195	hypothetical prote
172	7	1.0	1822	2	T50207	probable protein c	245	6	0.8	113	2	T45195	hypothetical prote
173	7	1.0	2605	2	T18552	saframycin Mxi syn	246	6	0.8	114	2	T26771	hypothetical prote
174	7	1.0	2907	2	A57278	fibrillin-2 precur	247	6	0.8	115	2	H72705	hypothetical prote
175	7	1.0	2918	2	A54105	fibrillin-2 precur	248	6	0.8	116	2	D96530	probable ribosomal

249	6	0.8	117	2	I51573	gene wnt-2 protein	322	159	2	A72709	hypothetical prote
250	6	0.8	117	2	H90021	50S ribosomal prot	323	159	2	D86743	hypothetical prote
251	6	0.8	117	2	C72511	hypothetical prote	324	159	2	D86286	Similar to gb - Ar
252	6	0.8	118	2	H71564	hypothetical prote	325	160	2	H55545	APA-III adhesin -
253	6	0.8	118	2	T14660	hypothetical prote	326	160	2	T35987	probable ribosome-
254	6	0.8	118	2	JC5793	elongin B - fruit	327	160	2	AC0835	Sara (tmRNA)-bindi
255	6	0.8	119	2	F70941	hypothetical prote	328	160	2	AE0135	Sara-binding prote
256	6	0.8	122	2	H64217	ribosomal protein	329	160	2	T48148	hypothetical prote
257	6	0.8	122	2	S62831	ribosomal protein	330	161	2	T31531	hypothetical prote
258	6	0.8	123	2	E71163	hypothetical prote	331	161	2	E90372	conserved hypotet
259	6	0.8	123	2	S72389	hypothetical prote	332	162	2	H75071	transcription regu
260	6	0.8	123	2	S75382	hypothetical prote	333	162	2	C97657	pexB protein limpo
261	6	0.8	124	1	MNIV71	nonstructural prot	334	162	2	AC2881	DNA-binding protei
262	6	0.8	124	2	A81163	conserved hypotet	335	162	2	H70803	probable transcrip
263	6	0.8	124	2	F81942	probable regulator	336	162	2	AB1950	hypothetical prote
264	6	0.8	126	2	T47297	hypothetical prote	337	162	2	H71093	hypothetical prote
265	6	0.8	127	2	T14956	hypothetical prote	338	163	2	B97290	3-isopropylmalate
266	6	0.8	127	2	F69377	molybdenum-pterin-	339	164	2	A45512	cold-regulated pro
267	6	0.8	127	2	T05261	cold-regulated pro	340	164	2	JC4675	transcription fact
268	6	0.8	129	2	T06188	probable DNA-dirc	341	165	2	AB0851	hypothetical prote
269	6	0.8	129	2	S52792	Ig kappa chain V r	342	165	2	S70217	sipE protein - Sal
270	6	0.8	129	2	C69488	LSU ribosomal prot	343	165	2	A57357	sicA protein - Sal
271	6	0.8	129	2	E75602	hypothetical prote	344	165	2	H86948	probable transcrip
272	6	0.8	130	2	S57896	polyketide synthas	345	165	2	I39546	hypothetical prote
273	6	0.8	130	2	T35906	probable quinone b	346	167	2	E71391	NADH2 dehydrogenas
274	6	0.8	130	2	B83992	hypothetical prote	347	167	2	AD0601	DNA protection dur
275	6	0.8	131	2	T49455	hypothetical prote	348	167	2	B90740	global regulator p
276	6	0.8	131	2	T29078	hypothetical prote	349	167	2	A46401	DNA-binding protei
277	6	0.8	132	2	T50416	40S ribosomal prot	350	167	2	D85590	global regulator,
278	6	0.8	132	2	H87626	hypothetical prote	351	167	2	AG0306	probable DNA-bind
279	6	0.8	133	2	E71062	hypothetical prote	352	167	2	S11411	hypothetical prote
280	6	0.8	133	2	F81748	conserved hypotet	353	168	2	A69708	signal peptidase I
281	6	0.8	133	2	H81191	hypothetical prote	354	169	2	B48489	nitrate reductase
282	6	0.8	134	2	E71945	hypothetical prote	355	170	2	A86638	protein F58F6.3 [i
283	6	0.8	134	2	F64561	conserved hypotet	356	171	2	S76982	hypothetical prote
284	6	0.8	134	2	B72651	hypothetical prote	357	171	2	T41924	hypothetical prote
285	6	0.8	136	2	E69376	hypothetical prote	358	172	2	AG3532	D-lactate dehydrog
286	6	0.8	136	2	E90394	ferric uptake regu	359	172	2	G82151	peptidoglycan-asso
287	6	0.8	137	2	A83852	hypothetical prote	360	172	2	G69087	conserved hypotet
288	6	0.8	138	2	D83824	transcription regu	361	172	2	AE2283	hypothetical prote
289	6	0.8	138	2	T29558	hypothetical prote	362	172	2	D71136	hypothetical prote
290	6	0.8	139	2	G90414	conserved hypotet	363	173	2	H70113	ribosomal protein
291	6	0.8	140	2	B81659	conserved hypotet	364	174	2	E69038	heat shock protein
292	6	0.8	141	2	T33271	hypothetical prote	365	175	2	T07877	self-pruning prote
293	6	0.8	141	2	S55247	hemoglobin alpha-A	366	175	2	AC3014	Mut7/nudix family
294	6	0.8	141	2	I39720	ORF10 - Agrobacter	367	175	2	G86458	unknown protein, 7
295	6	0.8	141	2	G72661	hypothetical prote	368	176	2	A34690	DNA-binding protei
296	6	0.8	143	2	S50549	hypothetical prote	369	176	2	AE0866	conserved hypotet
297	6	0.8	143	2	B72627	hypothetical prote	370	177	2	S45878	hypothetical prote
298	6	0.8	144	2	T49457	hypothetical prote	371	177	2	E95222	conserved hypotet
299	6	0.8	145	2	C64447	hypothetical prote	372	177	2	D75309	protein-tyrosine p
300	6	0.8	145	2	F84251	hypothetical prote	373	177	2	E98086	conserved hypotet
301	6	0.8	146	2	H64340	hypothetical prote	374	178	2	A95367	probable NADH2 deh
302	6	0.8	147	2	S01655	alpha-amylase/tryp	375	178	2	B42845	3-hydroxybutyrate
303	6	0.8	147	2	T35980	probable peptide t	376	178	2	H84789	hypothetical prote
304	6	0.8	149	2	T35846	probable integral	377	178	2	A86836	hypothetical prote
305	6	0.8	149	2	T49200	hypothetical prote	378	178	2	S26481	calcium-binding pr
306	6	0.8	150	2	AC1720	transcription regu	379	179	2	G75462	ribonuclease H - D
307	6	0.8	151	2	C71503	probable rRNA meth	380	179	2	G90003	ATP synthase delta
308	6	0.8	151	2	B87824	transcription regu	381	180	2	FC1305	genome polyprotein
309	6	0.8	151	2	A97008	transcription regu	382	180	2	PC1304	genome polyprotein
310	6	0.8	152	2	D98270	hypothetical prote	383	180	2	FC1303	genome polyprotein
311	6	0.8	153	2	T06564	alpha-amylase/tryp	384	180	2	T23339	hypothetical prote
312	6	0.8	153	2	C98238	hypothetical 16.4K	385	182	2	T39915	meiotic recombinat
313	6	0.8	153	2	AH3047	conserved hypotet	386	182	2	A72361	hypothetical prote
314	6	0.8	153	2	AB1907	hypothetical prote	387	183	2	E69432	hypothetical prote
315	6	0.8	154	2	E83634	hypothetical prote	388	183	2	T07677	piuII-specific pr
316	6	0.8	155	2	B90143	hypothetical prote	389	184	2	T09609	uroplakin II - hum
317	6	0.8	155	2	A82884	conserved hypotet	390	184	2	A54135	uroplakin II precu
318	6	0.8	156	2	G69233	N-terminal acetyl	391	184	2	JC7839	uroplakin II prote
319	6	0.8	157	2	T28321	ORF MSV160 hypothe	392	184	2	E87506	hypothetical prote
320	6	0.8	158	2	D82499	hypothetical prote	393	185	2	F04779	flavodoxin - Aquif
321	6	0.8	159	2	B70635	hypothetical prote	394	185	2	B81732	general stress pro

395	185	2	E71469	probable general s	468	208	2	D87565	conserved hypothet
396	185	2	A49713	uroplakin II precu	469	209	2	A99460	conserved hypothet
397	186	1	R5B8E	ribosomal protein	470	209	2	C87521	hypothetical prote
398	186	2	T41601	hypothetical prote	471	209	2	T07779	dehydrin homolog C
399	187	2	G75022	hypothetical prote	472	210	2	G95858	probable 3-octapre
400	187	2	B83084	hypothetical prote	473	210	2	D84238	hypothetical prote
401	188	2	S70580	bplJ protein - Bor	474	210	2	H75361	leu/phe-tRNA-prote
402	188	2	AMECRD	3-octaprenyl-4-hyd	475	211	1	ZKBP74	transcription regu
403	189	1	XB0801	probable decarboxy	476	211	2	T47580	ribosomal protein
404	189	2	C91028	3-octaprenyl-4-hyd	477	211	2	S45464	hypothetical prote
405	189	2	D85872	3-octaprenyl-4-hyd	478	212	1	QQLJZR	nef protein - huma
406	189	2	D71658	3-octaprenyl-4-hyd	479	212	2	S37973	DNA-directed RNA p
407	189	2	T51064	hypothetical prote	480	214	2	D45681	glutathione transf
408	189	2	AB0361	probable iron-sulp	481	214	2	E46681	glutathione transf
409	189	2	AE0338	probable 3-octapre	482	214	2	T14920	hypothetical prote
410	190	2	A97800	hypothetical prote	483	215	2	C46681	glutathione transf
411	191	2	C64574	hypothetical prote	484	215	2	AD0455	thiamine-phosphate
412	191	2	A45816	MHC class II histo	485	215	2	T45985	hypothetical prote
413	192	2	H72099	phenylacrylate dec	486	216	1	T16383	hypothetical prote
414	192	2	H86523	phenylacrylate dec	487	216	1	C64081	L-fucose-phospha
415	192	2	E75021	probable transcript	488	216	2	D85664	YagE family (impor
416	193	2	T30325	hypothetical prote	489	216	2	G72060	YagE family - Chla
417	194	1	HSU10	histone H1-0 - hum	490	216	2	G72509	hypothetical prote
418	194	2	C82041	general secretion	491	217	2	D82407	outer membrane pro
419	196	2	D98190	decarboxylase (imp	492	217	2	F85571	probable carboxyla
420	196	2	AE3096	phenylacrylic acid	493	218	2	H90720	probable carboxyla
421	196	2	AC3629	3-octaprenyl-4-hyd	494	218	2	F64806	YbgJ protein - Esc
422	197	1	R5MUL9	ribosomal protein	495	218	2	B64595	endonuclease III -
423	197	2	E95411	probable decarboxy	496	218	2	C71918	endonuclease III -
424	197	2	B70761	probable lipoprote	497	218	2	A70601	hypothetical prote
425	197	2	D87309	hypothetical prote	498	218	2	T50440	glycerone kinase (
426	197	2	H75188	hypothetical prote	499	218	2	AG3301	conserved hypothet
427	198	2	E81391	probable transcript	500	218	2	H87666	hypothetical prote
428	198	2	AC1890	hypothetical prote	501	218	2	E75389	hypothetical prote
429	199	2	A46681	glutathione transf	502	218	2	G69374	14-3-3 protein hom
430	199	2	G75575	hypothetical prote	503	218	2	AI3612	hypothetical cytos
431	200	2	B95349	Probable decarboxy	504	220	2	S20581	hypothetical prote
432	201	2	C36885	bo-type ubiquinol	505	220	2	T26991	hypothetical prote
433	201	2	AD2419	SOS function regul	506	221	2	B70890	oligopeptide ABC t
434	201	2	C69271	hypothetical prote	507	221	2	AI1232	glutamate-5-phospha
435	201	2	H81731	CDP-diacylglycerol	508	222	2	AC1495	ribulose-5-phospha
436	202	2	H81731	probable glycerol-	509	222	2	T35145	glutamate transpor
437	202	2	C71469	probable sigma fac	510	222	2	AH0991	cell division ATP-
438	202	2	T37025	hypothetical prote	511	222	2	AB1408	hypothetical prote
439	202	2	AD2197	hypothetical prote	512	223	2	AG1166	phosphoribosylform
440	202	2	D72573	hypothetical prote	513	223	2	C81397	potassium uptake p
441	203	2	S74809	lexA protein - Syn	514	223	2	T34828	hypothetical prote
442	203	2	AH0223	probable glycosida	515	223	2	D75040	hypothetical prote
443	204	2	C38129	bo-type ubiquinol	516	224	1	R5SP11	ribosomal protein
444	204	2	S03246	nef protein (clone	517	224	2	C86571	L4 ribosomal prote
445	205	1	XMBST1	hypothetical prote	518	224	2	H72055	ribosomal protein
446	205	1	ASLJH3	regulatory protein	519	224	2	C81417	probable transcript
447	205	2	D85764	nef protein - huma	520	224	2	T21101	hypothetical prote
448	205	2	G64914	probable oxidoredu	521	224	2	B97580	hypothetical prote
449	205	2	G90915	dimethylsulfoxide	522	225	2	AB2800	conserved hypothet
450	205	2	T01744	probable oxidoredu	523	225	2	AH2800	hypothetical prote
451	205	2	S43467	ribosomal protein	524	226	2	T29632	tox regulon trans
452	205	2	D69036	nef protein - huma	525	226	2	A35568	hypothetical prote
453	205	2	C82325	conserved hypothet	526	227	2	T22144	flagellar hook ass
454	205	2	JC7975	maf protein VC0418	527	227	2	A87361	hypothetical prote
455	206	1	ASLJ12	HIV accessory prot	528	227	2	T41133	conserved hypothet
456	206	1	ASLJFV	nef protein - huma	529	228	2	AB0438	probable smp prote
457	206	1	ASLJVL	nef protein - huma	530	228	2	B82087	cytochrome-c oxida
458	206	2	A86609	glycerol-3-P phosp	531	229	2	S70599	cytochrome-c oxida
459	206	2	B72016	CDP-diacylglycerol	532	229	2	S14207	probable antitermi
460	206	2	S03245	nef protein (clone	533	229	2	C90912	antiterminator lim
461	206	2	S33986	nef protein - huma	534	229	2	F90972	antiterminator lim
462	206	2	S03244	nef protein (clone	535	229	2	C85920	lysine decarboxyla
463	206	2	S03268	heterochromatin pr	536	230	1	T48348	nonstructural prot
464	208	1	A38432	heparin-binding EG	537	230	1	MNIV16	nonstructural prot
465	208	1	A41914	diphtheria toxin re	538	230	1	MNIV45	nonstructural prot
466	208	2	A41636	GTP-binding protei	539	230	1	MNIV46	nonstructural prot
467	208	2	B64357	ribosomal protein	540	230	1	MNIV47	nonstructural prot

541	6	0.8	230	1	MNIVAB	nonstructural prot	614	257	2	JQ0064	MERS5 protein - mou
542	6	0.8	230	2	A45575	nonstructural prot	615	257	2	T00780	myb-related protei
543	6	0.8	230	2	G70504	probable cmk prot	616	257	2	T33292	hypothetical prote
544	6	0.8	231	2	S57271	14-3-3 protein hom	617	258	2	T07389	14-3-3 protein tft
545	6	0.8	231	2	D49934	phosphoglycolate p	618	258	2	T04131	14-3-3 protein, is
546	6	0.8	231	2	B69858	hypothetical prote	619	258	2	AP0016	probable biotin bi
547	6	0.8	231	2	A13283	transcription regu	620	258	2	AH2615	hypothetical prote
548	6	0.8	232	2	AG2525	hypothetical prote	621	258	2	G86764	hypothetical prote
549	6	0.8	233	2	I55654	MHC class II prote	622	258	2	T31647	hypothetical prote
550	6	0.8	233	2	C82360	cell division ATP-	623	259	1	A47237	14-3-3 protein hom
551	6	0.8	233	2	A72786	probable transport	624	259	2	B69113	cell division inhi
552	6	0.8	233	2	H75359	hypothetical prote	625	259	2	G97397	ubiquinone/menaqui
553	6	0.8	234	2	S61309	nitrate reductase	626	259	2	D81083	conserved hypotnet
554	6	0.8	234	2	T07686	transcription fact	627	259	2	D81859	conserved hypotnet
555	6	0.8	234	2	F95952	transable membrane-	628	260	1	S30927	14-3-3 protein hom
556	6	0.8	234	2	C97001	ABC transporter, A	629	260	2	T07388	14-3-3 protein tft
557	6	0.8	235	2	B98108	response regulator	630	260	2	T02051	14-3-3 protein hom
558	6	0.8	235	2	E95243	response regulator	631	260	2	S20580	14-3-3 protein hom
559	6	0.8	235	2	C75030	hypothetical prote	632	260	2	D69299	hypothetical prote
560	6	0.8	236	2	AH3230	hypothetical prote	633	260	2	T51079	related to chitina
561	6	0.8	236	2	E42600	probable octopine	634	261	1	S18911	14-3-3 protein hom
562	6	0.8	236	2	T10417	p25 protein - Orgy	635	261	2	S52110	sepiapterin reduct
563	6	0.8	236	2	T02432	ethylene-responsiv	636	261	2	A71192	probable glucosae 1
564	6	0.8	237	2	E97712	transcription acti	637	261	2	S52899	14-3-3 protein hom
565	6	0.8	237	2	C70157	hypothetical prote	638	261	2	H83442	probable enoyl-CoA
566	6	0.8	238	2	I71907	MHC H2-IE-beta cel	639	261	2	H70100	conserved hypotnet
567	6	0.8	238	2	T14629	hypothetical prote	640	261	2	D64166	hypothetical prote
568	6	0.8	239	2	A72623	hypothetical prote	641	262	2	H71390	cytochrome-c oxida
569	6	0.8	239	2	D81351	hypothetical prote	642	262	2	T04406	14-3-3b protein -
570	6	0.8	240	2	T24239	hypothetical prote	643	262	2	S57276	14-3-3 protein hom
571	6	0.8	241	2	I48657	I-E(b-beta) protei	644	262	2	T47002	hypothetical prote
572	6	0.8	241	2	T23823	hypothetical prote	645	262	2	AH0238	probable phosphate
573	6	0.8	241	2	H81536	hypothetical prote	646	262	2	T22148	hypothetical prote
574	6	0.8	242	2	B82815	conserved hypotnet	647	263	2	F87043	ECF subfamily sigm
575	6	0.8	243	2	JX0162	lectin I - furze	648	263	2	T26031	hypothetical prote
576	6	0.8	244	2	C95901	probable,short cha	649	263	2	T18930	hypothetical prote
577	6	0.8	244	2	S76160	hypothetical prote	650	264	1	HLMSER1	H-2 class II histo
578	6	0.8	245	2	S28827	chlorophyll a/b-bi	651	264	1	HLMSER	H-2 class II histo
579	6	0.8	246	1	S56439	ammonium transport	652	264	1	C64368	cell division inhi
580	6	0.8	246	2	T51631	probable transcrip	653	264	2	A30529	H-2 class II histo
581	6	0.8	246	2	AF1054	cysQ protein [limpo	654	264	2	I56056	MHC E-beta-f - mou
582	6	0.8	246	2	H86118	ammonium transport	655	264	2	A81668	conserved hypotnet
583	6	0.8	247	2	H91277	ammonium transport	656	264	2	E71509	hypothetical prote
584	6	0.8	247	2	JT0555	MHC class II histo	657	264	2	T13116	protein gp30 - pha
585	6	0.8	247	2	S23474	rod-core linker po	658	264	2	D71037	hypothetical prote
586	6	0.8	247	2	H90419	hypothetical prote	659	265	2	T30246	NADH2 dehydrogenas
587	6	0.8	248	2	S53727	14-3-3 protein hom	660	265	2	T12599	NADH2 dehydrogenas
588	6	0.8	249	2	F87153	probable pseudouri	661	265	2	T12597	NADH2 dehydrogenas
589	6	0.8	249	2	H72200	conserved hypotnet	662	265	2	T12601	NADH2 dehydrogenas
590	6	0.8	250	2	T06338	probable vacuolar	663	266	2	D83210	hypothetical prote
591	6	0.8	250	2	S58362	nucleolar protein	664	266	2	T40318	hypothetical prote
592	6	0.8	250	2	S61626	hypothetical prote	665	266	2	AB3571	nickel transport A
593	6	0.8	250	2	T46912	hypothetical prote	666	266	2	H85090	probable 14-3-3 pr
594	6	0.8	250	2	H95161	conserved hypotnet	667	267	2	C86472	trypsin (EC 3.4.21
595	6	0.8	250	2	G98027	conserved hypotnet	668	267	2	S40006	hypothetical prote
596	6	0.8	250	2	E84708	probable signal pe	669	267	2	A98129	hypothetical prote
597	6	0.8	251	2	S47970	14-3-3 protein hom	670	267	2	AE3158	hypothetical prote
598	6	0.8	252	2	F84728	probable CCR4-asso	671	267	2	H90368	hypothetical prote
599	6	0.8	253	1	LD01A	discooidin I chain	672	267	2	G84862	probable clathrin
600	6	0.8	253	1	LD01C	discooidin I chain	673	268	2	H87708	exodeoxyribonuclea
601	6	0.8	253	2	AE0809	conserved hypotnet	674	268	2	A64123	tryptophan synthas
602	6	0.8	253	2	E64025	hypothetical prote	675	268	2	S11224	transcription fact
603	6	0.8	254	2	T07387	14-3-3 protein tft	676	268	2	T04966	hypothetical prote
604	6	0.8	254	2	S55375	14-3-3 protein - p	677	268	2	T40606	hypothetical prote
605	6	0.8	254	2	T07103	14-3-3 protein hom	678	269	2	T36639	probable substrate
606	6	0.8	255	2	T04127	14-3-3 protein, is	679	269	2	AG3538	ubiquinone/menaqui
607	6	0.8	255	2	T02050	14-3-3 protein hom	680	269	2	AE0466	probable haloacid
608	6	0.8	256	2	T04153	GF14-c protein - r	681	270	2	AB1308	conserved hypotnet
609	6	0.8	256	2	T10109	trypsin (EC 3.4.21	682	270	2	AB1680	conserved hypotnet
610	6	0.8	256	2	T44452	amidase yedB [limpo	683	270	2	F69362	conserved hypotnet
611	6	0.8	256	2	D70565	probable pseudouri	684	271	2	A85552	probable carboxyla
612	6	0.8	256	2	AI0267	probable membrane	685	271	2	F90701	probable carboxyla
613	6	0.8	256	2	G71121	hypothetical prote	686	271	2	G64783	probable carboxyla

687	6	0.8	272	2	B75293	amino acid ABC tra	760	6	0.8	295	2	F83412	probable transcrip
688	6	0.8	272	2	AG2819	conserved hypotet	761	6	0.8	295	2	T32202	hypothetical prote
689	6	0.8	272	2	G97597	hypothetical prote	762	6	0.8	297	2	AD3225	ABC transporter, m
690	6	0.8	273	2	D81878	probable oxidoredu	763	6	0.8	297	2	T45990	probable regulator
691	6	0.8	273	2	H81140	oxidoreductase, sh	764	6	0.8	297	2	S55063	conserved hypotet
692	6	0.8	273	2	T49994	14-3-3-like protei	765	6	0.8	297	2	H90154	hypothetical prote
693	6	0.8	273	2	F82999	CysQ protein PA517	766	6	0.8	297	2	D83357	hypothetical prote
694	6	0.8	273	2	A86280	Fla117.29 protein	767	6	0.8	297	2	T27525	probable sugar kin
695	6	0.8	273	2	AI3630	membrane protein n	768	6	0.8	298	2	AH0947	minor tail protein
696	6	0.8	273	2	AC3573	oligopeptide trans	769	6	0.8	298	2	C55223	chromosomal protei
697	6	0.8	273	2	G83403	conserved hypotet	770	6	0.8	298	2	A28260	conserved hypotet
698	6	0.8	274	2	C95924	probable response	771	6	0.8	299	2	AE0269	phosphorylase fami
699	6	0.8	274	2	G86977	probable methyltra	772	6	0.8	299	2	A87530	hypothetical prote
700	6	0.8	274	2	H83707	bacitracin resista	773	6	0.8	299	2	S30861	hypothetical prote
701	6	0.8	274	2	D96840	hypothetical prote	774	6	0.8	300	1	S40827	probable sugar kin
702	6	0.8	274	2	H70247	hypothetical prote	775	6	0.8	300	2	F91229	probable kinase [i
703	6	0.8	275	2	S40007	trypsin (EC 3.4.21	776	6	0.8	300	2	E86076	probable kinase yi
704	6	0.8	275	2	S40005	trypsin (EC 3.4.21	777	6	0.8	301	2	AD0660	probable transcrip
705	6	0.8	275	2	E70693	probable ugpE prot	778	6	0.8	301	2	E86486	protein F28J9.4 [i
706	6	0.8	275	2	G83522	conserved hypotet	779	6	0.8	302	2	S69188	probable flavonol
707	6	0.8	276	2	JE0218	28k surface antige	780	6	0.8	302	2	AF3306	dipeptide transpor
708	6	0.8	276	2	E84373	hypothetical prote	781	6	0.8	302	2	E84421	probable phosphati
709	6	0.8	278	2	AE0210	4-deoxy-L-threo-5-	782	6	0.8	302	2	B70888	hypothetical prote
710	6	0.8	278	2	AD0146	probable ABC trans	783	6	0.8	302	2	PC4287	protein kinase (EC
711	6	0.8	279	1	S74824	glutamate racemase	784	6	0.8	303	2	D83082	probable permease
712	6	0.8	279	2	C70458	diaminopimelate ep	785	6	0.8	303	2	S77278	lipic acid synthe
713	6	0.8	279	2	B70328	hypothetical prote	786	6	0.8	303	2	T36509	probable molybdopt
714	6	0.8	280	2	T36066	hypothetical prote	787	6	0.8	303	2	B72218	hypothetical prote
715	6	0.8	280	2	B84498	En/Spm-like transp	788	6	0.8	304	2	F83987	heat-shock protein
716	6	0.8	280	2	H72504	hypothetical prote	789	6	0.8	304	2	D72316	ribosomal large su
717	6	0.8	281	2	T43945	ribosomal protein	790	6	0.8	304	2	A96642	hypothetical prote
718	6	0.8	281	2	T05522	hypothetical prote	791	6	0.8	304	2	S75441	hypothetical prote
719	6	0.8	281	2	JE0418	aminoglycoside-N-a	792	6	0.8	305	2	T23022	hypothetical prote
720	6	0.8	282	2	AB1728	hypothetical prote	793	6	0.8	305	2	T20585	hypothetical prote
721	6	0.8	282	2	AC1054	conserved hypotet	794	6	0.8	306	2	A48652	transfer protein t
722	6	0.8	284	2	D81075	conserved hypotet	795	6	0.8	307	2	B83723	hypothetical prote
723	6	0.8	284	2	S75817	hypothetical prote	796	6	0.8	307	2	H70214	antigen, P35 homol
724	6	0.8	284	2	T24479	hypothetical prote	797	6	0.8	307	2	S55596	hypothetical prote
725	6	0.8	284	2	F81431	ABC transporter AT	798	6	0.8	308	2	I40166	aspartate carbamoy
726	6	0.8	285	2	B83588	hypothetical prote	799	6	0.8	308	2	S77938	EBNA-IP protein -
727	6	0.8	285	2	F70194	hypothetical prote	800	6	0.8	308	2	T05297	hypothetical prote
728	6	0.8	285	2	AH0200	conserved hypotet	801	6	0.8	308	2	E90670	probable transcrip
729	6	0.8	286	2	E97720	hflC protein (mpo	802	6	0.8	309	2	B84550	hypothetical prote
730	6	0.8	286	2	A71722	hflC protein (hflC	803	6	0.8	310	2	AE3398	N-acetyl-gamma-glu
731	6	0.8	286	2	B83343	hypothetical prote	804	6	0.8	311	2	G90407	homoserine kinase
732	6	0.8	286	2	E91277	probable oxidoredu	805	6	0.8	312	2	F82889	holliday junction
733	6	0.8	286	2	E86118	probable oxidoredu	806	6	0.8	312	2	T45834	hypothetical prote
734	6	0.8	287	2	E56436	hypothetical 29.7K	807	6	0.8	313	2	AI2202	hypothetical prote
735	6	0.8	287	2	E75202	dipeptide abc tran	808	6	0.8	314	2	C69286	probable tumor-rel
736	6	0.8	287	2	S03787	probable dimethyls	809	6	0.8	314	2	E96759	ABC-type MDR trans
737	6	0.8	287	2	AF0970	conserved hypotet	810	6	0.8	314	2	D97318	hypothetical prote
738	6	0.8	287	2	F65165	33.2 kD protein in	811	6	0.8	316	2	E70664	hypothetical prote
739	6	0.8	287	2	H86040	probable alpha hel	812	6	0.8	316	2	E97086	3',5'-cyclic-nucle
740	6	0.8	287	2	G91193	probable alpha hel	813	6	0.8	317	1	E87185	ATP sulfurylase, s
741	6	0.8	287	2	E69778	conserved hypotet	814	6	0.8	317	2	F82672	hypothetical prote
742	6	0.8	288	2	G64102	phosphatidate cyti	815	6	0.8	317	2	S72871	hypothetical prote
743	6	0.8	288	2	T22721	hypothetical prote	816	6	0.8	318	1	F70536	hypothetical prote
744	6	0.8	290	1	D47468	cytochrome-c oxida	817	6	0.8	318	2	C71168	hypothetical prote
745	6	0.8	290	2	E70141	oligopeptide trans	818	6	0.8	319	2	AC2536	hypothetical prote
746	6	0.8	290	2	T24747	hypothetical prote	819	6	0.8	320	2	T10281	exopolysphatase
747	6	0.8	290	2	F71546	probable DNA pol I	820	6	0.8	321	2	F97122	hypothetical prote
748	6	0.8	290	2	F81700	DNA polymerase III	821	6	0.8	321	2	T27463	hypothetical prote
749	6	0.8	291	2	S05508	photosystem II oxy	822	6	0.8	321	2	G72347	hypothetical prote
750	6	0.8	291	2	A97387	hypothetical prote	823	6	0.8	321	2	F81030	ABC transporter, p
751	6	0.8	291	2	AB2605	hypothetical prote	824	6	0.8	321	2	F81976	conserved hypotet
752	6	0.8	292	2	S54533	ribosomal protein	825	6	0.8	321	2	A69088	iron(III) ABC tran
753	6	0.8	292	2	T34529	hypothetical prote	826	6	0.8	322	2	G72421	hypothetical prote
754	6	0.8	292	2	T52257	CCR4-associated fa	827	6	0.8	322	2	E64238	conserved hypotet
755	6	0.8	292	2	H70513	hypothetical prote	828	6	0.8	322	2	E70306	transcription regu
756	6	0.8	293	1	D69300	4-hydroxybenzoate	829	6	0.8	322	2	AF2725	probable transcrip
757	6	0.8	293	2	T41928	hypothetical prote	830	6	0.8	322	2	B97507	hypothetical prote
758	6	0.8	293	2	T31618	hypothetical prote	831	6	0.8	323	2	T22492	probable transcrip
759	6	0.8	293	2	B75570	conserved hypotet	832	6	0.8	323	2	T47447	sulfotransferase-1

833	6	0.8	323	2	E83454	flagellar motor sw	906	6	0.8	344	2	C75203	hypothetical prote
834	6	0.8	324	2	T07832	probable steroid s	907	6	0.8	345	2	T17065	NADH2 dehydrogenas
835	6	0.8	324	2	F86788	transcription regu	908	6	0.8	345	2	JC1174	amidase (EC 3.5.1.1
836	6	0.8	325	1	A45470	hydroxymethylgluta	909	6	0.8	345	2	S73729	MG307 homolog H08
837	6	0.8	325	2	T11610	probable cinnamyl-	910	6	0.8	345	2	A98251	hypothetical prote
838	6	0.8	325	2	T07833	probable steroid s	911	6	0.8	345	2	AB3035	conserved hypothet
839	6	0.8	325	2	T57009	3-Hydroxy-3-methyl	912	6	0.8	345	2	JC7523	catabolite control
840	6	0.8	325	2	G90040	uroporphyrin-III C	913	6	0.8	346	2	C96739	hypothetical prote
841	6	0.8	326	2	T23426	hypothetical prote	914	6	0.8	346	2	D42087	al-phenomone recep
842	6	0.8	326	2	T03928	probable peroxidase	915	6	0.8	346	2	S64693	pheromone receptor
843	6	0.8	326	2	F86407	probable sulfotran	916	6	0.8	346	2	T46914	hypothetical prote
844	6	0.8	326	2	A84452	probable steroid s	917	6	0.8	347	2	T22555	hypothetical prote
845	6	0.8	326	2	A41732	heterogeneous ribo	918	6	0.8	348	2	D84798	probable mitochond
846	6	0.8	326	2	S49937	hypothetical prote	919	6	0.8	348	2	D84922	probable sugar tra
847	6	0.8	327	2	AB1822	pyruvate dehydroge	920	6	0.8	348	2	T31681	bacs protein - Bac
848	6	0.8	327	2	T19529	hypothetical prote	921	6	0.8	348	2	F96997	uncharacterized co
849	6	0.8	328	2	T27911	hypothetical prote	922	6	0.8	350	2	T25366	hypothetical prote
850	6	0.8	328	2	T50104	hypothetical prote	923	6	0.8	351	2	G96923	NADH-dependent fla
851	6	0.8	328	2	E95307	hypothetical prote	924	6	0.8	351	2	T01845	hypothetical prote
852	6	0.8	328	2	E95404	probable ABC trans	925	6	0.8	352	2	A39042	fatty-acid synthas
853	6	0.8	329	2	T47448	sulfotransferase-1	926	6	0.8	352	2	E83519	quinolinate synthe
854	6	0.8	329	2	C97264	UDP-galactose 4-ep	927	6	0.8	353	2	S74379	probable ATPase -
855	6	0.8	329	2	AD1170	lipote-protein li	928	6	0.8	353	2	F84252	phycocyanin alpha
856	6	0.8	329	2	AF1527	lipote-protein li	929	6	0.8	353	2	H71223	probable dolichol-
857	6	0.8	329	2	T09897	hypothetical prote	930	6	0.8	354	2	C81986	probable O-sialogl
858	6	0.8	329	2	H85520	probable LysR-like	931	6	0.8	354	2	C81040	O-sialoglycoprotei
859	6	0.8	330	2	G88115	protein F53C3.1 (i	932	6	0.8	355	2	C86592	aminopeptidase P (
860	6	0.8	330	2	F72428	oligopeptide ABC t	933	6	0.8	355	2	B72032	proline dipeptidas
861	6	0.8	330	2	A95074	ABC transporter, A	934	6	0.8	356	2	T36961	probable zinc-cont
862	6	0.8	331	2	E97941	hypothetical prote	935	6	0.8	356	2	H84934	UDP-N-acetylmuram
863	6	0.8	331	2	S70212	hypothetical prote	936	6	0.8	356	2	H72214	hypothetical prote
864	6	0.8	331	2	B87359	riboflavin biosynt	937	6	0.8	356	2	AC1888	hypothetical prote
865	6	0.8	331	2	E82170	peptide ABC transp	938	6	0.8	357	2	E64233	membrane transport
866	6	0.8	332	2	T47703	Ca-dependent solut	939	6	0.8	358	2	T45934	hypothetical prote
867	6	0.8	332	2	A11355	low-affinity inorg	940	6	0.8	358	2	JQ0596	hypothetical prote
868	6	0.8	332	2	AB1726	hypothetical prote	941	6	0.8	359	2	T36443	probable penicilli
869	6	0.8	333	1	H64400	hypothetical prote	942	6	0.8	359	2	T29647	hypothetical prote
870	6	0.8	333	2	A84523	probable steroid s	943	6	0.8	360	2	D83255	3-isopropylmalate
871	6	0.8	333	2	A41881	collagenase PrtC (944	6	0.8	361	1	SYEBKR	chorismate synthas
872	6	0.8	334	2	T19637	hypothetical prote	945	6	0.8	361	1	SYECKR	chorismate synthas
873	6	0.8	334	2	B87545	hypothetical prote	946	6	0.8	361	2	AF0804	chorismate synthas
874	6	0.8	334	2	A83414	probable transcrip	947	6	0.8	361	2	E91030	chorismate synthas
875	6	0.8	335	2	G70369	sialoglycoproteina	948	6	0.8	361	2	F85874	chorismate synthas
876	6	0.8	335	2	F96999	hydrogenase format	949	6	0.8	361	2	F82115	chorismate synthas
877	6	0.8	335	2	H81677	conserved hypothet	950	6	0.8	361	2	JC6314	major porin protei
878	6	0.8	335	2	H91191	hypothetical prote	951	6	0.8	361	2	A43510	basic membrane pro
879	6	0.8	335	2	A86039	probable LPS biosy	952	6	0.8	362	2	D72734	probable histidine
880	6	0.8	335	2	AB2093	hypothetical prote	953	6	0.8	362	2	G84526	hypothetical prote
881	6	0.8	335	2	T33457	hypothetical prote	954	6	0.8	364	2	AB2993	glycosyltransferas
882	6	0.8	335	2	E71215	hypothetical prote	955	6	0.8	364	2	H70776	hypothetical prote
883	6	0.8	336	2	S61299	lipopolysaccharide	956	6	0.8	365	1	A44974	ferredoxin-NADP re
884	6	0.8	336	2	C81073	ADP-heptose-LPS he	957	6	0.8	365	2	T23220	hypothetical prote
885	6	0.8	336	2	B81869	lipopolysaccharide	958	6	0.8	366	1	JN0146	translation releas
886	6	0.8	336	2	A97305	hypothetical prote	959	6	0.8	366	2	A64950	membrane-bound pen
887	6	0.8	337	2	AD0972	lipopolysaccharide	960	6	0.8	366	2	C85800	probable cycochrome
888	6	0.8	339	2	AD0009	glycerol-3-phospha	961	6	0.8	366	2	G90951	probable cycochrome
889	6	0.8	339	2	T46713	hypothetical prote	962	6	0.8	366	2	JE0105	testicular serine
890	6	0.8	339	2	E95962	probable taurine u	963	6	0.8	366	2	F87508	GTP-binding protei
891	6	0.8	339	2	E82211	conserved hypothet	964	6	0.8	367	2	S68680	stress-activated p
892	6	0.8	339	2	G82113	lipoprotein-34 Nlp	965	6	0.8	367	2	JE0104	testicular serine
893	6	0.8	339	2	F71121	probable membrane-	966	6	0.8	367	2	H83088	membrane-bound lyp
894	6	0.8	340	2	T35394	probable glycerol	967	6	0.8	368	2	G85587	hypothetical prote
895	6	0.8	340	2	T14774	hypothetical prote	968	6	0.8	368	2	F90737	hypothetical prote
896	6	0.8	341	2	T33221	hypothetical prote	969	6	0.8	368	2	H64815	ybhR protein - Esc
897	6	0.8	341	2	AB1394	galactosyltransfer	970	6	0.8	369	1	RDSPPX	ferredoxin-NADP re
898	6	0.8	341	2	AB1769	galactosyltransfer	971	6	0.8	369	2	F81674	conserved hypothet
899	6	0.8	342	2	H86893	elongation factor	972	6	0.8	369	2	S37314	cycH protein - Bra
900	6	0.8	342	2	A10043	conserved hypothet	973	6	0.8	369	2	H82404	hypothetical prote
901	6	0.8	342	2	AF1398	ATP binding protei	974	6	0.8	370	2	F95363	probable serine-py
902	6	0.8	342	2	AC1774	ATP binding protei	975	6	0.8	370	2	C96979	similar to spore g
903	6	0.8	342	2	C86811	hypothetical prote	976	6	0.8	370	2	AF1432	recF protein limpo
904	6	0.8	343	2	G72218	conserved hypothet	977	6	0.8	370	2	H72748	probable glycerol
905	6	0.8	344	1	S49978	aspartate-semialde	978	6	0.8	370	2	T33382	hypothetical prote

979	6	0.8	371	2	C70237	hypothetical prote	1052	393	2	AB1146	histidyl-tRNA synt
980	6	0.8	371	2	T18558	probable mitochond	1053	393	2	F91195	probable integrase
981	6	0.8	372	1	A55510	chorismate synthas	1054	393	2	G86042	probable integrase
982	6	0.8	372	1	D69442	conserved hypothet	1055	393	2	A55859	regulatory protein
983	6	0.8	372	2	S18953	fix23-1 protein -	1056	393	2	D96577	hypothetical prote
984	6	0.8	372	2	T09612	secreted glycoprot	1057	393	2	E97309	probable amidohydr
985	6	0.8	373	2	A82398	maltose/maltodextr	1058	394	2	JS0600	t-plasminogen acti
986	6	0.8	373	2	G90398	hypothetical prote	1059	394	2	T44463	integrase int limp
987	6	0.8	373	2	E72216	alanine-tRNA ligas	1060	394	2	S26431	intermediate filam
988	6	0.8	374	2	D90338	hypothetical prote	1061	394	2	S39739	efflux protein hom
989	6	0.8	374	2	G89846	hypothetical prote	1062	395	1	Q0ECTR	hypothetical 45.2K
990	6	0.8	375	2	S17253	alcohol dehydrogen	1063	395	2	F69148	hypothetical prote
991	6	0.8	375	2	D82585	imidazoleglycerolp	1064	395	2	T00574	probable protein k
992	6	0.8	375	2	A83802	NAD biosynthesis n	1065	395	2	A40270	cyclin E - human
993	6	0.8	375	2	C90746	probable enzyme (i	1066	395	2	A91129	hypothetical prote
994	6	0.8	375	2	G85596	probable enzyme yb	1067	395	2	H85973	hypothetical prote
995	6	0.8	375	2	C64824	probable RNA methy	1068	395	2	AB3543	succinyl-diaminopi
996	6	0.8	376	1	F64705	conserved hypothet	1069	395	2	A95860	hypothetical prote
997	6	0.8	376	2	F71815	hypothetical prote	1070	395	2	B83313	probable type II s
998	6	0.8	376	2	AD1915	hypothetical prote	1071	396	2	AB2309	hypothetical prote
999	6	0.8	377	2	G85975	hypothetical prote	1072	397	2	A82108	flagellar hook-ass
1000	6	0.8	379	2	T32778	hypothetical prote	1073	398	2	AE1142	penicillin-binding
1001	6	0.8	379	2	T21417	hypothetical prote	1074	398	2	C81729	Mtr/TnaB/Tyro perm
1002	6	0.8	380	2	A55259	kappa opioid recep	1075	398	2	D83506	conserved hypothet
1003	6	0.8	380	2	T43016	DNA mismatch repai	1076	398	2	AH1500	penicillin-binding
1004	6	0.8	380	2	G86556	ABC transporter pe	1077	399	2	F82657	beta-ketoacyl-(ACP
1005	6	0.8	380	2	A12185	hypothetical prote	1078	399	2	A31137	hemocyanin - giant
1006	6	0.8	381	2	A43769	fodrin alpha chain	1079	399	2	F89893	hypothetical prote
1007	6	0.8	381	2	S65212	hypothetical prote	1080	400	1	JC1428	keto1-acid reducto
1008	6	0.8	381	2	T34592	probable transmemb	1081	400	2	G64104	hypothetical prote
1009	6	0.8	382	2	E82249	mnp protein VCL037	1082	400	2	F86887	hypothetical prote
1010	6	0.8	382	2	G86791	hypothetical prote	1083	401	2	T25031	drug-efflux transp
1011	6	0.8	382	2	T38092	hypothetical prote	1084	402	2	AD1417	drug-efflux transp
1012	6	0.8	382	2	AI3175	conserved hypothet	1085	402	2	AF1792	ectin C1 - sea ur
1013	6	0.8	383	1	A25978	alcohol dehydrogen	1086	402	2	S71137	endosperm specific
1014	6	0.8	383	2	S32375	gene BCF2 protein	1087	402	2	T04348	hypothetical prote
1015	6	0.8	383	2	B83205	hypothetical prote	1088	402	2	C83881	hypothetical prote
1016	6	0.8	383	2	T23041	hypothetical prote	1089	403	1	S23802	homotic protein 1
1017	6	0.8	383	2	A71139	hypothetical prote	1090	403	1	S01828	probable high-affi
1018	6	0.8	384	2	G91130	N-acetylglactosam	1091	403	2	JQ0028	cytokeratin 19 - m
1019	6	0.8	385	2	T52483	hypothetical prote	1092	403	2	T45580	hypothetical prote
1020	6	0.8	385	2	T47535	hypothetical prote	1093	403	2	T27948	hypothetical prote
1021	6	0.8	385	2	T51127	G6PP synthase limp	1094	403	2	JC5171	D-galactose-bindin
1022	6	0.8	385	2	AE2651	hypothetical prote	1095	404	2	T40532	keto1-acid reducto
1023	6	0.8	385	2	D97433	polyamine transpor	1096	404	2	G01507	LiM domain transcr
1024	6	0.8	386	1	S22315	snRNP-associated p	1097	404	2	A55444	orf within vasotoc
1025	6	0.8	386	2	H71511	probable 2-compone	1098	404	2	B46189	ABC transporter rg
1026	6	0.8	386	2	T09598	cyclin 4, D-type -	1099	405	1	T00089	conserved hypothet
1027	6	0.8	387	2	H71708	pol (A) POLYMERASE	1100	405	2	AB2995	probable MR-MUE-fa
1028	6	0.8	387	2	T38876	probable ribosomal	1101	405	2	AB2995	homotic protein 1
1029	6	0.8	387	2	F82815	voltage-gated pota	1102	406	1	I58187	homotic protein 1
1030	6	0.8	387	2	C86640	multidrug efflux t	1103	406	1	I48186	homotic protein 1
1031	6	0.8	387	2	S00867	colicin N - Escher	1104	406	1	I48637	homotic protein 1
1032	6	0.8	387	2	T47013	hypothetical prote	1105	406	1	I50375	hypothetical prote
1033	6	0.8	387	2	E83679	multidrug-efflux t	1106	406	2	G70639	conserved hypothet
1034	6	0.8	387	2	E97028	probable amidohydr	1107	406	2	B89342	conserved hypothet
1035	6	0.8	387	2	AD0237	probable membrane	1108	406	2	AC2721	MFS permease limpo
1036	6	0.8	387	2	AD0237	FeA14.9 protein -	1109	407	2	G97502	probable mfs trans
1037	6	0.8	388	2	H83714	alanine racemase B	1110	407	2	E95214	hypothetical prote
1038	6	0.8	388	2	AG2663	mnp protein [mpor	1111	408	2	H98290	hypothetical prote
1039	6	0.8	389	2	E86017	probable 3-oxoacyl	1112	408	2	JC1378	aryldialkylphospha
1040	6	0.8	389	2	E91171	probable 3-oxoacyl	1113	409	2	C95042	hypothetical prote
1041	6	0.8	389	2	C83202	alginate biosynthe	1114	410	2	T34717	probable transmemb
1042	6	0.8	390	2	F97445	mnp protein homolo	1115	410	2	S68515	probable arginine
1043	6	0.8	390	2	AB3384	N-acetylmuramoyl-L	1116	410	2	D84785	hypothetical prote
1044	6	0.8	391	2	F83269	fatty-acid oxidati	1117	410	2	S38238	hypothetical prote
1045	6	0.8	391	2	F88778	protein T20D3.3 [i	1118	411	2	H95048	3-oxoacyl-(acyl-ca
1046	6	0.8	391	2	F70625	probable PPE prote	1119	411	2	PC2061	genome polypeptid
1047	6	0.8	392	2	F83610	probable fatty aci	1120	411	2	AB3485	florfenicol resist
1048	6	0.8	392	2	AB1505	histidyl-tRNA synt	1121	411	2	S40064	3-deoxy-manno-octu
1049	6	0.8	392	2	S72984	hypothetical prote	1122	412	2	H70915	probable pgk prote
1050	6	0.8	392	2	T34095	zinc finger protei	1123	412	2	H75484	hypothetical prote
1051	6	0.8	393	2	AB0035	cystathionine beta	1124				

1125	6	0.8	413	2	T43170	probable triacylglycerol	1198	6	0.8	431	2	T00698	methionyl aminopeptidase
1126	6	0.8	413	2	S61305	cycH protein - Par	1199	6	0.8	431	2	JS0599	t-plasminogen activator
1127	6	0.8	413	2	A82726	conserved hypothetical protein	1200	6	0.8	431	2	F86179	hypothetical protein
1128	6	0.8	413	2	T26915	hypothetical protein	1201	6	0.8	432	1	RWCOT4	T-cell surface glycoprotein
1129	6	0.8	414	2	H70667	probable oxidoreductase	1202	6	0.8	432	1	RWCOT4	probable asparaginase
1130	6	0.8	414	2	F97919	3-oxoacyl-[acyl-carrier protein]	1203	6	0.8	432	2	B71442	conserved hypothetical protein
1131	6	0.8	414	2	E90372	hypothetical protein	1204	6	0.8	432	2	E99954	u-plasminogen activator
1132	6	0.8	414	2	E87316	periplasmic phosphatase	1205	6	0.8	433	1	JN0560	UDP-N-acetylglucosamine 6-phosphate lyase
1133	6	0.8	414	2	E29829	SalI protein - Esc	1206	6	0.8	433	1	UKBAY	UDP-N-acetylglucosamine 6-phosphate lyase
1134	6	0.8	414	2	A29835	probable phage-related protein	1207	6	0.8	433	2	D75480	FGF1.5 protein - A
1135	6	0.8	415	2	I58144	corticosterone-releasing hormone	1208	6	0.8	435	2	A86305	nicotinate phosphoribosyltransferase
1136	6	0.8	415	2	D81909	probable integral membrane protein	1209	6	0.8	435	2	H82501	hypothetical protein
1137	6	0.8	415	2	D81107	conserved hypothetical protein	1210	6	0.8	435	2	T47737	hypothetical protein
1138	6	0.8	415	2	T49072	hypothetical protein	1211	6	0.8	435	2	AB1786	cellulose phosphorylase
1139	6	0.8	416	1	S06763	calreticulin precursor	1212	6	0.8	435	2	E83362	probable 2-ketoglutarate decarboxylase
1140	6	0.8	416	1	ACCH3N	nicotinic acetylcholine receptor subunit gamma	1213	6	0.8	436	2	G97701	polynucleotide adenylyltransferase
1141	6	0.8	416	2	D71277	tyrosine-tRNA ligase	1214	6	0.8	436	2	JC5599	hypothetical protein
1142	6	0.8	417	2	D98078	conserved oxidoreductase	1215	6	0.8	436	2	S74385	hypothetical protein
1143	6	0.8	417	2	G98200	sarcosine oxidase	1216	6	0.8	436	2	S48399	hypothetical protein
1144	6	0.8	417	2	AB3086	sarcosine oxidase	1217	6	0.8	436	2	F86486	protein F2809.3 [lipoxygenase]
1145	6	0.8	417	2	AE3056	sarcosine oxidase	1218	6	0.8	436	2	G97186	NADH2 dehydrogenase
1146	6	0.8	417	2	T05207	hypothetical protein	1219	6	0.8	437	2	S34959	keratin 13, type I
1147	6	0.8	417	2	A97063	NAD(PAD)-dependent enzyme	1220	6	0.8	437	2	A55682	transcription factor
1148	6	0.8	418	2	H97437	cyclopropane-fatty acid synthase	1221	6	0.8	438	1	S11225	transforming protein
1149	6	0.8	418	2	AC2656	hypothetical protein	1222	6	0.8	438	2	JC1179	hypothetical protein
1150	6	0.8	418	2	E96765	hypothetical protein	1223	6	0.8	438	2	AF3215	transforming protein
1151	6	0.8	418	2	H83126	probable secretion protein	1224	6	0.8	438	2	A22285	hypothetical protein
1152	6	0.8	419	2	C84813	probable protein kinase	1225	6	0.8	439	1	TVTMC	transforming protein
1153	6	0.8	419	2	D86785	diaminopimelate decarboxylase	1226	6	0.8	439	1	TVTMC	transforming protein
1154	6	0.8	419	2	JC4123	pregnancy-specific beta-1-glycoprotein	1227	6	0.8	439	2	T25494	probable cytochrome c
1155	6	0.8	419	2	S75647	glutamate N-acetyltransferase	1228	6	0.8	440	1	A35875	transcription factor
1156	6	0.8	419	2	B89788	hypothetical protein	1229	6	0.8	440	1	QOBYTY	TyA protein - years
1157	6	0.8	419	2	F83673	PTS system, galactose	1230	6	0.8	440	2	S43113	phosphopyruvate hydratase
1158	6	0.8	420	2	B98288	hypothetical protein	1231	6	0.8	440	2	I48291	transcription factor
1159	6	0.8	420	2	B95100	conserved hypothetical protein	1232	6	0.8	440	2	I50213	protein-tyrosine phosphatase
1160	6	0.8	420	2	D97368	hypothetical protein	1233	6	0.8	440	2	S57044	TyA protein - years
1161	6	0.8	420	2	B84702	hypothetical protein	1234	6	0.8	440	2	A22671	TyA protein - years
1162	6	0.8	421	2	H82236	iron-containing xanthine permease	1235	6	0.8	440	2	S69837	TyA protein - years
1163	6	0.8	422	2	F89805	xanthine permease	1236	6	0.8	440	2	S69837	TyA protein - years
1164	6	0.8	422	2	A93309	sarcosine oxidase	1237	6	0.8	440	2	S45866	TyA protein - years
1165	6	0.8	423	2	A93309	sarcosine oxidase	1238	6	0.8	440	2	S69964	TyA protein - years
1166	6	0.8	423	2	A93309	sarcosine oxidase	1239	6	0.8	440	2	S50947	TyA protein - years
1167	6	0.8	423	2	AH1407	PTS system galactose	1240	6	0.8	440	2	S51894	TyA protein - years
1168	6	0.8	423	2	AH1783	PTS system galactose	1241	6	0.8	440	2	S69840	TyA protein - years
1169	6	0.8	423	2	T31342	ragD protein - Bra	1242	6	0.8	440	2	S69985	TyA protein - years
1170	6	0.8	424	2	C64362	aconitate hydratase	1243	6	0.8	440	2	S69971	TyA protein - years
1171	6	0.8	424	2	T35535	probable secreted protein	1244	6	0.8	440	2	S69976	TyA protein - years
1172	6	0.8	424	2	AD2017	cell wall-binding protein	1245	6	0.8	440	2	S53588	TyA protein - years
1173	6	0.8	426	2	A81933	probable malate dehydrogenase	1246	6	0.8	440	2	S70228	TyA protein - years
1174	6	0.8	426	2	C81173	malate oxidoreductase	1247	6	0.8	440	2	S33553	TyA protein - years
1175	6	0.8	426	2	T52285	serine/threonine-specific phosphatase	1248	6	0.8	440	2	S51249	TyA protein - years
1176	6	0.8	426	2	E70058	ubiquinol-cytochrome c reductase	1249	6	0.8	440	2	S61577	TyA protein - years
1177	6	0.8	427	2	S55905	phosphotransferase	1250	6	0.8	440	2	S40909	TyA protein - years
1178	6	0.8	427	2	G69067	N-ethylmaleimide-sensitive protein	1251	6	0.8	440	2	D69596	branched-chain amino acid aminotransferase
1179	6	0.8	427	2	T29376	hypothetical protein	1252	6	0.8	440	2	D64186	conserved hypothetical protein
1180	6	0.8	427	2	A86493	polymorphic outer membrane protein	1253	6	0.8	440	2	C97620	probable proteinase
1181	6	0.8	428	1	TVHUEK	transforming protein	1254	6	0.8	441	1	A53988	transcription factor
1182	6	0.8	428	2	D70989	probable oxidoreductase	1255	6	0.8	441	1	TVCHTE	transcription factor
1183	6	0.8	428	2	D70343	glycine hydroxymethyltransferase	1256	6	0.8	441	1	TVHUEK	transcription factor
1184	6	0.8	428	2	JN0692	cholecystokinin receptor	1257	6	0.8	441	2	C38575	glucuronate 2-dehydrogenase
1185	6	0.8	428	2	F85458	flavoprotein, electron transfer	1258	6	0.8	441	2	E84264	isochlorogenic acid synthase
1186	6	0.8	428	2	F90634	flavoprotein (improvement)	1259	6	0.8	442	1	UKFG	u-plasminogen activator
1187	6	0.8	428	2	C64725	fixC protein - Esc	1260	6	0.8	442	2	G84465	probable cytochrome c
1188	6	0.8	428	2	B75133	cytochrome-c3 hydrolase	1261	6	0.8	443	2	G59102	hypothetical protein
1189	6	0.8	428	2	T06290	hypothetical protein	1262	6	0.8	443	2	F30010	NADH2 dehydrogenase
1190	6	0.8	428	2	G56273	protein-histidine kinase	1263	6	0.8	443	2	I35338	alpha-amylase - A
1191	6	0.8	429	2	E70979	carbon dioxide-fixing protein	1264	6	0.8	444	2	A24685	cholecystokinin receptor
1192	6	0.8	429	2	JC4965	elk1 protein - mouse	1265	6	0.8	444	2	H71243	probable helicase
1193	6	0.8	429	2	C84194	hypothetical protein	1266	6	0.8	445	2	T26762	hypothetical protein
1194	6	0.8	429	2	A70949	hypothetical protein	1267	6	0.8	446	2	E75075	hybrid cluster [4P]
1195	6	0.8	430	2	F87472	FMN oxidoreductase	1268	6	0.8	446	2	F86815	hypothetical protein
1196	6	0.8	431	1	UKGU	u-plasminogen activator	1269	6	0.8	446	2	T07907	hydroxyproline-rich glycoprotein
1197	6	0.8	431	2	F84077	homoserine dehydratase	1270	6	0.8	446	2	A75209	DNA repair protein

1271	6	0.8	447	2	C86233	hypothetical prote	1344	6	0.8	471	2	E83173	hypothetical prote
1272	6	0.8	448	2	AE1919	hypothetical prote	1345	6	0.8	471	2	A84741	probable myrosinas
1273	6	0.8	449	2	AC1019	probable xanthine/	1346	6	0.8	472	2	T47436	protein kinase-lik
1274	6	0.8	449	2	T23126	hypothetical prote	1347	6	0.8	472	2	E98020	hypothetical prote
1275	6	0.8	450	2	C87463	hypothetical prote	1348	6	0.8	472	2	TS1559	probable flavonol
1276	6	0.8	450	2	T08701	hypothetical prote	1349	6	0.8	473	2	E86955	conserved hypothet
1277	6	0.8	451	2	A85836	PTS system galacti	1350	6	0.8	473	2	G70975	hypothetical prote
1278	6	0.8	451	2	C64976	gatC protein - Esc	1351	6	0.8	474	2	S30227	transposase - Clos
1279	6	0.8	451	2	G90990	PTS system galacti	1352	6	0.8	474	2	H25664	3-isopropylmalate
1280	6	0.8	451	2	T36217	plasmid transfer p	1353	6	0.8	474	2	T26694	hypothetical prote
1281	6	0.8	452	2	I49595	cytokeatin 15 - m	1354	6	0.8	476	2	A70318	aldehyde dehydroge
1282	6	0.8	454	1	C69214	zinc metalloprotei	1355	6	0.8	476	2	T47606	UMP synthase - Ara
1283	6	0.8	454	2	F75580	probable sugar tra	1356	6	0.8	476	2	S46440	bifunctional UMP s
1284	6	0.8	455	2	B90619	NADH dehydrogenase	1357	6	0.8	477	1	A34369	t-plasminogen acti
1285	6	0.8	455	2	S50725	hypothetical prote	1358	6	0.8	477	2	JS0597	t-plasminogen acti
1286	6	0.8	456	1	KRHU5	hypothetical prote	1359	6	0.8	477	2	JS0598	hypothetical prote
1287	6	0.8	456	2	T40386	hypothetical prote	1360	6	0.8	477	2	T46304	aldehyde dehydroge
1288	6	0.8	456	2	H85022	hypothetical prote	1361	6	0.8	478	2	E90495	translation elonga
1289	6	0.8	456	2	T05612	hypothetical prote	1362	6	0.8	478	2	S36183	translation elonga
1290	6	0.8	456	2	S47924	MGAL protein - yea	1363	6	0.8	478	2	JQ2240	TYA protein - yea
1291	6	0.8	457	2	AC1056	murein peptide lig	1364	6	0.8	478	2	S52602	hypothetical prote
1292	6	0.8	457	2	B86121	probable ligase YJ	1365	6	0.8	478	2	T25899	related to aldehyd
1293	6	0.8	457	2	B91280	probable ligase [i	1366	6	0.8	479	2	TS1919	lipopolysaccharide
1294	6	0.8	457	2	S56459	UDP-N-acetylmuram	1367	6	0.8	479	2	D72354	serine/threonine p
1295	6	0.8	457	2	AH0898	PTS system, galact	1368	6	0.8	479	2	S48705	protein kinase hom
1296	6	0.8	457	2	B83643	potassium uptake p	1369	6	0.8	480	2	T04849	lipopolysaccharide
1297	6	0.8	457	2	B82268	conserved hypothet	1370	6	0.8	482	2	B35843	probable non-proce
1298	6	0.8	458	1	RWHUT4	T-cell surface gly	1371	6	0.8	482	2	E97012	altronate oxidorec
1299	6	0.8	458	2	B90621	NADH dehydrogenase	1372	6	0.8	483	2	A85723	tagaturonate reduc
1300	6	0.8	458	2	B90625	NADH dehydrogenase	1373	6	0.8	483	2	D64906	altronate oxidorec
1301	6	0.8	458	2	B90615	NADH dehydrogenase	1374	6	0.8	483	2	H90894	gag-myc polyprotei
1302	6	0.8	458	2	B90617	NADH dehydrogenase	1375	6	0.8	484	1	TMVVF7	hypothetical prote
1303	6	0.8	458	2	T11176	NADH2 dehydrogenas	1376	6	0.8	484	2	D89781	hypothetical prote
1304	6	0.8	458	2	T11528	NADH2 dehydrogenas	1377	6	0.8	484	2	T33492	transcription fact
1305	6	0.8	458	2	B99613	NADH dehydrogenase	1378	6	0.8	485	1	TVCHET	rhamnulokinase (EC
1306	6	0.8	458	2	B90627	NADH dehydrogenase	1379	6	0.8	485	2	AD0041	glutamyl-tRNA(Gln)
1307	6	0.8	458	2	B90623	NADH dehydrogenase	1380	6	0.8	485	2	B69795	probable phor prot
1308	6	0.8	458	2	B97324	sugar/Na+ (H+) simp	1381	6	0.8	485	2	A70706	probable cytochrom
1309	6	0.8	459	2	T10196	NADH2 dehydrogenas	1382	6	0.8	486	2	T32431	glutamyl-tRNA (Gln
1310	6	0.8	459	2	T11411	NADH2 dehydrogenas	1383	6	0.8	486	2	TS1582	coenzyme F420-quin
1311	6	0.8	459	2	T11189	NADH2 dehydrogenas	1384	6	0.8	487	2	H69477	hypothetical prote
1312	6	0.8	459	2	T11256	NADH2 dehydrogenas	1385	6	0.8	487	2	E98326	transcription fact
1313	6	0.8	459	2	T11084	NADH2 dehydrogenas	1386	6	0.8	488	1	TVFVES	hypothetical prote
1314	6	0.8	459	2	AE0679	probable membrane	1387	6	0.8	488	2	F95875	shaw protein - Cal
1315	6	0.8	459	2	G90080	probable thiophene	1388	6	0.8	489	2	JC4787	nicotinate phospho
1316	6	0.8	459	2	G81187	Na+/H+ antiporter	1389	6	0.8	490	2	D70008	hypothetical prote
1317	6	0.8	459	2	F81914	probable transmemb	1390	6	0.8	490	2	G70108	UDP-N-acetylmuram
1318	6	0.8	459	2	T24742	hypothetical prote	1391	6	0.8	491	2	AI0068	amino acid transpo
1319	6	0.8	459	2	D86256	hypothetical prote	1392	6	0.8	491	2	D97311	hypothetical prote
1320	6	0.8	460	2	T24248	hypothetical prote	1393	6	0.8	491	2	AG1838	hypothetical prote
1321	6	0.8	461	2	A43782	keratin, type II -	1394	6	0.8	492	2	S71112	catalase (EC 1.11.
1322	6	0.8	461	2	C86935	probable carboxype	1395	6	0.8	492	2	S41288	genome polyprotein
1323	6	0.8	461	2	D81418	hypothetical prote	1396	6	0.8	492	2	C86316	protein T10022.7 [
1324	6	0.8	461	2	T00621	hypothetical prote	1397	6	0.8	493	2	TS1453	serine/threonine s
1325	6	0.8	462	2	T28699	hypothetical prote	1398	6	0.8	495	2	A85441	cytochrome P450-11
1326	6	0.8	463	2	S72992	probable phosphory	1399	6	0.8	495	2	S60589	acetylcholine rece
1327	6	0.8	463	2	T39621	peptidyl prolyl ci	1400	6	0.8	495	2	G82371	FixG-related prote
1328	6	0.8	464	2	AG2774	glutathione-disulf	1401	6	0.8	496	2	T11376	cytochrome-c oxida
1329	6	0.8	464	2	E97554	glutathione-disulf	1402	6	0.8	496	2	H70668	probable polyketid
1330	6	0.8	464	2	AF0761	probable CoA-depen	1403	6	0.8	496	2	G87546	acid-CoA ligase, p
1331	6	0.8	464	2	C83328	hypothetical prote	1404	6	0.8	496	2	T17908	proline/lysine-ric
1332	6	0.8	465	2	S03325	transforming prote	1405	6	0.8	497	2	B81728	serine proteinase,
1333	6	0.8	465	2	T40697	conserved hypotet	1406	6	0.8	497	2	S27785	acetyl-CoA acetyl
1334	6	0.8	466	2	C64690	probable tata bind	1407	6	0.8	498	1	S52570	phosphoprotein pho
1335	6	0.8	467	2	B64974	sensory kinase Bae	1408	6	0.8	498	2	B95893	potassium channel
1336	6	0.8	468	2	AI2956	hypothetical prote	1409	6	0.8	498	2	A41359	nitrogenase (EC 1.
1337	6	0.8	469	2	AE1220	ethanolamine utili	1410	6	0.8	499	1	B29042	phosphoprotein pho
1338	6	0.8	469	2	AH1573	ethanolamine utili	1411	6	0.8	499	1	A55346	nicotinic acetylch
1339	6	0.8	470	2	B90481	glycosyltransferas	1412	6	0.8	499	2	A24572	glutelin 2 precurs
1340	6	0.8	470	2	D85111	hypothetical prote	1413	6	0.8	499	2	B34332	glutelin type I pr
1341	6	0.8	470	2	T31049	hypothetical prote	1414	6	0.8	499	2	S06350	glutelin precursor
1342	6	0.8	470	2	T49272	hypothetical prote	1415	6	0.8	499	2	A27033	hypothetical prote
1343	6	0.8	471	2	S35019	noIX protein - Rhi	1416	6	0.8	499	2	H87460	

1417 6 0.8 499 2 T47879
 1418 6 0.8 499 2 S22571
 1419 6 0.8 500 1 A44001
 1420 6 0.8 501 2 C82414
 1421 6 0.8 502 2 T35743
 1422 6 0.8 502 2 T35743
 1423 6 0.8 502 2 T35743
 1424 6 0.8 502 2 T35743
 1425 6 0.8 503 2 T35743
 1426 6 0.8 503 2 T35743
 1427 6 0.8 504 2 T35743
 1428 6 0.8 504 2 T35743
 1429 6 0.8 505 2 T35743
 1430 6 0.8 506 2 T35743
 1431 6 0.8 506 2 T35743
 1432 6 0.8 506 2 T35743
 1433 6 0.8 506 2 T35743
 1434 6 0.8 507 1 A39072
 1435 6 0.8 507 2 T35743
 1436 6 0.8 507 2 T35743
 1437 6 0.8 507 2 T35743
 1438 6 0.8 508 1 T35743
 1439 6 0.8 508 2 T35743
 1440 6 0.8 508 2 T35743
 1441 6 0.8 509 2 T35743
 1442 6 0.8 509 2 T35743
 1443 6 0.8 510 2 T35743
 1444 6 0.8 511 2 T35743
 1445 6 0.8 512 2 T35743
 1446 6 0.8 512 2 T35743
 1447 6 0.8 512 2 T35743
 1448 6 0.8 512 2 T35743
 1449 6 0.8 513 2 T35743
 1450 6 0.8 513 2 T35743
 1451 6 0.8 513 2 T35743
 1452 6 0.8 513 2 T35743
 1453 6 0.8 514 2 T35743
 1454 6 0.8 514 2 T35743
 1455 6 0.8 515 2 T35743
 1456 6 0.8 515 2 T35743
 1457 6 0.8 516 2 T35743
 1458 6 0.8 517 2 T35743
 1459 6 0.8 517 2 T35743
 1460 6 0.8 517 2 T35743
 1461 6 0.8 518 2 T35743
 1462 6 0.8 518 2 T35743
 1463 6 0.8 520 2 T35743
 1464 6 0.8 522 2 T35743
 1465 6 0.8 523 2 T35743
 1466 6 0.8 523 2 T35743
 1467 6 0.8 523 2 T35743
 1468 6 0.8 523 2 T35743
 1469 6 0.8 525 2 T35743
 1470 6 0.8 525 2 T35743
 1471 6 0.8 526 1 T35743
 1472 6 0.8 526 2 T35743
 1473 6 0.8 527 2 T35743
 1474 6 0.8 528 2 T35743
 1475 6 0.8 528 2 T35743
 1476 6 0.8 529 2 T35743
 1477 6 0.8 529 2 T35743
 1478 6 0.8 529 2 T35743
 1479 6 0.8 530 2 T35743
 1480 6 0.8 530 2 T35743
 1481 6 0.8 530 2 T35743
 1482 6 0.8 530 2 T35743
 1483 6 0.8 530 2 T35743
 1484 6 0.8 531 2 T35743
 1485 6 0.8 531 2 T35743
 1486 6 0.8 531 2 T35743
 1487 6 0.8 531 2 T35743
 1488 6 0.8 533 2 T35743
 1489 6 0.8 533 2 T35743

1490 6 0.8 534 2 D71598
 1491 6 0.8 535 2 C96518
 1492 6 0.8 536 2 T38210
 1493 6 0.8 536 2 AG1482
 1494 6 0.8 536 2 AB3038
 1495 6 0.8 538 2 G83653
 1496 6 0.8 538 2 T40992
 1497 6 0.8 539 2 G95405
 1498 6 0.8 540 1 OXECLE
 1499 6 0.8 540 2 H91058
 1500 6 0.8 540 2 AB0830

ALIGNMENTS

RESULT 1

T08805

hypothetical protein DKFp586H2123.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: T08805

R;Ansoorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A;Reference number: Z16472

A;Accession: T08805

A;Molecule type: mRNA

A;Residues: 1-181 <ANS>

A;Cross-references: UNIPROT:Q9Y432; EMBL:AL050214

A;Experimental source: adult uterus; clone DKFp586H2123

C;Genetics:

A;Note: DKFp586H2123.1

Query Match 24.7%; Score 178; DB 2; Length 181;

Best Local Similarity 100.0%; Pred. No. 2.4e-182;

Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 543 ISAILHPNYDPILLDADIAILKLDKARISTRVQVPCIAASRDLSSTSFQESHITVAGWN 602

Db 4 ISAILHPNYDPILLDADIAILKLDKARISTRVQVPCIAASRDLSSTSFQESHITVAGWN 63

QY 603 VLADVSPGFKNDTLRSVVVDSLLCEQHEHGHGIPVSVTDNMFCSWEPTAPSDICT 662

Db 64 VLADVSPGFKNDTLRSVVVDSLLCEQHEHGHGIPVSVTDNMFCSWEPTAPSDICT 123

QY 663 AETGGIAAVSFGRASPERVHLMGLVSVSYDKTCSHRLSTAFKVLFFKDWIERNNK 720

Db 124 AETGGIAAVSFGRASPERVHLMGLVSVSYDKTCSHRLSTAFKVLFFKDWIERNNK 181

RESULT 2

E70372

hypothetical protein aq_836 - Aquifex aeolicus

C;Species: Aquifex aeolicus

C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C;Accession: E70372

R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V.

Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:98196686; PMID:9537320

A;Accession: E70372

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-232 <AQF>

A;Cross-references: UNIPROT:O67008; GB:AE000709; NID:g2983373; PIDN:AAC06970.1; PID:g29

A;Experimental source: strain VF5

C;Genetics:

A;Gene: aq_836

Query Match

Best Local Similarity 100.0%; Score 9; DB 2; Length 232;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 FENCKSCRN 96
|||||
Db 23 FENCKSCRN 31

RESULT 3

T29125
ketoacyl reductase homolog - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C/Accession: T29125
R/Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A/Reference number: Z17215
A/Accession: T29125
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-276 <PAR>
A/Cross-references: UNIPROT:O86553; EMBL:AL031350; PIDN:CAA20507.1
C/Genetics:
A/Note: SC1F2.16c
C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homolog

Query Match 1.2% Score 9; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 0.53; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 670 AVSFPGRAS 678
|||||
Db 225 AVSFPGRAS 233

RESULT 4

BMHUI
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human
N/Alternate names: bone morphogenic protein 1 (BMP1)
C/Species: Homo sapiens (man)
C/Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C/Accession: A37278; E58788
R/Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1988
A/Title: Novel regulators of bone formation: molecular clones and activities.
A/Reference number: A37278; MUID:89072730; PMID:3201241
A/Accession: A37278
A/Molecule type: mRNA
A/Residues: 1-730 <WOZ>
A/Cross-references: GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500
C/Genetics:

A/Gene: GDB:BMP1
A/Cross-references: GDB:125203; OMIM:112264
A/Map position: 8p21-8p21
C/Function:
A/Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C/Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; B
C/Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F/1-22/Domain: signal sequence #status predicted <SIG>
F/23-730/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>
F/130-321/Domain: astacin homology <AST>
F/322-431/Domain: C1r/C1s repeat homology <C1R1>
F/435-544/Domain: C1r/C1s repeat homology <C1R2>
F/551-587/Domain: EGF homology <EGF>
F/591-700/Domain: C1r/C1s repeat homology <C1R3>
F/91,142,332,363,599/Binding site: carbohydate (Asn) (covalent) #status predicted
F/163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F/213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F/214/Active site: Glu #status predicted
F/565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 1.2% Score 9; DB 1; Length 730;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYEVRDG 187
|||||
Db 377 YDYEVRDG 385

RESULT 5

A58788
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human
N/Alternate names: bone morphogenic protein splice form BMP-1/HIS
C/Species: Homo sapiens (man)
C/Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999
C/Accession: A37278; A58788
R/Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; He;
Science 242, 1528-1534, 1988
A/Title: Novel regulators of bone formation: molecular clones and activities.
A/Reference number: A37278; MUID:89072730; PMID:3201241
A/Accession: A37278
A/Molecule type: mRNA
A/Residues: 1-702, 'EKRPALQPPGRPHQLKPRVQKRNPQ' <WOZ>
A/Cross-references: GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500
R/Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A/Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are enco
A/Reference number: A58788; MUID:95096114; PMID:7798260
A/Accession: A58788
A/Molecule type: mRNA
A/Residues: 703-823 <TAK>
A/Cross-references: GB:U35278; NID:G619423; PIDN:AAC41703.1; PID:G619424
C/Genetics:

A/Gene: GDB:BMP1; BMP-1
A/Cross-references: GDB:125203; OMIM:112264
A/Map position: 8p21-8p21
C/Function:
A/Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C/Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; g
C/Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g
F/1-22/Domain: signal sequence #status predicted <SIG>
F/23-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>
F/130-321/Domain: astacin homology <AST>
F/322-431/Domain: C1r/C1s repeat homology <C1R1>
F/435-544/Domain: C1r/C1s repeat homology <C1R2>
F/551-587/Domain: EGF homology <EGF>
F/591-700/Domain: C1r/C1s repeat homology <C1R3>
F/738-752/Region: histidine-rich
F/91,142,332,363,599/Binding site: carbohydate (Asn) (covalent) #status predicted
F/163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-6
F/213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F/214/Active site: Glu #status predicted
F/565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 1.2% Score 9; DB 1; Length 823;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYEVRDG 187
|||||
Db 377 YDYEVRDG 385

RESULT 6

B58788
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - human
N/Alternate names: bone morphogenic protein 1, tolloid-like splice form
C/Species: Homo sapiens (man)
C/Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004
C/Accession: A37278; B58788
R/Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; He;
Science 242, 1528-1534, 1988
A/Title: Novel regulators of bone formation: molecular clones and activities.
A/Reference number: A37278; MUID:89072730; PMID:3201241
A/Accession: A37278
A/Molecule type: mRNA
A/Residues: 1-702, 'EKRPALQPPGRPHQLKPRVQKRNPQ' <WOZ>

A;Cross-references: UNIPROT:P13497; GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
 R;Takahara, K.; Lyons, G.E.; Greenspan, D.S.
 J. Biol. Chem. 269, 32572-32578, 1994
 A;Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mtld) are encoded by two genes in the mouse genome
 A;Reference number: A58788; MUID:95096114; PMID:7798260
 A;Accession: B58788
 A;Molecule type: mRNA
 A;Residues: 703-986 <TK>
 A;Cross-references: GB:IJ35279; NID:g619860; PIDN:AAC41710.1; PID:g619861
 C;Genetics:
 A;Gene: GDB:BMPL1; BMP-1
 A;Cross-references: GDB:125203; OMIM:112264
 A;Map position: 8p21-8p21
 C;Function:
 A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type I
 C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; EGF homology
 C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
 F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-986/Product: procollagen C-endopeptidase tolloid-like splice form #status predicted
 F;130-321/Domain: astacin homology <AST>
 F;322-431/Domain: C1r/C1s repeat homology <C1R1>
 F;435-544/Domain: C1r/C1s repeat homology <C1R2>
 F;551-587/Domain: EGF homology <EG1>
 F;591-700/Domain: C1r/C1s repeat homology <C1R3>
 F;707-742/Domain: EGF homology <EG2>
 F;747-856/Domain: C1r/C1s repeat homology <C1R4>
 F;860-973/Domain: C1r/C1s repeat homology <C1R5>
 F;91-142/332,332,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
 F;213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
 F;214/Active site: Glu #status predicted
 F;565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
 Query Match 1.2%; Score 9; DB 1; Length 986;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 179 YDYVEVRDG 187
 DB 377 YDYVEVRDG 385
 RESULT 7
 I49540
 C;Superfamily: procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I49540
 R;Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.
 Dev. Biol. 163, 175-183, 1994
 A;Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rel
 A;Reference number: I49540; MUID:94229342; PMID:8174772
 A;Accession: I49540
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-991 <RES>
 A;Cross-references: UNIPROT:P98063; GB:L24755; NID:g439606; PIDN:AAA37306.1; PID:g439607
 C;Genetics:
 A;Gene: Bmp-1
 C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
 C;Keywords: hydrolase; metalloproteinase; zinc
 F;135-326/Domain: astacin homology <AST>
 F;556-592/Domain: EGF homology <EG1>
 F;596-705/Domain: C1r/C1s repeat homology <C1R>
 F;712-747/Domain: EGF homology <EG2>
 F;218,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted
 F;219/Active site: Glu #status predicted
 Query Match 1.2%; Score 9; DB 2; Length 991;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 179 YDYVEVRDG 187

DB 382 YDYVEVRDG 390
 |||||

RESULT 8
 S58984

development protein tolkin (EC 3.4.24.-) - fruit fly (Drosophila melanogaster)
 C;Species: Drosophila melanogaster
 C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C;Accession: S58984
 R;Finelli, A.L.; Xie, T.; Bossie, C.A.; Blackman, R.K.; Padgett, R.W.
 Genetics 141, 271-281, 1995
 A;Title: The tolkin gene is a tolloid/BMP-1 homologue that is essential for Drosophila
 A;Reference number: S58984; MUID:96042912; PMID:8536976
 A;Accession: S58984
 A;Molecule type: mRNA
 A;Residues: 1-1464 <FIN>
 A;Cross-references: UNIPROT:Q24132; EMBL:U34777; NID:g1002985; PIDN:AAC47015.1; PID:g10
 A;Note: the authors did not translate the codon for residue 722
 C;Genetics:
 A;Gene: tolkin
 A;Cross-references: FlyBase:FBgn0004885
 C;Keywords: hydrolase; metalloproteinase; zinc
 F;529-722/Domain: astacin homology <AST>
 F;958-993/Domain: EGF homology <EGF>
 F;118-1153/Domain: EGF homology <EGF1>
 F;614,618,624,673/Binding site: zinc (His, His, His, Tyr) #status predicted
 F;615/Active site: Glu #status predicted

Query Match 1.2%; Score 9; DB 2; Length 1464;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
 DB 897 YDYVEVRDG 905
 |||||

RESULT 9
 T31070

notch homolog - sea urchin (Lytechinus variegatus)
 C;Species: Lytechinus variegatus (variegated urchin)
 C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
 C;Accession: T31070
 R;Sherwood, D.R.; McClay, D.R.
 Development 124, 3363-3374, 1997
 A;Title: Identification and localization of a sea urchin Notch homologue: insights into
 A;Reference number: Z20966; MUID:97454256; PMID:9310331
 A;Accession: T31070
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-2531 <SHE>
 A;Cross-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN:AAB82088.1
 C;Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 1.2%; Score 9; DB 2; Length 2531;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 CACLAGYTG 268
 DB 537 CACLAGYTG 545
 |||||

RESULT 10
 S00996

Ig kappa chain precursor V region (A10) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Jul-1999
 C;Accession: S00996
 R;Straubinger, B.; Thiebe, R.; Huber, C.; Osterholzer, E.; Zachau, H.G.
 Biol. Chem. Hoppe-Seyler 369, 601-607, 1988
 A;Title: Two unusual human immunoglobulin V-kappa genes.

A;Reference number: S00996; MUID:89134397; PMID:2852016

A;Accession: S00996

A;Molecule type: DNA

A;Residues: 1-114 <STR>

A;Cross-references: EMBL:M27750; NID:g185914; PIDN:AAA58912.1; PID:g553479

A;Note: this sequence was determined from the germline gene

C;Genetics: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-114/Product: Ig kappa chain V region #status predicted <MAT>

F;42-107/Disulfide bonds: #status predicted

Query Match 1.1%; Score 8; DB 2; Length 114;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 QSIGSSSLH 215

|||||

DB 46 QSIGSSSLH 53

|||||

RESULT 11

G70323

conserved hypothetical protein aq_260 - Aquifex aeolicus

C;Species: Aquifex aeolicus

C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C;Accession: G70323

R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovi-

V.

Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Accession: G70323

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-158 <AQF>

A;Cross-references: UNIPROT:O66619; GB:AE000681; NID:g2982963; PIDN:AAC06588.1; PID:g298

A;Experimental source: strain VF5

C;Genetics:

C;Superfamily: nus operon 15K protein

Query Match 1.1%; Score 8; DB 2; Length 158;

Best Local Similarity 100.0%; Pred. No. 3.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 GKREVVGY 64

|||||

DB 114 GKREVVGY 121

|||||

RESULT 12

D42696

thrombin (EC 3.4.21.5) B chain - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004

C;Accession: D42696

R;Banfield, D.K.; MacGillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992

A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq

A;Reference number: A42696; MUID:92212913; PMID:1557383

A;Accession: D42696

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-235 <BAN>

A;Cross-references: UNIPROT:Q91001; GB:M81391

C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology

C;Keywords: hydrolase; serine proteinase

F;1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 1.1%; Score 8; DB 2; Length 235;

Best Local Similarity 100.0%; Pred. No. 5.4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 VTDNMFCA 650

|||||

DB 158 VTDNMFCA 165

|||||

RESULT 15

AB0338

probable membrane protein dedD [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AB0338

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Best Local Similarity 100.0%; Pred. No. 5.4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 VTDNMFCA 650

|||||

DB 157 VTDNMFCA 164

|||||

RESULT 13

H42696

thrombin (EC 3.4.21.5) B chain - white sturgeon (fragment)

C;Species: Acipenser transmontanus (white sturgeon)

C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004

C;Accession: H42696

R;Banfield, D.K.; MacGillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992

A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and se

A;Reference number: A42696; MUID:92212913; PMID:1557383

A;Accession: H42696

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr

A;Molecule type: mRNA

A;Residues: 1-235 <BAN>

A;Cross-references: UNIPROT:Q90244; GB:M81399

C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology

C;Keywords: hydrolase; serine proteinase

F;1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 1.1%; Score 8; DB 2; Length 235;

Best Local Similarity 100.0%; Pred. No. 5.4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 VTDNMFCA 650

|||||

DB 157 VTDNMFCA 164

|||||

RESULT 14

C42696

thrombin (EC 3.4.21.5) B chain - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004

C;Accession: C42696

R;Banfield, D.K.; MacGillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992

A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and se

A;Reference number: A42696; MUID:92212913; PMID:1557383

A;Accession: C42696

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr

A;Molecule type: mRNA

A;Residues: 1-236 <BAN>

A;Cross-references: UNIPROT:Q28731; GB:M81396

C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology

C;Keywords: hydrolase; serine proteinase

F;1-227/Domain: trypsin homology (fragment) <TRY>

Query Match 1.1%; Score 8; DB 2; Length 236;

Best Local Similarity 100.0%; Pred. No. 5.4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 VTDNMFCA 650

|||||

DB 158 VTDNMFCA 165

|||||

Nature 413, 523-527, 2001
A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0338
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-240 <KUR>
A;Cross-references: UNIPROT:Q8ZD23; GB:AL590842; PIDN:CAC93009.1; PID:gl5980748; GSPDB:G
C;Genetics:
A;Gene: dedD
C;Superfamily: dedD protein

Query Match 1.1%; Score 8; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 SKQKLQSA 387
|||||
Db 212 SKQKLQSA 219

Search completed: May 8, 2005, 16:11:41
Job time : 28 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 8, 2005, 16:08:34 ; Search time 50 Seconds
(without alignments)
7373.940 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 720

Sequence: 1 MELGCTQLGLFLQLLLIS.....LSTFTKVLPLFKDWIERNMK 720

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	720	100.0	720	2	Q6UXH9
2	563	78.2	720	2	Q6N062
3	446	61.9	737	2	Q96JW2
4	386	53.6	417	2	Q71RE9
5	178	24.7	181	2	Q9Y432
6	61	8.5	720	2	Q8BU25
7	41	5.7	720	2	Q8K2B8
8	24	3.3	722	2	Q6DIV5
9	9	1.2	222	2	Q91WZ0
10	9	1.2	232	1	Y836 AQUAE
11	9	1.2	276	2	Q6PUN5
12	9	1.2	593	2	Q6PUN5
13	9	1.2	639	1	BMPH STRPU
14	9	1.2	691	1	O57658
15	9	1.2	775	2	Q6P550
16	9	1.2	860	2	Q7QAH1
17	9	1.2	923	1	NRP1 BRARE
18	9	1.2	923	2	Q69DB8
19	9	1.2	986	1	BMP1 HUMAN
20	9	1.2	991	1	BMP1 MOUSE
21	9	1.2	991	2	Q6NZM2
22	9	1.2	1015	2	Q9Y6L7
23	9	1.2	1078	2	Q9UQ00
24	9	1.2	1464	2	Q23995
25	9	1.2	1464	2	Q24132
26	9	1.2	1464	2	Q9VC47
27	9	1.2	2531	2	O16004
28	8	1.1	81	2	Q79204
29	8	1.1	133	2	Q6LTX4
30	8	1.1	136	2	Q8CEX5
31	8	1.1	152	2	Q924X1

32	8	1.1	158	1	Y260 AQUAE
33	8	1.1	234	2	Q90244
34	8	1.1	235	2	Q28731
35	8	1.1	240	2	Q668X3
36	8	1.1	240	2	Q82D23
37	8	1.1	242	2	Q8DOT9
38	8	1.1	360	1	MTSB_LACLC
39	8	1.1	367	2	Q9XUN6
40	8	1.1	385	2	Q90WS2
41	8	1.1	395	1	VIBC VIBCH
42	8	1.1	407	1	PA7_BOVIN
43	8	1.1	411	2	Q67UZ3
44	8	1.1	413	2	Q7X370
45	8	1.1	486	1	YDBH SCHPO
46	8	1.1	556	2	Q7UX12
47	8	1.1	569	2	Q62KZ6
48	8	1.1	569	2	Q63TF6
49	8	1.1	607	2	Q91001
50	8	1.1	608	2	Q9PTW7
51	8	1.1	611	2	Q94HU9
52	8	1.1	611	2	Q7XG00
53	8	1.1	719	2	Q9PVY2
54	8	1.1	737	2	Q8YTB7
55	8	1.1	740	1	CATB STRRE
56	8	1.1	752	2	O42374
57	8	1.1	764	2	Q8XTM0
58	8	1.1	963	2	O44393
59	8	1.1	1019	1	LFC CARRO
60	8	1.1	1019	1	LFC TACTR
61	8	1.1	1019	2	Q8T5S1
62	8	1.1	1070	2	P91972
63	8	1.1	1083	2	Q26423
64	8	1.1	1238	2	Q9N614
65	8	1.1	1238	2	Q9VCD8
66	8	1.1	1316	2	Q96JU7
67	7	1.0	36	2	Q7UL51
68	7	1.0	37	2	Q8F0D9
69	7	1.0	47	2	Q75GQ9
70	7	1.0	50	2	Q6Z6D5
71	7	1.0	54	2	Q8NQ87
72	7	1.0	55	2	Q768X9
73	7	1.0	59	2	Q931M9
74	7	1.0	59	2	Q99SV1
75	7	1.0	59	2	Q7A0F7
76	7	1.0	59	2	Q6G7Z5
77	7	1.0	59	2	Q6GFB7
78	7	1.0	61	2	Q8GRP5
79	7	1.0	61	2	Q8GRP6
80	7	1.0	61	2	Q8GZF3
81	7	1.0	61	2	Q8GZF4
82	7	1.0	61	2	Q8GZF5
83	7	1.0	61	2	Q8GZF7
84	7	1.0	61	2	Q8GZF8
85	7	1.0	61	2	Q8GZF9
86	7	1.0	62	2	Q7PIZ1
87	7	1.0	67	2	Q9EMT6
88	7	1.0	71	2	Q855B3
89	7	1.0	75	2	Q9C8F3
90	7	1.0	81	2	Q7R3P2
91	7	1.0	81	2	Q9EMT8
92	7	1.0	81	2	Q79209
93	7	1.0	81	2	Q79303
94	7	1.0	82	2	Q90D16
95	7	1.0	86	2	Q7X3H3
96	7	1.0	91	2	Q9M9B7
97	7	1.0	106	2	Q87074
98	7	1.0	108	2	Q62QF8
99	7	1.0	109	2	Q966A7
100	7	1.0	112	2	P91967
101	7	1.0	114	2	Q9YCI9
102	7	1.0	120	2	Q8T6A0
103	7	1.0	123	2	Q6W1F1
104	7	1.0	124	2	Q7WC39

O66619	aquifex aeo
Q90244	acipenser t
Q28731	oryctolagus
Q668X3	versinia ps
Q82D23	versinia pe
Q8DOT9	versinia pe
Q9XUN6	lactococcus
Q90WS2	caenorhabdi
O07898	elaphe sp.
P22457	vibrio chol
Q67UZ3	bos taurus
Q7X370	oryza sativ
Q10367	uncultured
Q7UX12	schistosacch
Q62KZ6	rhodopiell
Q63TF6	burkholderi
Q91001	gallus gall
Q9PTW7	struthio ca
Q94HU9	oryza sativ
Q7XG00	oryza sativ
Q9PVY2	triakis scy
Q8YTB7	anabaena sp
O87854	streptomyce
O42374	brachydania
Q8XTM0	raletonia s
O44393	pisaster oc
Q26422	carcinosc
Q28175	tachypleus
Q8T91	tachypleus
P91972	aplysia cal
Q26423	carcinosc
Q9N614	drosophila
Q9VCD8	drosophila
Q96JU7	homo sapien
Q7UL51	rhodopiell
Q8F0D9	leptospira
Q75GQ9	oryza sativ
Q6Z6D5	oryza sativ
Q8NQ87	corynebacte
Q768X9	uncultured
Q931M9	staphylococ
Q99SV1	staphylococ
Q7A0F7	staphylococ
Q6G7Z5	staphylococ
Q6GFB7	staphylococ
Q8GRP5	arabidopsis
Q8GRP6	arabidopsis
Q8GZF3	arabidopsis
Q8GZF4	arabidopsis
Q8GZF5	arabidopsis
Q8GZF7	arabidopsis
Q8GZF8	arabidopsis
Q8GZF9	arabidopsis
Q7PIZ1	anopheles g
Q9EMT6	amsacta moo
Q855B3	mycobacteri
Q9C8F3	arabidopsi
Q7R3P2	giardia lam
Q9EMT8	amsacta moo
Q79209	human immun
Q79303	human immun
Q90D16	human immun
Q7X3H3	thiocapsa r
Q9M9B7	arabidopsis
Q87074	suid herpes
Q62QF8	bacillus li
Q966A7	caenorhabdi
P91967	trichinella
Q9YCI9	aeropyrum p
Q8T6A0	aplysia cal
Q6W1F1	rhizobium s
Q7WC39	bordetella

105	7	1.0	124	2	Q81G20	Q81g20 bacillus ce	178	7	1.0	211	2	Q8ZEH2	Q8zeh2 yersinia pe
106	7	1.0	124	2	Q8G3X3	Q8g3x3 bifidobacte	179	7	1.0	211	2	Q6D4T7	Q6ddt7 erwina car
107	7	1.0	126	2	Q6NQG5	Q6ngq5 arabidopsis	180	7	1.0	212	1	OMPW_ECOLI	P21364 escherichia
108	7	1.0	129	2	Q87FS3	Q87fs3 vibrio para	181	7	1.0	212	1	OMPW_SALTI	Q8zfe2 salmonella
109	7	1.0	132	2	Q8W9J7	Q8w9j7 apatania zo	182	7	1.0	212	1	OMPW_SALTY	Q8zps0 salmonella
110	7	1.0	132	2	Q8L158	Q8l158 streptomyce	183	7	1.0	212	2	Q7Q8A2	Q7q8a2 anopheles g
111	7	1.0	136	2	Q6SV41	Q6sv41 metarhizium	184	7	1.0	212	2	Q8XC86	Q8xc86 escherichia
112	7	1.0	141	2	Q6A6E6	Q6a6e6 propionibac	185	7	1.0	213	2	Q9CF55	Q9cf55 lactococcus
113	7	1.0	143	2	Q9S9X5	Q9s9x5 arabidopsis	186	7	1.0	214	2	Q87K02	Q87k02 vibrio para
114	7	1.0	144	2	Q8WG98	Q8wg98 moropsysche	187	7	1.0	215	2	Q74TX0	Q74tx0 yersinia pe
115	7	1.0	146	2	Q6RGN1	Q6rgn1 sus scrofa	188	7	1.0	215	2	Q8D0J8	Q8d0j8 yersinia pe
116	7	1.0	146	2	Q75Q50	Q75q50 hartigiola	189	7	1.0	215	2	Q9RKP8	Q9rkp8 streptomyce
117	7	1.0	146	2	Q75QF3	Q75qf3 rhopalomyia	190	7	1.0	221	2	Q9S824	Q9s824 drosophila
118	7	1.0	146	2	Q75QF4	Q75qf4 rhopalomyia	191	7	1.0	221	2	Q9VWV7	Q9vvw7 drosophila
119	7	1.0	146	2	Q75QF5	Q75qf5 rhopalomyia	192	7	1.0	222	2	Q871A9	Q871a9 neurospora
120	7	1.0	146	2	Q75QF6	Q75qf6 rhopalomyia	193	7	1.0	222	2	Q6ESR8	Q6esr8 oryza sativ
121	7	1.0	146	2	Q75QF7	Q75qf7 rhopalomyia	194	7	1.0	222	2	Q8KQW4	Q8kqw4 saccharopol
122	7	1.0	146	2	Q75QF8	Q75qf8 rhopalomyia	195	7	1.0	223	2	Q7Z7Z4	Q7z7z4 inocybe sie
123	7	1.0	146	2	Q75QF9	Q75qf9 rhopalomyia	196	7	1.0	223	2	Q8M0X1	Q8m0x1 gynodiastyl
124	7	1.0	146	2	Q75QG0	Q75qg0 rhopalomyia	197	7	1.0	225	2	Q8W5L0	Q8w5l0 oryza sativ
125	7	1.0	146	2	Q75QG1	Q75qg1 rhopalomyia	198	7	1.0	225	2	Q7XH60	Q7xh60 oryza sativ
126	7	1.0	146	2	Q75QG2	Q75qg2 rhopalomyia	199	7	1.0	226	2	Q632M1	Q632m1 bacillus ce
127	7	1.0	146	2	Q75QG3	Q75qg3 rhopalomyia	200	7	1.0	226	2	Q816L1	Q816l1 bacillus ce
128	7	1.0	146	2	Q75QG4	Q75qg4 rhopalomyia	201	7	1.0	226	2	Q81KC5	Q81kc5 bacillus an
129	7	1.0	146	2	Q75QG5	Q75qg5 rhopalomyia	202	7	1.0	226	2	Q6HC61	Q6hc61 bacillus th
130	7	1.0	146	2	Q69T63	Q69t63 oryza sativ	203	7	1.0	227	2	Q29875	Q29875 archaeoglob
131	7	1.0	147	2	Q67MY5	Q67my5 symbiobacte	204	7	1.0	227	2	Q7Z8D8	Q7z8d8 inocybe ada
132	7	1.0	154	2	Q50211	Q50211 mycobacteri	205	7	1.0	227	2	Q88Q18	Q88q18 pseudomonas
133	7	1.0	156	2	Q6PFF6	Q6pf6 xanthomonas	206	7	1.0	228	2	Q7Z825	Q7z825 inocybe che
134	7	1.0	156	2	Q8PU04	Q8pu04 oryza sativ	207	7	1.0	228	2	Q889S0	Q889s0 pseudomonas
135	7	1.0	157	2	Q95W21	Q95w21 anthonomus	208	7	1.0	231	2	Q7NBJ8	Q7nbj8 mycoplasma
136	7	1.0	158	2	Q9AV48	Q9av48 oryza sativ	209	7	1.0	231	2	Q9Z795	Q9z795 chlamydia p
137	7	1.0	158	2	Q654W6	Q654w6 oryza sativ	210	7	1.0	232	2	Q9HWW1	Q9hww1 pseudomonas
138	7	1.0	163	2	Q75L20	Q75l20 oryza sativ	211	7	1.0	233	2	Q7Z824	Q7z824 inocybe che
139	7	1.0	164	2	Q960K6	Q96qk6 homo sapien	212	7	1.0	235	2	Q8LD25	Q8ld25 arabidopsis
140	7	1.0	167	1	YPA2_ASCIM	P22375 ascobolus i	213	7	1.0	235	2	Q6VY63	Q6vy63 arabidopsis
141	7	1.0	168	2	Q8DJF0	Q8djf0 synechococc	214	7	1.0	235	2	Q6VTS3	Q6vts3 oryza sativ
142	7	1.0	168	2	Q9Z8U3	Q9z8u3 chlamydia p	215	7	1.0	236	2	Q91004	Q91004 gecko gecko
143	7	1.0	169	2	Q87NK8	Q87nk8 vibrio para	216	7	1.0	237	2	Q9HOG1	Q9h0g1 halobacteri
144	7	1.0	170	2	Q84RT8	Q84rt8 chamaemelum	217	7	1.0	237	2	Q7ZWL3	Q7zwl3 xenopus lae
145	7	1.0	170	2	Q84SG4	Q84sg4 chamaemelum	218	7	1.0	238	2	Q7Z7Z1	Q7z7z1 inocybe ste
146	7	1.0	171	2	Q9ROP0	Q9rqp0 vibrio chol	219	7	1.0	238	2	Q8CW43	Q8cw43 escherichia
147	7	1.0	171	2	Q9K279	Q9k279 chlamydia p	220	7	1.0	239	2	Q9KQD6	Q9kqd6 vibrio chol
148	7	1.0	172	2	Q9CLF6	Q9clf6 pasteurella	221	7	1.0	239	2	Q91218	Q91218 oncorhynchu
149	7	1.0	172	2	Q9DFD1	Q9dfd1 oncorhynchu	222	7	1.0	240	2	Q89IB3	Q89ib3 bradyrhizob
150	7	1.0	175	2	Q7NK23	Q7nk23 gloeobacter	223	7	1.0	241	2	Q8FRK8	Q8frk8 corynebacte
151	7	1.0	176	2	Q9PUC7	Q9puc7 gallus gall	224	7	1.0	242	2	Q7Z9K7	Q7z9k7 desulfovibr
152	7	1.0	178	2	Q9LMH2	Q9lmh2 arabidopsis	225	7	1.0	243	2	Q7M4I3	Q7m4i3 megabombus
153	7	1.0	181	2	Q87NZ6	Q87nz6 vibrio para	226	7	1.0	244	2	Q7X990	Q7x990 oryza sativ
154	7	1.0	185	2	Q9KWV2	Q9kwv2 salmonella	227	7	1.0	244	2	Q6DIS2	Q6dis2 xenopus tro
155	7	1.0	186	2	Q6BL42	Q6bl42 debaromyce	228	7	1.0	247	2	Q6FCS3	Q6fc3 escherichia
156	7	1.0	187	2	Q84S30	Q84s30 matricaria	229	7	1.0	247	2	Q8FCQ3	Q8fcq3 escherichia
157	7	1.0	187	2	Q6MTT3	Q6mtt3 mycoplasma	230	7	1.0	247	2	Q8X6U7	Q8x6u7 escherichia
158	7	1.0	189	2	Q84S31	Q84s31 matricaria	231	7	1.0	248	2	Q83P08	Q83pu8 shigella fl
159	7	1.0	190	1	YR15_GLOVI	Q7nh22 gloeobacter	232	7	1.0	248	2	Q83P08	Q83pu8 arabidopsis
160	7	1.0	190	2	Q6BSX0	Q6bsx0 debaromyce	233	7	1.0	249	2	Q6IE63	Q6ie63 rattus norv
161	7	1.0	191	1	MAF_BACAN	Q81ld6 bacillus an	234	7	1.0	249	2	Q8C1Q8	Q8clq8 mus musculu
162	7	1.0	191	2	Q633Y9	Q633y9 bacillus ce	235	7	1.0	250	2	Q8ZFK6	Q8zfk6 yersinia pe
163	7	1.0	191	2	Q9RSA2	Q9rsa2 deinococcus	236	7	1.0	253	2	Q89UG6	Q89ug6 bradyrhizob
164	7	1.0	191	2	Q6HD71	Q6hd71 bacillus th	237	7	1.0	254	2	Q74MV1	Q74mvl nanoarchaeu
165	7	1.0	193	1	Y377_MYCGE	P47617 mycoplasma	238	7	1.0	255	1	V29K_PERV	Q6n3m7 rhodopseudo
166	7	1.0	195	2	Q6AMF5	Q6amf5 desulfocalé	239	7	1.0	255	2	Q9Y7A9	P14850 pea early b
167	7	1.0	196	1	CRBD_CHICK	P49152 gallus gall	240	7	1.0	255	2	Q84700	Q84700 pea early b
168	7	1.0	198	2	Q8XR75	Q8xr75 ralstonia s	241	7	1.0	259	2	Q69EZ7	Q69ez7 homo sapien
169	7	1.0	201	1	ABP1_MAIZE	P13689 zea mays (m	242	7	1.0	260	1	COLI_RANRI	Q8udl2 agrobacteri
170	7	1.0	202	2	Q6ZSF8	Q6zsf8 homo sapien	243	7	1.0	260	1	COLI_RANCI	P22923 r corticotr
171	7	1.0	203	2	Q72ZX1	Q72zx1 bacillus ce	244	7	1.0	263	1	COLI_RANCA	P11885 r corticotr
172	7	1.0	204	2	Q8JIS7	Q8jis7 xenopus lae	245	7	1.0	263	2	Q6LJ76	Q6lj76 photobacter
173	7	1.0	208	2	Q9Z3I5	Q9z3i5 bradyrhizob	246	7	1.0	265	2	Q07812	Q07812 mycobacteri
174	7	1.0	209	1	NODS_BRAJA	P26026 bradyrhizob	247	7	1.0	265	2	Q68AV7	Q68av7 uncultured
175	7	1.0	210	2	Q75C67	Q75c67 ashbya goss	248	7	1.0	265	2	Q07181	Q07181 mycobacteri
176	7	1.0	211	2	Q6ESR9	Q6esr9 oryza sativ	249	7	1.0	265	2	Q7U190	Q7u190 mycobacteri
177	7	1.0	211	2	Q66AK7	Q66ak7 yersinia ps	250	7	1.0	266	2	Q8I916	Q8i916 blomia trop

251	7	1.0	266	2	O6JYB6	Q6jye6 elasmosteth	324	7	1.0	355	2	O47485	O47485 carabus cra
252	7	1.0	266	2	Q73QA7	Q73qa7 treponema d	325	7	1.0	355	2	O47486	O47486 carabus sic
253	7	1.0	266	2	Q9QU80	Q9qu80 tt virus. o	326	7	1.0	355	2	O47487	O47487 carabus tat
254	7	1.0	268	2	Q9XY56	Q9xy56 ctenocephal	327	7	1.0	355	2	O78724	O78724 carabus bla
255	7	1.0	268	2	Q6N9D3	Q6n9d3 rhodopsueto	328	7	1.0	355	2	O79585	O79585 carabus tit
256	7	1.0	271	2	Q9NPW7	Q9npw7 homo sapien	329	7	1.0	355	2	O79586	O79586 carabus sui
257	7	1.0	272	2	O51013	Q51013 neisseries g	330	7	1.0	355	2	O99052	O99052 carabus por
258	7	1.0	273	2	Q83DW2	Q83dw2 coxiella bu	331	7	1.0	355	2	O99053	O99053 carabus por
259	7	1.0	278	2	Q84C08	Q84c08 pseudomonas	332	7	1.0	355	2	O99054	O99054 carabus por
260	7	1.0	280	2	Q87X78	Q87x78 pseudomonas	333	7	1.0	355	2	P92098	P92098 carabus mar
261	7	1.0	281	2	O8U4H8	Q8u4h8 pyrococcus	334	7	1.0	355	2	P92100	P92100 carabus wag
262	7	1.0	281	2	O6JYN8	Q6jyn8 lestonia ha	335	7	1.0	355	2	P92101	P92101 carabus lep
263	7	1.0	282	2	O8JXE9	Q8jxe9 roselinia	336	7	1.0	355	2	P92102	P92102 carabus lud
264	7	1.0	284	2	Q96089	Q96089 haemaphysal	337	7	1.0	355	2	P92103	P92103 carabus bor
265	7	1.0	286	2	Q9H7G9	Q9h7g9 homo sapien	338	7	1.0	355	2	Q37388	Q37388 carabus geh
266	7	1.0	291	1	PCAR_PSRPU	Q52154 pseudomonas	339	7	1.0	355	2	Q37389	Q37389 carabus geh
267	7	1.0	291	2	Q9R9T0	Q9r9t0 pseudomonas	340	7	1.0	355	2	Q37428	Q37428 carabus fru
268	7	1.0	291	2	O88N41	O88n41 pseudomonas	341	7	1.0	355	2	Q37441	Q37441 carabus van
269	7	1.0	292	2	O54441	O54441 bacillus ps	342	7	1.0	355	2	Q37443	Q37443 carabus bla
270	7	1.0	294	1	PEPM_MYTED	P56839 mytilus edu	343	7	1.0	355	2	Q37444	Q37444 carabus bla
271	7	1.0	295	2	Q69E28	Q69e28 homo sapien	344	7	1.0	355	2	Q37445	Q37445 carabus bla
272	7	1.0	295	2	O6D6J3	Q6d6j3 erwinia car	345	7	1.0	355	2	Q37446	Q37446 carabus bla
273	7	1.0	299	2	Q8T8D9	Q8t8d9 trypanosoma	346	7	1.0	355	2	Q37447	Q37447 carabus bla
274	7	1.0	299	2	O7PMA7	Q7pma7 anopheles g	347	7	1.0	355	2	Q37448	Q37448 carabus bla
275	7	1.0	300	2	Q8IN70	Q8in70 drosophila	348	7	1.0	355	2	Q37449	Q37449 carabus bla
276	7	1.0	301	2	Q7ZSX7	Q7zxs7 fugu rubrip	349	7	1.0	355	2	Q37453	Q37453 carabus bla
277	7	1.0	303	1	LPXC_XANAC	Q8ppa3 xanthomonas	350	7	1.0	355	2	Q37454	Q37454 carabus bla
278	7	1.0	303	2	Q74ZD4	Q74zd4 ashbya goss	351	7	1.0	355	2	Q37457	Q37457 carabus bla
279	7	1.0	303	2	Q6VQ99	Q6vq99 tetraodon n	352	7	1.0	355	2	Q37459	Q37459 carabus bla
280	7	1.0	304	2	O8XXF6	O8xxf6 ralstonia s	353	7	1.0	355	2	Q37465	Q37465 carabus por
281	7	1.0	305	1	LPXC_RALSO	Q9khi6 ralstonia s	354	7	1.0	355	2	Q37518	Q37518 carabus mae
282	7	1.0	306	2	Q8LSB0	Q8lsb0 oryza sativ	355	7	1.0	355	2	Q37542	Q37542 carabus maa
283	7	1.0	307	2	Q7QK28	Q7qk28 anopheles g	356	7	1.0	355	2	O85A26	O85a26 carabus sac
284	7	1.0	307	2	Q9KV89	Q9kv89 vibrio chol	357	7	1.0	355	2	O85BA4	O85ba4 carabus cha
285	7	1.0	308	1	T2RC_MOUSE	P59532 mus musculu	358	7	1.0	355	2	O85GL4	O85gl4 carabus sma
286	7	1.0	308	2	Q7MT04	Q7mt04 mus musculu	359	7	1.0	355	2	O85GL5	O85gl5 carabus sma
287	7	1.0	312	2	Q12125	Q12125 saccharomyc	360	7	1.0	355	2	O85GL6	O85gl6 carabus kub
288	7	1.0	314	2	Q6F0P3	Q6fup3 candida gla	361	7	1.0	355	2	O85GL7	O85gl7 carabus for
289	7	1.0	315	1	Y001_CAUCR	Q9acs9 caulobacter	362	7	1.0	355	2	O85GL8	O85gl8 carabus jan
290	7	1.0	315	2	Q55220	Q55220 streptomyce	363	7	1.0	355	2	O85GL9	O85gl9 carabus osa
291	7	1.0	317	2	Q9KWA7	Q9kwa7 agrobacteri	364	7	1.0	355	2	O85GM0	O85gm0 carabus nan
292	7	1.0	318	2	O6CP66	O6cp66 kluyveromyc	365	7	1.0	355	2	O85GM1	O85gm1 carabus kae
293	7	1.0	321	2	Q67LF3	Q67lf3 symbiobacte	366	7	1.0	355	2	O85GM2	O85gm2 carabus rem
294	7	1.0	324	2	Q90Z55	Q90z55 scophthalmu	367	7	1.0	355	2	O85GM3	O85gm3 carabus alp
295	7	1.0	329	2	O8U2M3	Q8u2m3 pyrococcus	368	7	1.0	355	2	O85GM4	O85gm4 carabus wag
296	7	1.0	329	2	O89MG1	O89mg1 bradyrhizob	369	7	1.0	355	2	O85GM5	O85gm5 carabus lam
297	7	1.0	330	2	O30523	O30523 vibrio shil	370	7	1.0	355	2	O85GM6	O85gm6 carabus dra
298	7	1.0	332	2	O8NXI9	O8nxi9 staphylococ	371	7	1.0	355	2	O85GM7	O85gm7 carabus ben
299	7	1.0	333	2	Q9K7W7	Q9k7w7 bacillus ha	372	7	1.0	355	2	O85GM8	O85gm8 carabus wen
300	7	1.0	336	2	O69510	O69510 mycobacteri	373	7	1.0	355	2	O85GM9	O85gm9 carabus gan
301	7	1.0	336	2	O8PR42	O8pr42 xanthomonas	374	7	1.0	355	2	O85GN0	O85gn0 carabus lam
302	7	1.0	336	2	O6MS16	O6ms16 mycoplasma	375	7	1.0	355	2	O85GN1	O85gn1 carabus cra
303	7	1.0	336	2	Q7WL07	Q7wl07 bordetella	376	7	1.0	355	2	O85GN2	O85gn2 carabus vir
304	7	1.0	337	2	Q9YDH3	Q9ydh3 aeropyrum p	377	7	1.0	355	2	O85GN3	O85gn3 carabus vir
305	7	1.0	338	2	O8PE85	O8pes5 xanthomonas	378	7	1.0	355	2	O85GN4	O85gn4 carabus vir
306	7	1.0	342	2	Q7XE33	Q7xe33 oryza sativ	379	7	1.0	355	2	O85GN5	O85gn5 carabus sun
307	7	1.0	343	2	Q7VV13	Q7vv13 bordetella	380	7	1.0	355	2	O85GN6	O85gn6 carabus sun
308	7	1.0	343	2	O8D7G2	O8d7g2 vibrio vuln	381	7	1.0	355	2	O85GN7	O85gn7 carabus erw
309	7	1.0	344	2	O84QA9	O84qa9 oryza sativ	382	7	1.0	355	2	O85GN8	O85gn8 carabus bur
310	7	1.0	344	2	O92M18	Q92m18 rhizobium m	383	7	1.0	355	2	O85GN9	O85gn9 carabus tal
311	7	1.0	345	2	Q7W7L8	Q7w7l8 bordetella	384	7	1.0	355	2	O85GS4	O85gs4 carabus pun
312	7	1.0	346	2	O6UY16	O6jy16 eupolemus s	385	7	1.0	355	2	O85GS5	O85gs5 carabus mul
313	7	1.0	347	2	O6E2C2	O6e2c2 escherichia	386	7	1.0	355	2	O85GS6	O85gs6 carabus imp
314	7	1.0	347	2	Q7P022	Q7p022 chromobacte	387	7	1.0	355	2	O85GS7	O85gs7 carabus hem
315	7	1.0	348	1	RTCA_PYRAE	O8zet4 pyrobaculum	388	7	1.0	355	2	O85GS8	O85gs8 carabus mul
316	7	1.0	349	2	Q9YBV1	Q9ybv1 aeropyrum p	389	7	1.0	355	2	O85GS9	O85gs9 carabus mul
317	7	1.0	349	2	Q6NDF7	Q6ndf7 rhodopseudo	390	7	1.0	355	2	O85GT0	O85gt0 carabus syr
318	7	1.0	350	2	O18122	O18122 caenorhabdi	391	7	1.0	355	2	O85GT1	O85gt1 carabus pio
319	7	1.0	351	1	MSS2_YEAST	P40990 saccharomyc	392	7	1.0	355	2	O85GT2	O85gt2 carabus pio
320	7	1.0	352	2	O8C9H0	O8c9h0 mus musculu	393	7	1.0	355	2	O85GT5	O85gt5 carabus tor
321	7	1.0	354	2	Q99Q08	Q99q08 bradyrhizob	394	7	1.0	355	2	O85GT6	O85gt6 carabus ere
322	7	1.0	354	2	Q99QE0	Q99qe0 bradyrhizob	395	7	1.0	355	2	O85GT7	O85gt7 carabus nor
323	7	1.0	355	2	O47484	O47484 carabus vir	396	7	1.0	355	2	O85GT8	O85gt8 carabus nor

397	7	1.0	355	2	Q85GT9	Q85gt9 carabus tor	470	7	1.0	355	2	Q9MR78	Q9mr78 carabus por
398	7	1.0	355	2	Q85GU0	Q85gu0 carabus tor	471	7	1.0	355	2	Q9MR79	Q9mr79 carabus por
399	7	1.0	355	2	Q85GU1	Q85gu1 carabus tor	472	7	1.0	355	2	Q9MR80	Q9mr80 carabus por
400	7	1.0	355	2	Q85GU2	Q85gu2 carabus cha	473	7	1.0	355	2	Q9MR81	Q9mr81 carabus por
401	7	1.0	355	2	Q85GU3	Q85gu3 carabus tor	474	7	1.0	355	2	Q9T227	Q9t227 carabus bla
402	7	1.0	355	2	Q85GU4	Q85gu4 carabus pra	475	7	1.0	355	2	Q9T391	Q9t391 carabus bla
403	7	1.0	355	2	Q8HAX6	Q8hax6 carabus tit	476	7	1.0	355	2	Q9T392	Q9t392 carabus bla
404	7	1.0	355	2	Q8HDX2	Q8hdx2 carabus asc	477	7	1.0	355	2	Q9T393	Q9t393 carabus bla
405	7	1.0	355	2	Q8HDX3	Q8hdx3 carabus mas	478	7	1.0	355	2	Q9T3V1	Q9t3v1 carabus bla
406	7	1.0	355	2	Q8HDX4	Q8hdx4 carabus mas	479	7	1.0	355	2	Q9T3V2	Q9t3v2 carabus bla
407	7	1.0	355	2	Q8HDX5	Q8hdx5 carabus inf	480	7	1.0	355	2	Q9T3V3	Q9t3v3 carabus bla
408	7	1.0	355	2	Q8HDX6	Q8hdx6 carabus inf	481	7	1.0	355	2	Q9T3V4	Q9t3v4 carabus bla
409	7	1.0	355	2	Q8HDX7	Q8hdx7 carabus min	482	7	1.0	355	2	Q9T3V5	Q9t3v5 carabus bla
410	7	1.0	355	2	Q8HDX8	Q8hdx8 carabus tic	483	7	1.0	355	2	Q9T3Z7	Q9t3z7 carabus bla
411	7	1.0	355	2	Q8HDX9	Q8hdx9 carabus tic	484	7	1.0	355	2	Q9T4D6	Q9t4d6 carabus del
412	7	1.0	355	2	Q8HDX10	Q8hdx10 carabus hum	485	7	1.0	355	2	Q9T4K2	Q9t4k2 carabus bla
413	7	1.0	355	2	Q8HDX11	Q8hdx11 carabus hum	486	7	1.0	355	2	Q9T4R4	Q9t4r4 carabus bla
414	7	1.0	355	2	Q8HDX12	Q8hdx12 carabus hum	487	7	1.0	355	2	Q9T4R5	Q9t4r5 carabus bla
415	7	1.0	355	2	Q8HDX13	Q8hdx13 carabus hum	488	7	1.0	355	2	Q9T4T8	Q9t4t8 carabus sem
416	7	1.0	355	2	Q8HDX14	Q8hdx14 carabus hum	489	7	1.0	355	2	Q9T4V4	Q9t4v4 carabus bla
417	7	1.0	355	2	Q8HDX15	Q8hdx15 carabus hum	490	7	1.0	355	2	Q9T4V8	Q9t4v8 carabus cla
418	7	1.0	355	2	Q8HDX16	Q8hdx16 carabus hum	491	7	1.0	355	2	Q9TDX8	Q9tdx8 carabus mao
419	7	1.0	355	2	Q8HDX17	Q8hdx17 carabus hum	492	7	1.0	355	2	Q9TDX9	Q9tdx9 carabus cle
420	7	1.0	355	2	Q8HDX18	Q8hdx18 carabus hum	493	7	1.0	355	2	Q9TDY1	Q9tdy1 carabus iri
421	7	1.0	355	2	Q8HDX19	Q8hdx19 carabus hum	494	7	1.0	355	2	Q9TDY2	Q9tdy2 carabus arr
422	7	1.0	355	2	Q8HDX20	Q8hdx20 carabus hum	495	7	1.0	355	2	Q9TDY3	Q9tdy3 carabus lao
423	7	1.0	355	2	Q8HDX21	Q8hdx21 carabus hum	496	7	1.0	355	2	Q9TDY4	Q9tdy4 carabus lao
424	7	1.0	355	2	Q8HDX22	Q8hdx22 carabus hum	497	7	1.0	355	2	Q9TDY5	Q9tdy5 carabus cya
425	7	1.0	355	2	Q8HDX23	Q8hdx23 carabus hum	498	7	1.0	355	2	Q9TDY6	Q9tdy6 carabus tou
426	7	1.0	355	2	Q8HDX24	Q8hdx24 carabus hum	499	7	1.0	355	2	Q9TDY7	Q9tdy7 carabus tux
427	7	1.0	355	2	Q8HDX25	Q8hdx25 carabus hum	500	7	1.0	355	2	Q9TDY8	Q9tdy8 carabus ton
428	7	1.0	355	2	Q8HDX26	Q8hdx26 carabus hum	501	7	1.0	355	2	Q9TDY9	Q9tdy9 carabus ton
429	7	1.0	355	2	Q8HDX27	Q8hdx27 carabus hum	502	7	1.0	355	2	Q9TE01	Q9te01 carabus tru
430	7	1.0	355	2	Q8HDX28	Q8hdx28 carabus hum	503	7	1.0	355	2	Q9TE02	Q9te02 carabus can
431	7	1.0	355	2	Q8HDX29	Q8hdx29 carabus hum	504	7	1.0	355	2	Q9TE03	Q9te03 carabus can
432	7	1.0	355	2	Q8HDX30	Q8hdx30 carabus hum	505	7	1.0	355	2	Q9TE04	Q9te04 carabus can
433	7	1.0	355	2	Q8HDX31	Q8hdx31 carabus hum	506	7	1.0	355	2	Q9TE05	Q9te05 carabus can
434	7	1.0	355	2	Q8HDX32	Q8hdx32 carabus hum	507	7	1.0	355	2	Q9TE08	Q9te08 carabus sei
435	7	1.0	355	2	Q8HDX33	Q8hdx33 carabus hum	508	7	1.0	355	2	Q9TE09	Q9te09 carabus sei
436	7	1.0	355	2	Q8HDX34	Q8hdx34 carabus hum	509	7	1.0	355	2	Q9TE10	Q9te10 carabus sei
437	7	1.0	355	2	Q8HDX35	Q8hdx35 carabus hum	510	7	1.0	355	2	Q9TE11	Q9te11 carabus sei
438	7	1.0	355	2	Q8HDX36	Q8hdx36 carabus hum	511	7	1.0	355	2	Q9TE12	Q9te12 carabus sei
439	7	1.0	355	2	Q8HDX37	Q8hdx37 carabus hum	512	7	1.0	355	2	Q9TE13	Q9te13 carabus sei
440	7	1.0	355	2	Q8HDX38	Q8hdx38 carabus hum	513	7	1.0	355	2	Q9TE14	Q9te14 carabus sei
441	7	1.0	355	2	Q8HDX39	Q8hdx39 carabus hum	514	7	1.0	355	2	Q9TE15	Q9te15 carabus sei
442	7	1.0	355	2	Q8HDX40	Q8hdx40 carabus hum	515	7	1.0	355	2	Q9TE16	Q9te16 carabus sei
443	7	1.0	355	2	Q8HDX41	Q8hdx41 carabus hum	516	7	1.0	355	2	Q9TE17	Q9te17 carabus sei
444	7	1.0	355	2	Q8HDX42	Q8hdx42 carabus hum	517	7	1.0	355	2	Q9TE18	Q9te18 carabus sei
445	7	1.0	355	2	Q8HDX43	Q8hdx43 carabus hum	518	7	1.0	355	2	Q9TE19	Q9te19 carabus sei
446	7	1.0	355	2	Q8HDX44	Q8hdx44 carabus hum	519	7	1.0	355	2	Q9TE20	Q9te20 carabus sei
447	7	1.0	355	2	Q8HDX45	Q8hdx45 carabus hum	520	7	1.0	355	2	Q9TE21	Q9te21 carabus sei
448	7	1.0	355	2	Q8HDX46	Q8hdx46 carabus hum	521	7	1.0	355	2	Q9TE22	Q9te22 carabus sei
449	7	1.0	355	2	Q8HDX47	Q8hdx47 carabus hum	522	7	1.0	355	2	Q9TE23	Q9te23 carabus sei
450	7	1.0	355	2	Q8HDX48	Q8hdx48 carabus hum	523	7	1.0	355	2	Q9TE24	Q9te24 carabus sei
451	7	1.0	355	2	Q8HDX49	Q8hdx49 carabus hum	524	7	1.0	355	2	Q9TE25	Q9te25 carabus sei
452	7	1.0	355	2	Q8HDX50	Q8hdx50 carabus hum	525	7	1.0	355	2	Q9TE26	Q9te26 carabus sei
453	7	1.0	355	2	Q8HDX51	Q8hdx51 carabus hum	526	7	1.0	355	2	Q9TE27	Q9te27 carabus sei
454	7	1.0	355	2	Q8HDX52	Q8hdx52 carabus hum	527	7	1.0	355	2	Q9TE28	Q9te28 carabus sei
455	7	1.0	355	2	Q8HDX53	Q8hdx53 carabus hum	528	7	1.0	355	2	Q9TE29	Q9te29 carabus sei
456	7	1.0	355	2	Q8HDX54	Q8hdx54 carabus hum	529	7	1.0	355	2	Q9TE30	Q9te30 carabus sei
457	7	1.0	355	2	Q8HDX55	Q8hdx55 carabus hum	530	7	1.0	355	2	Q9TE31	Q9te31 carabus sei
458	7	1.0	355	2	Q8HDX56	Q8hdx56 carabus hum	531	7	1.0	355	2	Q9TE32	Q9te32 carabus sei
459	7	1.0	355	2	Q8HDX57	Q8hdx57 carabus hum	532	7	1.0	355	2	Q9TE33	Q9te33 carabus sei
460	7	1.0	355	2	Q8HDX58	Q8hdx58 carabus hum	533	7	1.0	355	2	Q9TE34	Q9te34 carabus sei
461	7	1.0	355	2	Q8HDX59	Q8hdx59 carabus hum	534	7	1.0	355	2	Q9TE35	Q9te35 carabus sei
462	7	1.0	355	2	Q8HDX60	Q8hdx60 carabus hum	535	7	1.0	355	2	Q9TE36	Q9te36 carabus sei
463	7	1.0	355	2	Q8HDX61	Q8hdx61 carabus hum	536	7	1.0	355	2	Q9TE37	Q9te37 carabus sei
464	7	1.0	355	2	Q8HDX62	Q8hdx62 carabus hum	537	7	1.0	355	2	Q9TE38	Q9te38 carabus sei
465	7	1.0	355	2	Q8HDX63	Q8hdx63 carabus hum	538	7	1.0	355	2	Q9TE39	Q9te39 carabus sei
466	7	1.0	355	2	Q8HDX64	Q8hdx64 carabus hum	539	7	1.0	355	2	Q9TE40	Q9te40 carabus sei
467	7	1.0	355	2	Q8HDX65	Q8hdx65 carabus hum	540	7	1.0	355	2	Q9TE41	Q9te41 carabus sei
468	7	1.0	355	2	Q8HDX66	Q8hdx66 carabus hum	541	7	1.0	355	2	Q9TE42	Q9te42 carabus sei
469	7	1.0	355	2	Q8HDX67	Q8hdx67 carabus hum	542	7	1.0	355	2	Q9TE43	Q9te43 carabus sei
												Q9TE44	Q9te44 carabus bla
												Q9TE45	Q9te45 carabus bla

543	7	1.0	355	2	Q9TEA6	Q9tea6 carabus bla	616	7	1.0	446	2	Q6FCC9	Q6fcc9 acinetobact
544	7	1.0	355	2	Q9TEA7	Q9tea7 carabus bla	617	7	1.0	447	2	Q8TAS5	Q8tas5 homo sapien
545	7	1.0	355	2	Q9TEA8	Q9tea8 carabus bla	618	7	1.0	449	2	Q8BI18	Q8bi18 mus musculu
546	7	1.0	355	2	Q9TEA9	Q9tea9 carabus bla	619	7	1.0	453	2	Q6CVL9	Q6cvl9 kluyveromyc
547	7	1.0	355	2	Q9TEB0	Q9teb0 carabus bla	620	7	1.0	453	2	Q6VAT4	Q6vat4 umbraculum
548	7	1.0	355	2	Q9TEB1	Q9teb1 carabus bla	621	7	1.0	453	2	Q8P704	Q8p704 xanthomonas
549	7	1.0	355	2	Q9TEB2	Q9teb2 carabus bla	622	7	1.0	453	2	Q8PIB8	Q8pi18 xanthomonas
550	7	1.0	355	2	Q9TEB2	Q9teb2 carabus bla	623	7	1.0	455	2	Q6LEF23	Q6lef23 photobacter
551	7	1.0	357	2	Q6ZSC3	Q6zsc3 homo sapien	624	7	1.0	459	2	Q96349	Q96349 brassica na
552	7	1.0	358	2	Q882Y3	Q882y3 pseudomonas	625	7	1.0	459	2	Q67L10	Q67l10 symbiobacte
553	7	1.0	359	2	Q882Y3	Q882y3 pseudomonas	626	7	1.0	461	2	Q7D565	Q7d565 mycobacteri
554	7	1.0	359	2	Q6JYI3	Q6jy13 amphaces sp	627	7	1.0	461	2	Q06380	Q06380 mycobacteri
555	7	1.0	359	2	Q6JYI5	Q6jy15 stauralia c	628	7	1.0	461	2	Q744A5	Q744a5 mycobacteri
556	7	1.0	359	2	Q6JYI5	Q6jy15 stauralia c	629	7	1.0	461	2	Q7TW31	Q7tw31 mycobacteri
557	7	1.0	360	1	Q65XU7	Q65xu7 oryza sativ	630	7	1.0	462	2	Q7SEJ7	Q7sej7 aahbya goos
558	7	1.0	360	1	AROBU CAP	Q8k939 buchnera ap	631	7	1.0	462	2	Q6PAG2	Q6pag2 xenopus lae
559	7	1.0	363	2	Q8WP22	Q8wp22 macaca fasc	632	7	1.0	463	1	FMNL HUMAN	Q95466 homo sapien
560	7	1.0	364	2	Q7MEH3	Q7meh3 vibrio vuln	633	7	1.0	463	2	Q8N671	Q8n671 homo sapien
561	7	1.0	367	2	Q8N7P6	Q8n7f6 homo sapien	634	7	1.0	463	2	Q84XL8	Q84xl8 xerophyta h
562	7	1.0	367	2	Q8N7P6	Q8n7f6 homo sapien	635	7	1.0	465	2	Q8GW44	Q8gw44 arabidopsis
563	7	1.0	368	2	Q32860	Q32860 mycobacteri	636	7	1.0	468	2	Q6K2N9	Q6k2n9 oryza sativ
564	7	1.0	372	2	Q9H2B5	Q9h2b5 pseudomonas	637	7	1.0	469	2	Q8LEG9	Q8leg9 arabidopsis
565	7	1.0	373	2	Q704D8	Q704d8 thermoprote	638	7	1.0	469	2	Q81NL2	Q81nl2 bacillus an
566	7	1.0	373	2	Q803P1	Q803f1 brachydanio	639	7	1.0	472	2	Q6DQ98	Q6dq98 nicotiana t
567	7	1.0	374	1	TGT ANASP	Q8yvt9 anabaena sp	640	7	1.0	472	2	Q09657	Q09657 caenorhabdi
568	7	1.0	375	2	Q9JX36	Q9jx36 neisseria m	641	7	1.0	475	1	GID BRAJA	Q89121 bradyrhizob
569	7	1.0	375	2	Q9KIG5	Q9kl95 neisseria m	642	7	1.0	476	2	Q6HMS5	Q6hms5 bacillus an
570	7	1.0	376	2	Q7VX11	Q7vx11 bordetella	643	7	1.0	476	2	Q735G8	Q735g8 bacillus ce
571	7	1.0	377	2	Q7NY19	Q7ny19 chromobacte	644	7	1.0	476	2	Q81BL6	Q81bl6 bacillus ce
572	7	1.0	378	2	Q8XQ55	Q8xq55 ralstonia s	645	7	1.0	476	2	Q6HGR8	Q6hgr8 bacillus th
573	7	1.0	382	2	Q88BC3	Q88bc3 pseudomonas	646	7	1.0	478	2	Q6FPY7	Q6fp7 candida gla
574	7	1.0	382	2	Q90WT4	Q90wt4 crocodylus	647	7	1.0	479	2	Q99RL5	Q99rl5 staphylococ
575	7	1.0	383	2	Q65Q28	Q65q28 manheimia	648	7	1.0	479	2	Q7A3S4	Q7a3s4 staphylococ
576	7	1.0	383	2	Q7W5V6	Q7w5v6 bordetella	649	7	1.0	483	2	Q89BC3	Q89bc3 bradyrhizob
577	7	1.0	387	2	Q7W6K8	Q7w6k8 bordetella	650	7	1.0	484	2	Q7PHP7	Q7php7 anopheles g
578	7	1.0	387	2	Q8GJM2	Q8gjm2 synechococc	651	7	1.0	487	2	Q8ET76	Q8et76 oceanobacil
579	7	1.0	387	2	P73853	P73853 synechocyst	652	7	1.0	489	1	MEP3 YEAST	P53390 saccharomyc
580	7	1.0	387	2	Q8Z0N9	Q8z0n9 anabaena sp	653	7	1.0	489	2	Q6B2F5	Q6b2f5 saccharomyc
581	7	1.0	387	2	Q7U697	Q7u697 synechococc	654	7	1.0	489	2	Q91QQ1	Q91qq1 soybean dwa
582	7	1.0	387	2	Q7U6M7	Q7u6m7 prochloroco	655	7	1.0	490	2	Q74I35	Q74i35 lactobacill
583	7	1.0	387	2	Q8DGX2	Q8dgx2 synechococc	656	7	1.0	490	2	Q7VHI3	Q7vhi3 helicobacte
584	7	1.0	388	2	O44330	O44330 manduca sex	657	7	1.0	491	1	MURC PHOLL	Q7n148 photorhabdu
585	7	1.0	389	1	PYRC SULTO	Q970x5 sulfolobus	658	7	1.0	492	1	MEPI YEAST	P40260 saccharomyc
586	7	1.0	391	2	Q91V12	Q91v12 mus musculu	659	7	1.0	492	2	O45659	O45659 caenorhabdi
587	7	1.0	392	2	Q63W65	Q63w65 burkholderi	660	7	1.0	492	2	Q88215	Q88215 lactobacill
588	7	1.0	394	2	P91817	P91817 tachypleus	661	7	1.0	493	1	CAMA CHICK	P05099 gallus gall
589	7	1.0	396	2	Q7XTQ4	Q7xtq4 oryza sativ	662	7	1.0	493	2	Q972W0	Q972w0 sulfolobus
590	7	1.0	397	2	Q94J66	Q94j66 oryza sativ	663	7	1.0	493	2	Q90XP7	Q90xp7 brachydanio
591	7	1.0	397	2	Q8RJW1	Q8rjw1 xanthomonas	664	7	1.0	494	1	CDS MOUSE	P13379 mus musculu
592	7	1.0	398	2	Q91374	Q91374 pseudomonas	665	7	1.0	494	2	Q8VDV0	Q8vdv0 mus musculu
593	7	1.0	399	2	Q7RY56	Q7ry56 neurospora	666	7	1.0	494	2	Q91X69	Q91x69 mus musculu
594	7	1.0	407	2	Q627S5	Q627s5 oryza sativ	667	7	1.0	494	2	Q8BMS0	Q8bms0 mus musculu
595	7	1.0	408	2	Q9VMA6	Q9vma6 dristophila	668	7	1.0	494	2	Q9ER20	Q9er20 mus musculu
596	7	1.0	408	2	Q8XWX2	Q8xwx2 ralstonia s	669	7	1.0	497	2	Q54706	Q54706 streptococc
597	7	1.0	410	2	Q6E824	Q6e824 umbonia cra	670	7	1.0	497	2	Q54749	Q54749 streptococc
598	7	1.0	410	2	Q6E826	Q6e826 umbonia cra	671	7	1.0	497	2	Q5A1S4	Q5a1s4 streptococc
599	7	1.0	410	2	Q6E838	Q6e838 platycotis	672	7	1.0	497	2	Q93VS8	Q93vs8 mycobacteri
600	7	1.0	413	2	Q6E840	Q6e840 platycotis	673	7	1.0	497	2	Q6C1P0	Q6c1p0 yarrowia li
601	7	1.0	413	2	O29192	O29192 archaeoglob	674	7	1.0	498	2	Q9NDD6	Q9ndd6 riftia pach
602	7	1.0	414	2	Q6LYH5	Q6lyh5 methanococc	675	7	1.0	501	2	Q9NDD6	Q9ndd6 riftia pach
603	7	1.0	414	2	Q6UDM0	Q6udm0 psittacid h	676	7	1.0	504	1	GPMT RHOPA	Q98qa7 rhodospseudo
604	7	1.0	416	2	Q88RT5	Q88rt5 pseudomonas	677	7	1.0	505	1	GPMT MYCPU	Q9m3n0 spinacia ol
605	7	1.0	420	1	O63A DROME	Q9vzw8 dristophila	678	7	1.0	505	1	MATK SPIOL	Q95ea3 gymnocalyci
606	7	1.0	421	2	Q73KB7	Q73kb7 treponema d	679	7	1.0	505	2	Q95EA3	Q95ea3 brownlingia
607	7	1.0	426	2	Q6BX74	Q6bx74 debaryomyce	680	7	1.0	507	1	MATK BROHE	Q94nc4 stetsonia c
608	7	1.0	429	2	Q7SYF9	Q7syf9 acipenser b	681	7	1.0	507	2	Q94NC4	Q94nc4 stetsonia c
609	7	1.0	432	2	Q73AL5	Q73al5 bacillus ce	682	7	1.0	507	2	Q94P31	Q94p31 haagocoreu
610	7	1.0	436	2	Q67NQ5	Q67nq5 symbiobacte	683	7	1.0	507	2	Q94P94	Q94p94 eriosyce na
611	7	1.0	437	2	Q51640	Q51640 burkholderi	684	7	1.0	507	2	Q94PY9	Q94py9 acanthocaly
612	7	1.0	439	2	Q7UDY7	Q7udy7 rhodopirell	685	7	1.0	507	2	Q95B87	Q95b87 neowderma
613	7	1.0	439	2	Q9LV67	Q9lv67 arabidopsis	686	7	1.0	507	2	Q95E88	Q95e88 eriosyce au
614	7	1.0	441	2	Q62LB1	Q62lb1 burkholderi	687	7	1.0	507	2	Q95E89	Q95e89 eriosyce is
615	7	1.0	442	2	Q804X1	Q804x1 fugu rubrip	688	7	1.0	507	2	Q95E90	Q95e90 eriosyce au
			445	2	Q67RK6	Q67rk6 symbiobacte							

589	7	1.0	507	2	Q95E93	Q95e93	parodia maa	762	7	1.0	544	2	Q8TFN9	Q8tfn9	emericeella
590	7	1.0	507	2	Q95E96	Q95e96	matucana in	763	7	1.0	545	2	Q67LM0	Q67lm0	ymbiobacte
591	7	1.0	507	2	Q95E97	Q95e97	rauhocereus	764	7	1.0	549	2	Q9DW53	Q9dw53	rat cytomec
592	7	1.0	507	2	Q95EA0	Q95ea0	trichocereu	765	7	1.0	553	2	Q97S10	Q97s10	streptococc
593	7	1.0	507	2	Q95EA1	Q95ea1	uebelmannia	766	7	1.0	553	2	Q8DQR3	Q8dq3	streptococc
594	7	1.0	507	2	Q95EA2	Q95ea2	coleocephal	767	7	1.0	556	1	NUZM_PODAN	P15578	podospora a
595	7	1.0	507	2	Q95EA4	Q95ea4	browningia	768	7	1.0	556	2	Q6DEK7	Q6dek7	brachydanio
596	7	1.0	507	2	Q95EC4	Q95ec4	copiapoa la	769	7	1.0	560	2	Q49141	Q49141	arabidopsis
597	7	1.0	507	2	Q95EC5	Q95ec5	copiapoa br	770	7	1.0	560	2	O50057	O50057	arabidopsis
598	7	1.0	507	2	Q95EC6	Q95ec6	copiapoa so	771	7	1.0	561	2	Q9KYS9	Q9kys9	streptomyc
599	7	1.0	507	2	Q95EC6	Q95ec6	peresklopsi	772	7	1.0	561	2	Q9RXS1	Q9rxs1	delinococcus
600	7	1.0	507	2	Q95ED8	Q95ed8	peresklopsi	773	7	1.0	563	2	Q74JC6	Q74jc6	lactobacill
700	7	1.0	507	2	Q7HFB7	Q7hfb7	parodia mag	773	7	1.0	568	2	Q88W64	Q88w64	lactobacill
701	7	1.0	507	2	Q7HFB8	Q7hfb8	oreocereus	774	7	1.0	576	2	Q6YID6	Q6yid6	penaeus mon
702	7	1.0	507	2	Q7HFB9	Q7hfb9	samaipatice	775	7	1.0	579	2	Q65XT5	Q65xt5	oryza sativ
703	7	1.0	507	2	Q7HFC0	Q7hfc0	micranthoce	776	7	1.0	580	2	Q9ZQP6	Q9zqp6	arabidopsis
704	7	1.0	507	2	Q7HFC1	Q7hfc1	cereus alac	777	7	1.0	581	1	YD15_SCHPO	Q10238	schizosacch
705	7	1.0	508	2	Q95EB2	Q95eb2	pfeiffera m	778	7	1.0	581	2	Q9LKH1	Q9lkh1	mesembryant
706	7	1.0	508	2	Q93SM9	Q93sm9	staphylococ	779	7	1.0	581	2	Q8D7C1	Q8d7c1	vibrio vuln
707	7	1.0	508	2	Q6GB44	Q6gb44	staphylococ	780	7	1.0	581	2	O23492	O23492	arabidopsis
708	7	1.0	509	2	Q95EB3	Q95eb3	lepisium c	781	7	1.0	584	2	Q9SQZ0	Q9sqz0	arabidopsis
709	7	1.0	509	2	Q95EB5	Q95eb5	rhipealis f	782	7	1.0	584	2	Q67RH6	Q67rh6	ymbiobacte
710	7	1.0	509	2	Q95EB6	Q95eb6	hattoria sal	783	7	1.0	585	2	Q17491	Q17491	caenorhabdi
711	7	1.0	509	2	Q95EB9	Q95eb9	parodia ott	784	7	1.0	585	2	Q8SZY4	Q8szy4	drosophila
712	7	1.0	509	2	Q95E92	Q95e92	parodia mic	785	7	1.0	600	2	Q93GX8	Q93gx8	streptomyc
713	7	1.0	509	2	Q95EA6	Q95ea6	disocactus	786	7	1.0	600	2	Q6AZT2	Q6azt2	xenopus lae
714	7	1.0	509	2	Q95EA7	Q95ea7	selenicereu	787	7	1.0	602	2	Q65DM0	Q65dm0	bacillus li
715	7	1.0	509	2	Q95EA8	Q95ea8	hylocereus	788	7	1.0	607	2	Q6DFJ5	Q6dfj5	xenopus lae
716	7	1.0	509	2	Q95EA9	Q95ea9	pachycereus	789	7	1.0	608	2	Q9GMB0	Q9gmb0	sub scrofa
717	7	1.0	509	2	Q95EB1	Q95eb1	echinocereu	790	7	1.0	611	2	Q7MEC8	Q7mec8	vibrio vuln
718	7	1.0	509	2	Q95EB3	Q95eb3	pfeiffera m	791	7	1.0	612	2	Q804W7	Q804w7	fugu rubrip
719	7	1.0	509	2	Q95EB4	Q95eb4	pfeiffera i	792	7	1.0	614	1	SPAS_MOUSE	Q9qy78	mus musculu
720	7	1.0	509	2	Q95EB5	Q95eb5	corryocactu	793	7	1.0	615	2	Q6GNK4	Q6gnk4	xenopus lae
721	7	1.0	509	2	Q95EB6	Q95eb6	corryocactu	794	7	1.0	616	1	SPAS_HUMAN	Q9ubp0	homo sapien
722	7	1.0	509	2	Q95EB7	Q95eb7	eulychnia i	795	7	1.0	617	1	THRB_RAT	P18292	rattus norv
723	7	1.0	509	2	Q95EB8	Q95eb8	austrocactu	796	7	1.0	617	2	Q97UG5	Q97ug5	sulfolobus
724	7	1.0	509	2	Q95EB9	Q95eb9	neoraimondi	797	7	1.0	618	1	CTR3_MOUSE	P70423	mus musculu
725	7	1.0	509	2	Q95EC0	Q95ec0	castellanos	798	7	1.0	618	1	THRB_MOUSE	P19221	mus musculu
726	7	1.0	509	2	Q95EC1	Q95ec1	leptocereus	799	7	1.0	620	2	Q38940	Q38940	arabidopsis
727	7	1.0	509	2	Q95EC2	Q95ec2	armatocereu	800	7	1.0	622	1	THRB_HUMAN	P00734	homo sapien
728	7	1.0	509	2	Q95EC3	Q95ec3	acanthocereu	801	7	1.0	622	2	Q727P3	Q727p3	homo sapien
729	7	1.0	509	2	Q95EC7	Q95ec7	calymmanthi	802	7	1.0	624	2	Q94CF4	Q94cf4	arabidopsis
730	7	1.0	509	2	Q95EC8	Q95ec8	aztekium ri	803	7	1.0	625	1	THIC_BOVIN	P00735	bos taurus
731	7	1.0	509	2	Q95ED0	Q95ed0	astrophytum	804	7	1.0	629	1	THIC_PSESM	Q87vg1	pseudomonas
732	7	1.0	509	2	Q95ED1	Q95ed1	echinocactu	805	7	1.0	633	2	Q90Z56	Q90z56	scophthalmu
733	7	1.0	509	2	Q95ED2	Q95ed2	frailea pha	806	7	1.0	638	2	Q9NKD7	Q9nk47	drosophila
734	7	1.0	509	2	Q95ED3	Q95ed3	frailea gra	807	7	1.0	651	2	Q7NGA4	Q7nga4	gloeobacter
735	7	1.0	509	2	Q95ED4	Q95ed4	blossfeldia	808	7	1.0	658	2	O65466	O65466	arabidopsis
736	7	1.0	509	2	Q95ED5	Q95ed5	blossfeldia	809	7	1.0	663	2	Q8U2H8	Q8u2h8	pyrococcus
737	7	1.0	509	2	Q95ED9	Q95ed9	opuntia qui	810	7	1.0	674	2	Q9CS59	Q9c599	arabidopsis
738	7	1.0	509	2	Q95EE0	Q95ee0	austrocylin	811	7	1.0	678	2	Q9A4E2	Q9a4e2	caulobacter
739	7	1.0	509	2	Q95EE2	Q95ee2	pereskia st	812	7	1.0	680	2	Q8GX18	Q8gx18	arabidopsis
740	7	1.0	509	2	Q95EE3	Q95ee3	pereskia gu	813	7	1.0	682	2	Q6DKG5	Q6dkg5	homo sapien
741	7	1.0	509	2	Q95EE4	Q95ee4	talinum pan	814	7	1.0	682	2	Q8EWF4	Q8ewf4	mycoplasma
742	7	1.0	510	1	MATK_GRABR	Q95ee5	grahamia br	815	7	1.0	684	2	O80709	O80709	arabidopsis
743	7	1.0	510	2	Q7SEH0	Q7seh0	neurospora	816	7	1.0	700	2	Q8ECU0	Q8ecu0	shewanella
744	7	1.0	517	2	Q67SW0	Q67sw0	ymbiobacte	817	7	1.0	703	2	Q8R917	Q8r917	thermoanaer
745	7	1.0	521	1	GM12_METAC	Q8tiy2	methanosarc	818	7	1.0	705	2	Q7R5J9	Q7r5j9	giardia lam
746	7	1.0	521	1	GFMI_METMA	Q8pyf8	methanosarc	819	7	1.0	707	1	BMPI_XENLA	P80700	xenopus lae
747	7	1.0	524	2	Q7SXH8	Q7sxh8	brachydanio	820	7	1.0	708	2	O87239	O87239	lactococcus
748	7	1.0	525	2	Q6BJ17	Q6bj17	debaromyce	821	7	1.0	713	2	Q62A96	Q62a96	burkholderi
749	7	1.0	526	2	Q96AV5	Q96av5	homo sapien	822	7	1.0	720	2	Q63NR2	Q63nr2	burkholderi
750	7	1.0	527	2	Q8P606	Q8p606	xanthomonas	823	7	1.0	732	2	O65QI8	O65qi8	mannheimia
751	7	1.0	529	2	Q17403	Q17403	caenorhabdi	824	7	1.0	735	2	O57381	O57381	xenopus lae
752	7	1.0	529	2	Q7ND04	Q7nd04	gloeobacter	825	7	1.0	735	2	Q66K13	Q66k13	xenopus lae
753	7	1.0	530	2	Q94900	Q94900	homo sapien	826	7	1.0	746	2	O6M7J3	O6m7j3	corynebacte
754	7	1.0	532	2	Q9YDB4	Q9ydb4	aeropyrum p	827	7	1.0	746	2	Q97R74	Q97r74	streptococc
755	7	1.0	533	2	Q9BI47	Q9bi47	caenorhabdi	828	7	1.0	749	2	Q9YGE8	Q9yge8	oncorhynch
756	7	1.0	535	2	Q9JP77	Q9jp77	thermonomon	829	7	1.0	754	2	O49144	O49144	arabidopsis
757	7	1.0	535	2	Q6MR14	Q6mr14	bdellovibri	830	7	1.0	754	2	O7G196	O7g196	arabidopsis
758	7	1.0	541	2	Q7P546	Q7p546	fusobacteri	831	7	1.0	765	2	O8XY74	O8xy74	raistonia s
759	7	1.0	541	2	Q8RFL3	Q8rf13	fusobacteri	832	7	1.0	778	2	Q6CP63	Q6cp63	kiuyveromyc
760	7	1.0	541	2	Q7WPA4	Q7wpa4	borderetella	833	7	1.0	783	1	YX11_PSEAE	Q9hrc3	pseudomonas
761	7	1.0	542	1	MODU_DROME	P13469	drosophila	834	7	1.0					

835	7	1.0	783	2	Q7R5Y0	Q7r5y0 giardia lam	908	7	1.0	1450	2	Q6BCK1	Q6bck1 tetrahymena
836	7	1.0	783	2	Q86LL3	Q86ll3 giardia lam	909	7	1.0	1506	2	Q6NS59	Q6ns59 mus musculus
837	7	1.0	783	2	Q6DW76	Q6dw76 glycine max	910	7	1.0	1522	1	DNA2 YEAST	P38859 saccharomyc
838	7	1.0	783	2	Q9E1Z6	Q9e1z6 cercopitheci	911	7	1.0	1527	2	Q6FII8	Q6fi18 candida gla
839	7	1.0	786	2	Q6DW74	Q6dw74 lotus japon	912	7	1.0	1544	2	Q86ZB3	Q86zb3 botrytis ci
840	7	1.0	787	2	Q9VIE8	Q9vie8 drosophila	913	7	1.0	1569	2	Q9FHD0	Q9fhd0 arabidopsis
841	7	1.0	787	2	CADI HUMAN	Q13634 homo sapien	914	7	1.0	1608	2	Q9SVAS	Q9svas drosophila
842	7	1.0	790	2	Q8NS52	Q8ns52 homo sapien	915	7	1.0	1631	2	Q8DZ37	Q8dz37 streptococc
843	7	1.0	791	2	Q49137	Q49137 arabidopsis	916	7	1.0	1640	2	Q86Z91	Q86z91 gibberella
844	7	1.0	791	2	O49139	Q49139 arabidopsis	917	7	1.0	1660	2	Q94729	Q94729 oryza sativ
845	7	1.0	791	2	O50073	O50073 arabidopsis	918	7	1.0	1660	2	Q7XPK3	Q7xpk3 oryza sativ
846	7	1.0	793	2	Q7QUH8	Q7quh8 giardia lam	919	7	1.0	1666	2	Q8LP68	Q8lp68 chlamydomon
847	7	1.0	799	2	Q7SAU1	Q7sau1 ashbya goss	920	7	1.0	1666	2	Q8LVX2	Q8lvx2 homo sapien
848	7	1.0	799	2	Q8NSU9	Q8neu9 corynebacte	921	7	1.0	1755	2	Q7RV31	Q7rv31 neurospora
849	7	1.0	803	2	Q6FV15	Q6fv15 candida gla	922	7	1.0	1768	2	Q9N8K7	Q9n8k7 trypanosoma
850	7	1.0	805	2	Q95RK7	Q95rk7 drosophila	923	7	1.0	1822	1	SC72 SCHPO	Q9p7v5 schizosacch
851	7	1.0	805	2	Q636U8	Q636u8 bacillus ce	924	7	1.0	1826	2	Q7RXK8	Q7rxk8 neurospora
852	7	1.0	805	2	Q733A2	Q733a2 bacillus ce	925	7	1.0	1831	2	Q86T77	Q86t77 homo sapien
853	7	1.0	805	2	Q81WV6	Q81wv6 bacillus th	926	7	1.0	1863	2	Q8IVX2	Q8ivx2 homo sapien
854	7	1.0	805	2	Q6HF81	Q6hf81 bacillus th	927	7	1.0	1865	2	Q7Z401	Q7z401 homo sapien
855	7	1.0	806	2	Q81A60	Q81a60 bacillus ce	928	7	1.0	1877	2	Q9XXW1	Q9xxw1 plasmodium
856	7	1.0	808	2	Q9S7D1	Q9s7d1 arabidopsis	929	7	1.0	1879	2	Q7PDP1	Q7pdp1 plasmodium
857	7	1.0	826	2	Q8PUF4	Q8puf4 methanosarc	930	7	1.0	1903	2	Q9UON7	Q9uon7 plasmodium
858	7	1.0	826	2	Q8TQX6	Q8tqx6 methanosarc	931	7	1.0	1952	2	Q95SN5	Q95sn5 drosophila
859	7	1.0	826	2	Q9TU41	Q9tu41 arabidopsis	932	7	1.0	1961	2	Q6WG89	Q6wg89 rattus norv
860	7	1.0	841	1	TRK1 SCHPO	Q9t041 arabidopsis	933	7	1.0	1966	2	Q81QA6	Q81qa6 drosophila
861	7	1.0	842	2	Q9LS88	P47946 schizosacch	934	7	1.0	1966	2	Q9NHX6	Q9nhx6 drosophila
862	7	1.0	859	1	ALR1 YEAST	Q91a88 arabidopsis	935	7	1.0	1968	2	Q8XOC5	Q8xoc5 neurospora
863	7	1.0	864	2	Q68VK4	Q68vk4 arabidopsis	936	7	1.0	1985	2	Q8T9N4	Q8t9n4 drosophila
864	7	1.0	867	2	Q21186	Q21186 caenorhabdi	937	7	1.0	1985	2	Q9VSK5	Q9vsk5 drosophila
865	7	1.0	869	2	Q8IG55	Q8ig55 caenorhabdi	938	7	1.0	1988	2	Q86BH2	Q86bh2 drosophila
866	7	1.0	873	2	Q9S0Z4	Q9s0z4 escherichia	939	7	1.0	2381	2	Q7R4R8	Q7r4r8 giardia lam
867	7	1.0	917	2	Q9V4B8	Q9v4b8 drosophila	940	7	1.0	2393	2	Q8IA61	Q8ia61 plasmodium
868	7	1.0	921	2	Q9VJ29	Q9vj29 drosophila	941	7	1.0	2549	2	Q7PPU7	Q7ppu7 anopheles g
869	7	1.0	921	2	Q9BDU0	Q9bdu0 dendrohyrax	942	7	1.0	2605	2	O50858	O50858 myxococcus
870	7	1.0	922	2	Q6BTJ4	Q6btj4 debaryomyce	943	7	1.0	2906	2	Q9WUH9	Q9wuh9 rattus norv
871	7	1.0	950	2	Q8RXZ0	Q8rxz0 oryza sativ	944	7	1.0	2907	1	FBN2 MOUSE	Q61555 mus musculu
872	7	1.0	955	2	Q726R1	Q726r1 desulfovibr	945	7	1.0	3011	1	FBN2 HUMAN	P35556 homo sapien
873	7	1.0	961	2	Q8SVH3	Q8svh3 enccephaloti	946	7	1.0	3306	2	Q9FT44	Q9ft44 arabidopsis
874	7	1.0	970	2	Q7XP23	Q7xf23 oryza sativ	947	7	1.0	3446	2	Q86AC8	Q86ac8 dictyosteli
875	7	1.0	970	2	Q9AYF2	Q9ayf2 oryza sativ	948	7	1.0	3523	2	Q7QCP4	Q7qcp4 anopheles g
876	7	1.0	977	2	Q91925	Q91925 xenopus lae	949	7	1.0	3564	1	CSM1 MOUSE	Q92313 mus musculu
877	7	1.0	980	2	Q22088	Q22088 caenorhabdi	950	7	1.0	3666	2	Q6UDX0	Q6udx0 plasmodium
878	7	1.0	982	2	Q6CWM6	Q6cwm6 kluyveromyc	951	7	1.0	3972	2	Q9S0R8	Q9s0r8 streptomyce
879	7	1.0	991	2	Q8TDH1	Q8tdh1 homo sapien	952	7	1.0	3996	2	Q7KTP2	Q7ktp2 drosophila
880	7	1.0	995	1	YPD1 CAEEL	P48053 caenorhabdi	953	7	1.0	4547	2	Q9W343	Q9w343 drosophila
881	7	1.0	1007	2	Q8JT28	Q8jt28 xenopus lae	954	7	1.0	4569	2	Q7PS35	Q7ps35 anopheles g
882	7	1.0	1013	2	Q6MP67	Q6mf67 parachlamyid	955	7	1.0	4899	2	Q9VR91	Q9vr91 drosophila
883	7	1.0	1022	1	TLD BRARE	O57460 brachydanio	956	7	1.0	23015	2	Q8IQ18	Q8iq18 drosophila
884	7	1.0	1031	2	Q8G5K2	Q8g5k2 bifidobacte	957	6	0.8	27	1	ANF ANGJA	P18144 anguilla ja
885	7	1.0	1046	2	Q6C1R8	Q6c1r8 yarrowia li	958	6	0.8	33	2	Q8FZE0	Q8fze0 bruceella su
886	7	1.0	1047	2	Q9PKW9	Q9fkw9 arabidopsis	959	6	0.8	33	2	Q8B9R2	Q8b9r2 emiliania h
887	7	1.0	1048	2	Q9NA71	Q9na71 caenorhabdi	960	6	0.8	33	2	Q8B9R3	Q8b9r3 emiliania h
888	7	1.0	1074	2	Q831Z5	Q831z5 enterococcu	961	6	0.8	33	2	Q8B9R4	Q8b9r4 emiliania h
889	7	1.0	1079	2	Q6MLZ8	Q6mlz8 bdellovibri	962	6	0.8	33	2	Q8B9R5	Q8b9r5 emiliania h
890	7	1.0	1081	2	Q8BZL9	Q8bz19 mus musculu	963	6	0.8	33	2	Q8B9R6	Q8b9r6 emiliania h
891	7	1.0	1100	2	Q86UH1	Q86uh1 homo sapien	964	6	0.8	33	2	Q8B9R7	Q8b9r7 emiliania h
892	7	1.0	1111	2	Q8S5Z2	Q8s5z2 mycobacteri	965	6	0.8	33	2	Q8B9R8	Q8b9r8 emiliania h
893	7	1.0	1120	2	Q8FPS7	Q8fp87 corynebacte	966	6	0.8	35	2	Q8B9R9	Q8b9r9 emiliania h
894	7	1.0	1135	2	Q7Q137	Q7q137 anopheles g	967	6	0.8	35	2	Q9KSL5	Q9ksl5 vibrio chol
895	7	1.0	1136	2	Q81UD8	Q81jd8 plasmodium	968	6	0.8	36	2	Q9W336	Q9w336 ophiostoma
896	7	1.0	1158	2	Q7Q253	Q7q253 anopheles g	969	6	0.8	36	2	Q72CQ3	Q72cq3 desulfovibr
897	7	1.0	1201	2	Q71RU0	Q71ru0 nitrobaacter	970	6	0.8	37	2	Q7DRP2	Q7drp2 human immun
898	7	1.0	1233	2	Q6CAC2	Q6cac2 yarrowia li	971	6	0.8	38	2	Q7VM96	Q7vm96 haemophilus
899	7	1.0	1234	2	Q7SF30	Q7sf30 neurospora	972	6	0.8	39	2	Q23160	Q23160 sus scrofa
900	7	1.0	1240	1	DLT DROME	Q8t626 drosophila	973	6	0.8	39	2	Q61E99	Q61e99 macaca mula
901	7	1.0	1240	2	Q65468	Q65468 arabidopsis	974	6	0.8	40	2	Q9R4D0	Q9rad0 thermus aqu
902	7	1.0	1243	2	O35954	O35954 mus musculu	975	6	0.8	40	2	Q73510	Q73510 bacillus ce
903	7	1.0	1300	2	Q8XOV5	Q8xov5 neurospora	976	6	0.8	40	2	Q9KLT1	Q9klt1 vibrio chol
904	7	1.0	1327	2	Q6C4J5	Q6c4j5 yarrowia li	977	6	0.8	40	2	Q8UM87	Q8um87 human immun
905	7	1.0	1340	2	Q9GTY4	Q9gyt4 anopheles g	978	6	0.8	40	2	Q8USM4	Q8usm4 human immun
906	7	1.0	1346	2	Q9ZG12	Q9zg12 streptomyce	979	6	0.8	41	2	Q90SM4	Q90sm4 human immun
907	7	1.0	1355	2	Q7Q7S9	Q7q7s9 anopheles g	980	6	0.8	41	2	Q90SM5	Q90sm5 human immun

981	6	0.8	41	2	Q90SM6	Q90sm6 human immun	1054	6	0.8	56	2	Q97AA0	Q97aa0 thermoplas
982	6	0.8	41	2	Q78226	Q78226 human immun	1055	6	0.8	56	2	Q81PA7	Q81pa7 bacillus
983	6	0.8	41	2	Q9QG57	Q9QG57 human immun	1056	6	0.8	56	2	Q9CBE3	Q9cbe3 mycobacteri
984	6	0.8	42	2	Q85WV3	Q85WV3 pinus korai	1057	6	0.8	57	2	Q38990	Q38990 arabidopsis
985	6	0.8	42	2	Q67PK6	Q67pk6 symbiobacte	1058	6	0.8	57	2	Q38991	Q38991 arabidopsis
986	6	0.8	43	2	Q704X0	Q704x0 bos taurus	1059	6	0.8	57	2	Q38992	Q38992 arabidopsis
987	6	0.8	44	2	Q8F2V9	Q8f2v9 leptospira	1060	6	0.8	57	2	Q8DB59	Q8db59 vibrio vuln
988	6	0.8	44	2	Q8F9N3	Q8f9n3 leptospira	1061	6	0.8	57	2	Q81Z30	Q81z30 bacillus an
989	6	0.8	45	2	Q80HK8	Q80hk8 hepatitis c	1062	6	0.8	59	2	Q9HYB3	Q9hyb3 pseudomonas
990	6	0.8	45	2	Q80I53	Q80i53 hepatitis c	1063	6	0.8	60	2	Q6ZGX7	Q6zgx7 oryza sativ
991	6	0.8	45	2	Q80I54	Q80i54 hepatitis c	1064	6	0.8	60	2	Q6Z9X7	Q6z9x7 rattus norv
992	6	0.8	45	2	Q80I55	Q80i55 hepatitis c	1065	6	0.8	60	2	Q6SPV9	Q6spv9 human immun
993	6	0.8	45	2	Q80I56	Q80i56 hepatitis c	1066	6	0.8	60	2	Q6Z4L9	Q6z4l9 oryza sativ
994	6	0.8	45	2	Q80I57	Q80i57 hepatitis c	1067	6	0.8	61	2	Q45045	Q45045 borrelia bu
995	6	0.8	45	2	Q80I58	Q80i58 hepatitis c	1068	6	0.8	61	2	Q77577	Q77577 human immun
996	6	0.8	45	2	Q80I59	Q80i59 hepatitis c	1069	6	0.8	61	2	Q77577	Q77577 human immun
997	6	0.8	45	2	Q80I60	Q80i60 hepatitis c	1070	6	0.8	62	1	Q77577	Q77577 human immun
998	6	0.8	45	2	Q80I61	Q80i61 hepatitis c	1071	6	0.8	62	1	Q77577	Q77577 human immun
999	6	0.8	45	2	Q80I62	Q80i62 hepatitis c	1072	6	0.8	62	1	Q77577	Q77577 human immun
1000	6	0.8	45	2	Q9QGf1	Q9qgf1 human immun	1073	6	0.8	62	1	Q77577	Q77577 human immun
1001	6	0.8	47	2	Q71IY3	Q71iy3 lactobacilli	1074	6	0.8	63	2	Q77577	Q77577 human immun
1002	6	0.8	48	2	Q9PII5	Q9pii5 homo sapien	1075	6	0.8	63	2	Q77577	Q77577 human immun
1003	6	0.8	48	2	Q9B8D3	Q9bad3 candida alb	1076	6	0.8	63	2	Q77577	Q77577 human immun
1004	6	0.8	48	2	Q9K201	Q9k201 chlamydia p	1077	6	0.8	63	2	Q77577	Q77577 human immun
1005	6	0.8	49	2	P74885	P74885 salmonella	1078	6	0.8	63	2	Q77577	Q77577 human immun
1006	6	0.8	49	2	Q9F800	Q9f800 erwinia amy	1079	6	0.8	63	2	Q77577	Q77577 human immun
1007	6	0.8	50	2	Q18986	Q18986 canis famli	1080	6	0.8	63	2	Q77577	Q77577 human immun
1008	6	0.8	50	2	Q72Yp1	Q72yp1 bacillus ce	1081	6	0.8	63	2	Q77577	Q77577 human immun
1009	6	0.8	51	2	Q9QGE5	Q9qge5 human immun	1082	6	0.8	63	2	Q77577	Q77577 human immun
1010	6	0.8	51	2	Q9QGE7	Q9qge7 human immun	1083	6	0.8	63	2	Q77577	Q77577 human immun
1011	6	0.8	51	2	Q9QGE9	Q9qge9 human immun	1084	6	0.8	63	2	Q77577	Q77577 human immun
1012	6	0.8	51	2	Q9QGF3	Q9qgf3 human immun	1085	6	0.8	63	2	Q77577	Q77577 human immun
1013	6	0.8	51	2	Q9QGF5	Q9qgf5 human immun	1086	6	0.8	63	2	Q77577	Q77577 human immun
1014	6	0.8	51	2	Q9QGF7	Q9qgf7 human immun	1087	6	0.8	63	2	Q77577	Q77577 human immun
1015	6	0.8	51	2	Q9QGG1	Q9qgg1 human immun	1088	6	0.8	63	2	Q77577	Q77577 human immun
1016	6	0.8	51	2	Q9QGG3	Q9qgg3 human immun	1089	6	0.8	63	2	Q77577	Q77577 human immun
1017	6	0.8	51	2	Q9QGG5	Q9qgg5 human immun	1090	6	0.8	63	2	Q77577	Q77577 human immun
1018	6	0.8	52	2	Q76IQ6	Q76iq6 bacterioph	1091	6	0.8	63	2	Q77577	Q77577 human immun
1019	6	0.8	52	2	Q77369	Q77369 human immun	1092	6	0.8	63	2	Q77577	Q77577 human immun
1020	6	0.8	53	2	Q9PGC6	Q9pgc6 xylella fas	1093	6	0.8	63	2	Q77577	Q77577 human immun
1021	6	0.8	54	2	Q6JLK6	Q6jlk6 penicillium	1094	6	0.8	63	2	Q77577	Q77577 human immun
1022	6	0.8	54	2	Q6JLK9	Q6jlk9 penicillium	1095	6	0.8	63	2	Q77577	Q77577 human immun
1023	6	0.8	54	2	Q6JLL1	Q6jll1 penicillium	1096	6	0.8	64	2	Q77577	Q77577 human immun
1024	6	0.8	54	2	Q6JLL2	Q6jll2 penicillium	1097	6	0.8	64	2	Q77577	Q77577 human immun
1025	6	0.8	54	2	Q6JLL3	Q6jll3 penicillium	1098	6	0.8	64	2	Q77577	Q77577 human immun
1026	6	0.8	54	2	Q6JLL5	Q6jll5 penicillium	1099	6	0.8	64	2	Q77577	Q77577 human immun
1027	6	0.8	54	2	Q6JLL6	Q6jll6 penicillium	1100	6	0.8	64	2	Q77577	Q77577 human immun
1028	6	0.8	54	2	Q6JLL7	Q6jll7 penicillium	1101	6	0.8	64	2	Q77577	Q77577 human immun
1029	6	0.8	54	2	Q6JLL9	Q6jll9 penicillium	1102	6	0.8	64	2	Q77577	Q77577 human immun
1030	6	0.8	54	2	Q6JLM1	Q6jlm1 penicillium	1103	6	0.8	64	2	Q77577	Q77577 human immun
1031	6	0.8	54	2	Q6JLM2	Q6jlm2 penicillium	1104	6	0.8	64	2	Q77577	Q77577 human immun
1032	6	0.8	54	2	Q6JLM3	Q6jlm3 penicillium	1105	6	0.8	64	2	Q77577	Q77577 human immun
1033	6	0.8	54	2	Q6JLM4	Q6jlm4 penicillium	1106	6	0.8	64	2	Q77577	Q77577 human immun
1034	6	0.8	54	2	Q6JLM5	Q6jlm5 penicillium	1107	6	0.8	64	2	Q77577	Q77577 human immun
1035	6	0.8	54	2	Q6JLM6	Q6jlm6 penicillium	1108	6	0.8	67	2	Q77577	Q77577 human immun
1036	6	0.8	54	2	Q6JLM7	Q6jlm7 penicillium	1109	6	0.8	67	2	Q77577	Q77577 human immun
1037	6	0.8	54	2	Q6JLM8	Q6jlm8 penicillium	1110	6	0.8	67	2	Q77577	Q77577 human immun
1038	6	0.8	54	2	Q6JLM9	Q6jlm9 penicillium	1111	6	0.8	67	2	Q77577	Q77577 human immun
1039	6	0.8	54	2	Q6JLM1	Q6jlm1 penicillium	1112	6	0.8	68	2	Q77577	Q77577 human immun
1040	6	0.8	54	2	Q6JLM2	Q6jlm2 penicillium	1113	6	0.8	68	2	Q77577	Q77577 human immun
1041	6	0.8	54	2	Q6JLM3	Q6jlm3 penicillium	1114	6	0.8	68	2	Q77577	Q77577 human immun
1042	6	0.8	54	2	Q9XCE2	Q9xce2 micromonos	1115	6	0.8	68	2	Q77577	Q77577 human immun
1043	6	0.8	54	2	Q8NUH5	Q8nuh5 ataphylococ	1116	6	0.8	68	2	Q77577	Q77577 human immun
1044	6	0.8	54	2	Q97P43	Q97p43 streptococ	1117	6	0.8	68	2	Q77577	Q77577 human immun
1045	6	0.8	54	2	Q7UTY8	Q7uty8 rhodopirell	1118	6	0.8	68	2	Q77577	Q77577 human immun
1046	6	0.8	54	2	Q8FYT6	Q8fyt6 bruceella su	1119	6	0.8	68	2	Q77577	Q77577 human immun
1047	6	0.8	54	2	Q9JTC3	Q9jtc3 neisseria m	1120	6	0.8	68	2	Q77577	Q77577 human immun
1048	6	0.8	54	2	Q6GSY7	Q6gsy7 streptococ	1121	6	0.8	68	2	Q77577	Q77577 human immun
1049	6	0.8	55	1	FER_CLOAC	P00198 clostridium	1122	6	0.8	68	2	Q77577	Q77577 human immun
1050	6	0.8	55	2	Q76955	P76955 escherichia	1123	6	0.8	68	2	Q77577	Q77577 human immun
1051	6	0.8	55	2	Q6TF66	Q6tf66 aeromonas h	1124	6	0.8	68	2	Q77577	Q77577 human immun
1052	6	0.8	55	2	Q8V9P1	Q8v9p1 sulfolobus	1125	6	0.8	68	2	Q77577	Q77577 human immun
1053	6	0.8	55	2	Q6SPW5	Q6spw5 human immun	1126	6	0.8	68	2	Q77577	Q77577 human immun

RL31_ECOLI

1127	6	0.8	71	2	Q77JL5	Q77JL5 bacterioph	1200	6	0.8	81	2	OL0811	O10811 human immun
1128	6	0.8	71	2	Q77JMS	Q77JMS bacterioph	1201	6	0.8	81	2	Q91893	Q91893 human immun
1129	6	0.8	71	2	Q9XJ51	Q9XJ51 lactococcus	1202	6	0.8	81	2	Q04271	Q04271 human immun
1130	6	0.8	71	2	Q75I61	Q75I61 oryza sativ	1203	6	0.8	81	2	Q90MJ9	Q90MJ9 human immun
1131	6	0.8	71	2	Q6FCL0	Q6FCL0 acinetobact	1204	6	0.8	81	2	Q90VH8	Q90VH8 human immun
1132	6	0.8	71	2	Q6ZEL3	Q6ZEL3 synechocyst	1205	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1133	6	0.8	71	2	Q7MYC6	Q7MYC6 photorhabdu	1206	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1134	6	0.8	71	2	Q83N1J	Q83N1J tropheryma	1207	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1135	6	0.8	71	2	Q9CB16	Q9CB16 lactococcus	1208	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1136	6	0.8	71	2	Q79955	Q79955 human immun	1209	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1137	6	0.8	71	2	Q79957	Q79957 human immun	1210	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1138	6	0.8	71	2	Q79959	Q79959 human immun	1211	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1139	6	0.8	71	2	Q79965	Q79965 human immun	1212	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1140	6	0.8	71	2	Q79967	Q79967 human immun	1213	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1141	6	0.8	71	2	Q79969	Q79969 human immun	1214	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1142	6	0.8	71	2	Q79970	Q79970 human immun	1215	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1143	6	0.8	71	2	Q79971	Q79971 human immun	1216	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1144	6	0.8	71	2	Q79974	Q79974 human immun	1217	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1145	6	0.8	71	2	Q79976	Q79976 human immun	1218	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1146	6	0.8	71	2	Q79979	Q79979 human immun	1219	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1147	6	0.8	71	2	Q79982	Q79982 human immun	1220	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1148	6	0.8	71	2	Q9P1H3	Q9P1H3 homo sapien	1221	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1149	6	0.8	71	2	Q26687	Q26687 trypanosoma	1222	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1150	6	0.8	71	2	Q49229	Q49229 mycoplasma	1223	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1151	6	0.8	71	2	Q64F11	Q64F11 bacteroides	1224	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1152	6	0.8	71	2	Q8K7S9	Q8K7S9 streptococc	1225	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1153	6	0.8	71	2	Q7NLJ8	Q7NLJ8 gloeobacter	1226	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1154	6	0.8	71	2	Q83214	Q83214 enterococcu	1227	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1155	6	0.8	71	2	Q87X19	Q87X19 pseudomonas	1228	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1156	6	0.8	71	2	P90297	P90297 human immun	1229	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1157	6	0.8	71	2	Q78461	Q78461 human immun	1230	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1158	6	0.8	71	2	Q79534	Q79534 human immun	1231	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1159	6	0.8	71	2	Q79551	Q79551 human immun	1232	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1160	6	0.8	71	2	Q79561	Q79561 human immun	1233	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1161	6	0.8	71	2	Q8RXW8	Q8RXW8 arabidopsis	1234	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1162	6	0.8	71	2	Q69U82	Q69U82 oryza sativ	1235	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1163	6	0.8	71	2	Q97HT9	Q97HT9 clostridium	1236	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1164	6	0.8	71	2	Q8F557	Q8F557 leptospira	1237	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1165	6	0.8	71	2	Q9HY80	Q9HY80 pseudomonas	1238	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1166	6	0.8	71	2	Q8TKU9	Q8TKU9 methanosaer	1239	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1167	6	0.8	71	2	Q8FWB5	Q8FWB5 brucella eu	1240	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1168	6	0.8	71	2	P88432	P88432 human immun	1241	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1169	6	0.8	71	2	YOR4_SMYEA	YOR4_SMYEA strawberry	1242	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1170	6	0.8	71	2	Q8PYR9	Q8PYR9 methanosaer	1243	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1171	6	0.8	71	2	Q9P169	Q9P169 homo sapien	1244	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1172	6	0.8	71	2	Q7PGQ2	Q7PGQ2 anophelies g	1245	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1173	6	0.8	71	2	Q69UW9	Q69UW9 oryza sativ	1246	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1174	6	0.8	71	2	Q8U5R3	Q8U5R3 agrobacteri	1247	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1175	6	0.8	71	2	Q83SD8	Q83SD8 enterococcu	1248	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1176	6	0.8	71	2	Q87C72	Q87C72 xylella fas	1249	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1177	6	0.8	71	2	Q9PB10	Q9PB10 xylella fas	1250	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1178	6	0.8	71	2	Q41279	Q41279 strawberry	1251	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1179	6	0.8	71	2	Q84XF0	Q84XF0 oryza sativ	1252	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1180	6	0.8	71	2	Q09529	Q09529 human immun	1253	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1181	6	0.8	71	2	YXCB_CVAPA	YXCB_CVAPA cyanophora	1254	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1182	6	0.8	71	2	Q6ZD12	Q6ZD12 oryza sativ	1255	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1183	6	0.8	71	2	Q9LDK3	Q9LDK3 oryza sativ	1256	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1184	6	0.8	71	2	Q8YU14	Q8YU14 anabaena sp	1257	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1185	6	0.8	71	2	YVFB_VACCC	YVFB_VACCC vaccinia vi	1258	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1186	6	0.8	71	2	Q96HW0	Q96HW0 homo sapien	1259	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1187	6	0.8	71	2	Q6YL42	Q6YL42 homo sapien	1260	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1188	6	0.8	71	2	Q7THW1	Q7THW1 cowpox viru	1261	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1189	6	0.8	71	2	Y476_ARCFU	Y476_ARCFU archaeoglob	1262	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1190	6	0.8	71	2	Q8C3F5	Q8C3F5 mus musculu	1263	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1191	6	0.8	71	2	NUSM_CERCA	NUSM_CERCA ceratitidis c	1264	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1192	6	0.8	71	2	Q8U4J1	Q8U4J1 pyrococcus	1265	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1193	6	0.8	71	2	Q8KJW5	Q8KJW5 proteus vul	1266	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1194	6	0.8	71	2	Q7U3T4	Q7U3T4 synechococc	1267	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1195	6	0.8	71	2	Q7UUG1	Q7UUG1 rhodopirell	1268	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1196	6	0.8	71	2	Q8DQ12	Q8DQ12 streptococc	1269	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1197	6	0.8	71	2	Q99IV0	Q99IV0 uncultured	1270	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1198	6	0.8	71	2	Q7ZP14	Q7ZP14 human immun	1271	6	0.8	81	2	Q6JN14	Q6JN14 human immun
1199	6	0.8	71	2	Q7ULV1	Q7ULV1 rhodopirell	1272	6	0.8	81	2	Q6JN14	Q6JN14 human immun

1273	6	0.8	90	2	Q9IQN8	Q9icn8 human immun	1346	6	0.8	102	2	Q87GJ3	Q87gJ3 vibrio para
1274	6	0.8	91	2	Q8Z6F7	Q8z6f7 salmonella	1347	6	0.8	102	2	Q89H29	Q89h29 bradyrhizob
1275	6	0.8	91	2	Q8ZPV4	Q8zpv4 salmonella	1348	6	0.8	102	2	Q9K8L0	Q9k8l0 bacillus ha
1276	6	0.8	91	2	Q9JVM4	Q9jvm4 neisseria m	1349	6	0.8	103	2	Q972J7	Q972j7 sulfobolus
1277	6	0.8	91	2	Q70004	Q70004 human immun	1350	6	0.8	103	2	Q95M89	Q95m89 equus cabal
1278	6	0.8	91	2	Q70009	Q70009 human immun	1351	6	0.8	103	2	Q74GQ6	Q74gq6 geobacter s
1279	6	0.8	91	2	Q72787	Q72787 human immun	1352	6	0.8	103	2	Q7UGU8	Q7ugU8 rhodopirell
1280	6	0.8	92	1	YLXP_BACSU	P32730 bacillus eu	1353	6	0.8	103	2	Q877Q6	Q877q6 vibrio para
1281	6	0.8	92	2	Q8HQJ5	Q8hqj5 nitrothodoro	1354	6	0.8	103	2	Q6D9M5	Q6d9m5 erwinia car
1282	6	0.8	92	2	Q93KE9	Q93ke9 chlamydia p	1355	6	0.8	103	2	Q9D5D6	Q9d5d6 mus musculu
1283	6	0.8	92	2	Q65JIO	Q65jio bacillus li	1356	6	0.8	104	2	Q8SQY2	Q8sqy2 encephalito
1284	6	0.8	92	2	Q8VIZ9	Q8viz9 emiliania h	1357	6	0.8	104	2	Q8SX12	Q8sx12 drosophila
1285	6	0.8	93	2	Q85FIO	Q85fi0 adiantum ca	1358	6	0.8	104	2	Q6IK98	Q6ik98 drosophila
1286	6	0.8	93	2	Q8LMZ6	Q8lmz6 oryza sativ	1359	6	0.8	104	2	Q7R8C5	Q7r8c5 plasmodium
1287	6	0.8	93	2	Q42278	Q42278 aradidopsis	1360	6	0.8	104	2	Q38556	Q38556 bacterioph
1288	6	0.8	93	2	Q629K2	Q629k2 haemophilus	1361	6	0.8	104	2	Q6V8N3	Q6v8n3 malus domes
1289	6	0.8	93	2	Q41565	Q41565 human immun	1362	6	0.8	104	2	Q45117	Q45117 bacteroides
1290	6	0.8	94	2	Q6IL90	Q6il90 drosophila	1363	6	0.8	104	2	Q73I39	Q73i39 wolbachia p
1291	6	0.8	94	2	Q7QWN1	Q7qwn1 giardia lam	1364	6	0.8	104	2	Q7POH7	Q7poh7 chromobacte
1292	6	0.8	94	2	Q9BDR2	Q9bdr2 bos taurus	1365	6	0.8	104	2	Q8B594	Q8b594 mus musculu
1293	6	0.8	94	2	Q94MT3	Q94mt3 bacterioph	1366	6	0.8	105	2	Q27553	Q27553 methanobact
1294	6	0.8	94	2	Q49475	Q49475 mycoplasma	1367	6	0.8	105	2	Q97C63	Q97c63 thermoplasm
1295	6	0.8	94	2	Q9ZBM8	Q9zbm8 mycobacteri	1368	6	0.8	105	2	Q23899	Q23899 dictyostell
1296	6	0.8	94	2	Q8VIZ6	Q8viz6 emiliania h	1369	6	0.8	105	2	Q8S005	Q8s005 oryza sativ
1297	6	0.8	94	2	Q8VIZ8	Q8viz8 emiliania h	1370	6	0.8	105	2	Q6ZLD9	Q6zld9 oryza sativ
1298	6	0.8	94	2	Q8VZ02	Q8vz02 emiliania h	1371	6	0.8	105	2	Q9LHN1	Q9lhn1 aradidopsis
1299	6	0.8	94	2	Q8VZ03	Q8vz03 emiliania h	1372	6	0.8	105	2	Q7N4V8	Q7n4v8 photorhabdu
1300	6	0.8	94	2	Q8VZ04	Q8vz04 emiliania h	1373	6	0.8	105	2	Q7NT32	Q7nt32 chromobacte
1301	6	0.8	94	2	Q41599	Q41599 human immun	1374	6	0.8	106	1	Q8BP51	Q8bp51 mus musculu
1302	6	0.8	94	2	Q70001	Q70001 human immun	1375	6	0.8	106	1	RNPA_SULSO	Q97WJ1 sulfolobus
1303	6	0.8	95	2	Q9I4U5	Q9i4u5 pseudomonas	1376	6	0.8	106	2	Q74KE5	Q74ke5 lactobacill
1304	6	0.8	95	2	Q80X28	Q80x28 mus musculu	1377	6	0.8	107	1	RL21_CHLTR	Q84425 chlamydia t
1305	6	0.8	95	2	Q6IEC0	Q6iec0 ictalurur p	1378	6	0.8	107	2	Q6IGL6	Q6igl6 drosophila
1306	6	0.8	96	2	Q7PFK0	Q7pfk0 anopheles g	1379	6	0.8	107	2	Q8E7H9	Q8e7h9 streptococc
1307	6	0.8	96	2	Q7QSG2	Q7qsg2 giardia lam	1380	6	0.8	107	2	Q9CEP1	Q9ceb1 mycobacteri
1308	6	0.8	96	2	Q9MPY9	Q9mpy9 anopheles c	1381	6	0.8	107	2	Q6AKQ7	Q6akq7 desulfotale
1309	6	0.8	96	2	Q9C7L8	Q9c7l8 aradidopsis	1382	6	0.8	107	2	Q8BM14	Q8bm14 mus musculu
1310	6	0.8	96	2	Q7NWJ1	Q7nwj1 chromobacte	1383	6	0.8	108	1	PT05_STVPL	Q28197 styela plic
1311	6	0.8	96	2	Q7UGN6	Q7ugn6 rhodopirell	1384	6	0.8	108	2	Q6UAT7	Q6uar7 bacterioph
1312	6	0.8	97	2	Q7RIM5	Q7rim5 giardia lam	1385	6	0.8	108	2	Q82328	Q82328 aradidopsis
1313	6	0.8	97	2	Q7YVG4	Q7yvg4 trypanosoma	1386	6	0.8	108	2	Q6K4F7	Q6k4f7 oryza sativ
1314	6	0.8	97	2	Q884H1	Q884h1 pseudomonas	1387	6	0.8	108	2	Q7NMX6	Q7nmx6 gloeobacter
1315	6	0.8	98	2	Q8Q0E3	Q8q0e3 methanosarc	1388	6	0.8	108	2	Q10826	Q10826 human immun
1316	6	0.8	98	2	Q6R223	Q6rz23 endoxyla sp	1389	6	0.8	108	2	Q9QN58	Q9qn58 human immun
1317	6	0.8	98	2	Q25731	Q25731 plasmodium	1390	6	0.8	108	2	Q9QN68	Q9qn68 human immun
1318	6	0.8	98	2	Q9NPH0	Q9nfh0 plasmodium	1391	6	0.8	109	1	TCMT_STRGA	Q39890 streptomyc
1319	6	0.8	98	2	Q6SEG0	Q6seg0 lactobacill	1392	6	0.8	109	2	Q92LF5	Q92lf5 rhizobium m
1320	6	0.8	98	2	Q52096	Q52096 pseudomonas	1393	6	0.8	110	1	M280_ARATH	Q92322 aradidopsis
1321	6	0.8	98	2	Q69509	Q69509 mycobacteri	1394	6	0.8	110	2	Q46207	Q46207 clostridium
1322	6	0.8	98	2	Q7TUT9	Q7tut9 prochloroco	1395	6	0.8	110	2	Q92SA8	Q92sa8 rhizobium m
1323	6	0.8	98	2	Q9KMT4	Q9kmt4 vibrio chol	1396	6	0.8	110	2	Q9FSI4	Q9fsi4 bradyrhizob
1324	6	0.8	98	2	Q65PM7	Q65pm7 lactobacill	1397	6	0.8	110	2	Q8CDY6	Q8cdy6 mus musculu
1325	6	0.8	98	2	Q6D5N1	Q6d5n1 erwinia car	1398	6	0.8	110	2	Q89141	Q89141 human herpe
1326	6	0.8	98	1	YOJ2_CABEL	P34625 caenorhabdi	1399	6	0.8	110	2	Q8TQ56	Q8tq56 methanosarc
1327	6	0.8	99	2	Q9LS64	Q9ls64 aradidopsis	1400	6	0.8	111	2	Q6IHE6	Q6ihe6 drosophila
1328	6	0.8	99	2	Q82VD8	Q82vd8 nitrosomona	1401	6	0.8	111	2	Q6DN49	Q6dn49 streptomyc
1329	6	0.8	99	2	Q89H95	Q89h95 bradyrhizob	1402	6	0.8	111	2	Q72SM5	Q72sm5 desulfovibr
1330	6	0.8	99	2	Q924W3	Q924w3 rattus norv	1403	6	0.8	111	2	Q8FLL7	Q8fll7 corynebacte
1331	6	0.8	99	2	P88433	P88433 human immun	1404	6	0.8	111	2	Q9JBB8	Q9jbb8 spodoptera
1332	6	0.8	100	2	Q64DE3	Q64de3 uncultured	1405	6	0.8	111	2	Q8FLL7	Q8fll7 corynebacte
1333	6	0.8	100	2	Q50101	Q50101 pyrococcus	1406	6	0.8	112	1	PT17_STVPL	Q9J888 spodoptera
1334	6	0.8	100	2	Q6YVY4	Q6yvy4 oryza sativ	1407	6	0.8	112	2	Q9GLK5	Q9glk5 felis silve
1335	6	0.8	100	2	Q7MS23	Q7ms23 wolfinella s	1408	6	0.8	112	2	P72474	P72474 streptococc
1336	6	0.8	101	2	Q979B6	Q979b6 thermoplasm	1409	6	0.8	112	2	Q62J69	Q62j69 burkholderi
1337	6	0.8	101	2	Q9JPF2	Q9jpf2 neisseria m	1410	6	0.8	112	2	Q63SW1	Q63sw1 sulfolobus
1338	6	0.8	101	2	Q91Z64	Q91z64 sigmodon hi	1411	6	0.8	112	2	Q684B5	Q684b5 burkholderi
1339	6	0.8	101	2	Q8BTV4	Q8btv4 mus musculu	1412	6	0.8	112	2	Q8LSK1	Q8lsk1 xenopus lae
1340	6	0.8	101	2	Q8K3D7	Q8k3d7 mus musculu	1413	6	0.8	113	2	Q84V28	Q84v28 crypthecodi
1341	6	0.8	102	2	Q14278	Q14278 homo sapien	1414	6	0.8	113	2	Q49970	Q49970 mycobacteri
1342	6	0.8	102	2	Q7R3J1	Q7r3j1 giardia lam	1415	6	0.8	113	2	Q925X2	Q925x2 frankia sp.
1343	6	0.8	102	2	Q67TQ7	Q67tq7 oryza sativ	1416	6	0.8	113	2	Q925X2	Q925x2 frankia sp.
1344	6	0.8	102	2	Q925K2	Q925k2 mycobacteri	1417	6	0.8	113	2	Q64GA6	Q64ga6 cylindrospe
1345	6	0.8	102	2	Q65RC9	Q65rc9 mannheimia	1418	6	0.8	113	2	Q87DR0	Q87dr0 xylella fas

1419	6	0.8	113	2	Q8FJ25	Q8fj25 escherichia
1420	6	0.8	114	2	Q8GUR2	Q8gur2 axonopus co
1421	6	0.8	114	2	Q6MMV6	Q6mmv6 bdellovibri
1422	6	0.8	114	2	Q89D11	Q89d11 bradyrhizob
1423	6	0.8	114	2	Q8Q6K9	Q8q6k9 human immun
1424	6	0.8	115	1	CTE9 MOUSE	Q8cr37 mus musculu
1425	6	0.8	115	2	Q9YD49	Q9yd49 aeropyrum p
1426	6	0.8	115	2	Q9BTD1	Q9btd1 homo sapien
1427	6	0.8	115	2	Q8LTJ8	Q8ltj8 lactococcus
1428	6	0.8	115	2	Q38132	Q38132 bacterioph
1429	6	0.8	115	2	Q8D410	Q8d410 vibrio vuln
1430	6	0.8	115	2	Q6PBI2	Q6pb12 brachydanio
1431	6	0.8	115	2	Q67257	Q67257 human immun
1432	6	0.8	116	1	RL22_GLOVI	Q9nek7 gloeobacter
1433	6	0.8	116	2	Q9HLD4	Q9hld4 thermoplas
1434	6	0.8	116	2	Q6B883	Q6b883 ixodes paci
1435	6	0.8	116	2	Q6B8C4	Q6b8c4 ixodes paci
1436	6	0.8	116	2	Q6B8E6	Q6b8e6 ixodes paci
1437	6	0.8	116	2	Q8HAR2	Q8har2 salmonella
1438	6	0.8	116	2	Q9XIA6	Q9xi86 arabidopsis
1439	6	0.8	116	2	Q67R66	Q67r66 symbiobacte
1440	6	0.8	116	2	Q7MFI1	Q7mf11 vibrio vuln
1441	6	0.8	116	2	P87922	P87922 human immun
1442	6	0.8	116	2	Q902G8	Q902g8 human immun
1443	6	0.8	116	2	Q6Q453	Q6q453 human immun
1444	6	0.8	117	1	RL22_STAAM	Q99826 staphylococ
1445	6	0.8	117	1	RL22_STAAN	Q7a460 staphylococ
1446	6	0.8	117	1	RL22_STAAN	Q7a079 staphylococ
1447	6	0.8	117	1	RL22_STAEP	Q8cr95 staphylococ
1448	6	0.8	117	2	Q9YA74	Q9ya74 aeropyrum p
1449	6	0.8	117	2	Q7S013	Q7s013 neurospora
1450	6	0.8	117	2	Q7QON3	Q7qon3 anopheles g
1451	6	0.8	117	2	Q7QKI5	Q7qk15 anopheles g
1452	6	0.8	117	2	Q7RPA0	Q7rpa0 plasmodium
1453	6	0.8	117	2	Q6G776	Q6g776 staphylococ
1454	6	0.8	117	2	Q6GRI8	Q6gei8 staphylococ
1455	6	0.8	118	2	Q44226	Q44226 drosophila
1456	6	0.8	118	2	Q61GT2	Q6igt2 drosophila
1457	6	0.8	118	2	Q7QIG7	Q7qig7 anopheles g
1458	6	0.8	118	2	Q69UD4	Q69ud4 oryza sativ
1459	6	0.8	118	2	Q6ZAF7	Q6zaf7 oryza sativ
1460	6	0.8	118	2	Q7BTW1	Q7btw1 yersinia pe
1461	6	0.8	118	2	Q84040	Q84040 chlamydia t
1462	6	0.8	118	2	Q72MY2	Q72my2 leptospira
1463	6	0.8	118	2	Q8F8Q9	Q8f8q9 leptospira
1464	6	0.8	119	2	Q9MG24	Q9mg24 callithrix
1465	6	0.8	119	2	Q9MG25	Q9mg25 callithrix
1466	6	0.8	119	2	Q46457	Q46457 chlamydia t
1467	6	0.8	119	2	Q53469	Q53469 mycobacteri
1468	6	0.8	119	2	Q7T250	Q7t250 mycobacteri
1469	6	0.8	119	2	Q35755	Q35755 rattus norv
1470	6	0.8	120	2	Q05715	Q05715 saccharomyc
1471	6	0.8	120	2	Q74LT1	Q74lt1 lactobacill
1472	6	0.8	120	2	Q8C3D7	Q8c3d7 mus musculu
1473	6	0.8	120	2	Q6D028	Q6dj28 xenopus tro
1474	6	0.8	121	2	Q6BN47	Q6bn47 debaryomyce
1475	6	0.8	121	2	Q7YXC5	Q7yxc5 cryptotlagus
1476	6	0.8	121	2	Q867A3	Q867a3 oenotrabid
1477	6	0.8	121	2	Q7V633	Q7v633 prochloroco
1478	6	0.8	121	2	Q91450	Q91450 salvelinus
1479	6	0.8	121	2	Q79786	Q79786 human immun
1480	6	0.8	122	1	RL14_MYCGE	Q50308 mycoplasma
1481	6	0.8	122	1	RL14_MYCPN	Q50308 mycoplasma
1482	6	0.8	122	2	Q9MP21	Q9mp21 anopheles f
1483	6	0.8	122	2	Q9TGJ5	Q9tgj5 taenia hyda
1484	6	0.8	122	2	P96093	P96093 thioabacillu
1485	6	0.8	123	1	NEF_HV1B1	P03404 human immun
1486	6	0.8	123	1	NEF_HV1H2	P04601 human immun
1487	6	0.8	123	2	O58242	O58242 pyrococcus
1488	6	0.8	123	2	P95954	P95954 sulfolobus
1489	6	0.8	123	2	Q9TCK1	Q9tck1 taenia soli
1490	6	0.8	123	2	Q47794	Q47794 enterococcu
1491	6	0.8	123	2	Q63DY7	Q63dy7 bacillus ce

ALIGNMENTS

RESULT 1

Q6UXH9	PRELIMINARY;	PRT;	720 AA.
AC Q6UXH9			
DT 05-JUL-2004	(TREMBLrel. 27, Created)		
DT 05-JUL-2004	(TREMBLrel. 27, Last sequence update)		
DE 05-JUL-2004	(TREMBLrel. 27, Last annotation update)		
DE ELGC699			
GN ORFNames=UNO699;			
OS Homo sapiens (Human)			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
NCBI_TaxID=9606;			
[1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=2887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA Huang A., Kim H.S., Klimowski L., Lin Y., Johnson S., Lee J.,			
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA Vandenberg R., Watanabe C., Wileand D., Woods K., Xie M.H., Yansura D.,			
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA Godowski P.,			
RT "The secreted protein discovery initiative (SPDI), a large-scale			
RT effort to identify novel human secreted and transmembrane proteins: a			
RT bioinformatics assessment."			
RL Genome Res. 13:2265-2270(2003).			
CC -I- SIMILARITY: Belongs to peptidase family S1.			
CC -I- SIMILARITY: Contains 1 EGF-like domain.			
DR EMBL: AY358346; AAQ88712.1; -			
DR HSSP: P00734; 1BB0			
DR GO: GO:0005509; F:calcium ion binding; IEA.			
DR GO: GO:0004363; F:chymotrypsin activity; IEA.			
DR GO: GO:0008233; F:peptidase activity; IEA.			
DR GO: GO:0004295; F:trypsin activity; IEA.			
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR InterPro: IPR000859; CUB			
DR InterPro: IPR000742; EGF_2.			
DR InterPro: IPR001881; EGF_Ca.			
DR InterPro: IPR006209; EGF-like.			
DR InterPro: IPR006210; IEGF.			
DR InterPro: IPR001254; Peptidase S1.			
DR InterPro: IPR001314; Peptidase S1A.			
DR InterPro: IPR009003; Pept_Ser_Cys.			
DR InterPro: IPR000436; Sushi_SCR_CCP.			
DR Pfam: PF00431; CUB; 1.			
DR Pfam: PF00008; EGF; 1.			
DR Pfam: PF00084; Sushi; 1.			
DR PRINTS; PR00722; CHYMOTRYPSIN.			
DR SMART; SM00032; CCP; 2.			
DR SMART; SM00042; CUB; 1.			
DR SMART; SM00181; EGF; 2.			
DR SMART; SM00179; EGF_Ca; 1.			
DR SMART; SM00020; Tryp_SPC; 1.			
DR PROSITE; PS01180; CUB; 1.			
DR PROSITE; PS00022; EGF_1; 1.			
DR PROSITE; PS01186; EGF_2; 1.			

DR PROSITE; PS50026; EGF 3; 1.
DR PROSITE; PS50923; SUSHI; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 720 AA; 80196 MW; DC898BC7241289D3 CRC64;

Query Match 100.0%; Score 720; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGCTQLGLTFLQLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60
DB 1 MELGCTQLGLTFLQLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60

QY 61 VVGYYTPCCRNENECDCLIHGCTIFENCKSCRNCSWGGLTDDFFVYKGYCAECRAGW 120
DB 61 VVGYYTPCCRNENECDCLIHGCTIFENCKSCRNCSWGGLTDDFFVYKGYCAECRAGW 120

QY 121 YGDCMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYD 180
DB 121 YGDCMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYD 180

QY 181 YVEVRDGDNRDGOIIRKVCNERNPAPIQSIGSSILHVLFHSDDGSKNFGDGHAIYEEITACS 240
DB 181 YVEVRDGDNRDGOIIRKVCNERNPAPIQSIGSSILHVLFHSDDGSKNFGDGHAIYEEITACS 240

QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI 300
DB 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI 300

QY 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPICIKACREPKISDLVRRRL 360
DB 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPICIKACREPKISDLVRRRL 360

QY 361 PMOVQSRRETLHQLYSAAFSKQKLSQAPTCKKPPALPFGDLPMGYQHLHTQLQYECISPFYR 420
DB 361 PMOVQSRRETLHQLYSAAFSKQKLSQAPTCKKPPALPFGDLPMGYQHLHTQLQYECISPFYR 420

QY 421 RLSSRRRTCLRTGKWSRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRTSGVHDGSL 480
DB 421 RLSSRRRTCLRTGKWSRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRTSGVHDGSL 480

QY 481 HKGAWFLVCSGALVNERTVVVAACHVTDLGKVTMIKTADLKVLGKPYRDDRDEKTIQS 540
DB 481 HKGAWFLVCSGALVNERTVVVAACHVTDLGKVTMIKTADLKVLGKPYRDDRDEKTIQS 540

QY 541 LQISAIIILHNPYDPIILLDADIALIKLLDKARISTRVQPICLAASRDISTSFQESHITVAG 600
DB 541 LQISAIIILHNPYDPIILLDADIALIKLLDKARISTRVQPICLAASRDISTSFQESHITVAG 600

QY 601 WNVLDVRSFGKNDLTRSGVSVVDSLLCEEQHEHDHGIPIVSVTDNMFCASWEPAPSIDI 660
DB 601 WNVLDVRSFGKNDLTRSGVSVVDSLLCEEQHEHDHGIPIVSVTDNMFCASWEPAPSIDI 660

QY 661 CTAETGIAAVSPGRASPRRHLMLGVSWSYDKTCSHRLSTAFKVLFPKDWIERNMK 720
DB 661 CTAETGIAAVSPGRASPRRHLMLGVSWSYDKTCSHRLSTAFKVLFPKDWIERNMK 720

RESULT 2

Q6N062 PRELIMINARY; PRT; 720 AA.
ID Q6N062
AC Q6N062;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686N24154.
GN Name=DKFZp686N24154;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Colon endothel;
RG The German cDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Belongs to peptidase family S1.
CC 1- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; BX640676; CAE45808.1; -.
DR HSSP; P00734; IBB0.
DR GO; GO:000509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sushi; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_Ca; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS50923; SUSHI; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW EGF-like domain; Hydrolase; Hypothetical protein; Protease;
KW Serine protease.
SQ SEQUENCE 720 AA; 80196 MW; E98A9F9948EE777D CRC64;

Query Match 78.2%; Score 563; DB 2; Length 720;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 663; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MELGCTQLGLTFLQLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60
DB 1 MELGCTQLGLTFLQLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60

QY 61 VVGYYTPCCRNENECDCLIHGCTIFENCKSCRNCSWGGLTDDFFVYKGYCAECRAGW 120
DB 61 VVGYYTPCCRNENECDCLIHGCTIFENCKSCRNCSWGGLTDDFFVYKGYCAECRAGW 120

QY 121 YGDCMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYD 180
DB 121 YGDCMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYD 180

QY 181 YVEVRDGDNRDGOIIRKVCNERNPAPIQSIGSSILHVLFHSDDGSKNFGDGHAIYEEITACS 240
DB 181 YVEVRDGDNRDGOIIRKVCNERNPAPIQSIGSSILHVLFHSDDGSKNFGDGHAIYEEITACS 240

QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI 300
DB 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI 300

QY 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPICIKACREPKISDLVRRRL 360
DB 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPICIKACREPKISDLVRRRL 360

QY 361 PMOVQSRRETLHQLYSAAFSKQKLSQAPTCKKPPALPFGDLPMGYQHLHTQLQYECISPFYR 420
DB 361 PMOVQSRRETLHQLYSAAFSKQKLSQAPTCKKPPALPFGDLPMGYQHLHTQLQYECISPFYR 420

Db 361 PMQVSRTPPLHQLYSAPFSKQKLSQAPTKKPALPFGDLPNGYQHLHTLQYECISPFYR 420
 Qy 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRTSGVHDGSL 480
 Db 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRTSGVHDGSL 480
 Qy 481 HKGAWFLVCSGALNERTVVAACHVTLGKVTMIKTADLVKLVGKPYRDDREKTIQS 540
 Db 481 HKGAWFLVCSGALNERTVVAACHVTLGKVTMIKTADLVKLVGKPYRDDREKTIQS 540
 Qy 541 LQISAILHPNYDPILLDADIAILKLDKARISTRVOPICLAASRDLSLTFQESHITVAG 600
 Db 541 LQISAILHPNYDPILLDADIAILKLDKARISTRVOPICLAASRDLSLTFQESHITVAG 600
 Qy 601 WNVLDVRSFGKNDLTRSGVSVVSDLLCEEQHEHGIPVSVTDNMFCASWEPTAPSDI 660
 Db 601 WNVLDVRSFGKNDLTRSGVSVVSDLLCEEQHEHGIPVSVTDNMFCASWEPTAPSDI 660
 Qy 661 CTAE 664
 Db 661 CTAE 664

RESULT 3
 Q96JW2 PRELIMINARY; PRT; 737 AA.
 ID Q96JW2
 AC Q96JW2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein FLJ14935.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi Y., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Sato K., Kawai T., Isono Y., Nakamura Y., Negahari K.,
 RA Murakami K., Satou T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosiiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshina A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakaigawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hakiiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushina-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45 (2004).
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 DR EMBL; AK027841; BAB55404.1; -;

DR HSSP; P00736; IQPZ.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00084; Sushi; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCF; 2.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS50923; SUSHI; 2.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR EGF-like domain; Hydrolase; Protease; Serine protease.
 KW EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 737 AA; 81952 MW; 4F51689C5EB32B44 CRC64;

Query Match 61.9%; Score 446; DB 2; Length 737;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 275 LEERNCSDPGGVNGYQKITGGPGLNGRHAQITGVVSPFCNNSYVLSGNEKRTCCQNGE 334
 Db 292 LEERNCSDPGGVNGYQKITGGPGLNGRHAQITGVVSPFCNNSYVLSGNEKRTCCQNGE 351
 Qy 335 WSGKQPIKACREPISDLVRRVRLPMQVQSRRTPLHQLYSAPFSKQKLSQAPTKKPAL 394
 Db 352 WSGKQPIKACREPISDLVRRVRLPMQVQSRRTPLHQLYSAPFSKQKLSQAPTKKPAL 411
 Qy 395 PFGDLPNGYQHLHTLQYECISPFYRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITA 454
 Db 412 PFGDLPNGYQHLHTLQYECISPFYRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITA 471
 Qy 455 PKTQGLRWPQAAIYRTSGVHDGSLHKGAWFLVCSGALNERTVVAACHVTLGKVTM 514
 Db 472 PKTQGLRWPQAAIYRTSGVHDGSLHKGAWFLVCSGALNERTVVAACHVTLGKVTM 531
 Qy 515 IKTADLVKLVGKPYRDDREKTIQSLQISAILHPNYDPILLDADIAILKLDKARIST 574
 Db 532 IKTADLVKLVGKPYRDDREKTIQSLQISAILHPNYDPILLDADIAILKLDKARIST 591
 Qy 575 RVQIPICLAASRDLSLTFQESHITVAGNVNLDVRSFGKNDLTRSGVSVVSDLLCEEQH 634
 Db 592 RVQIPICLAASRDLSLTFQESHITVAGNVNLDVRSFGKNDLTRSGVSVVSDLLCEEQH 651
 Qy 635 EDHGIPVSVTDNMFCASWEPTAPSDICTARTGIAAVSPFGRASPEPRHMLGLVSVSYD 694
 Db 652 EDHGIPVSVTDNMFCASWEPTAPSDICTARTGIAAVSPFGRASPEPRHMLGLVSVSYD 711
 Qy 695 KTCSHRLSTAFKVLPPKOWIERNMK 720
 Db 712 KTCSHRLSTAFKVLPPKOWIERNMK 737

RESULT 4
 Q71RE9
 ID Q71RE9 PRELIMINARY; PRT; 417 AA.
 AC Q71RE9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)

```
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 03-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FP938.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF370388; AAQ15224.1; -.
DR HSSP; P00734; 1BB0.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept Ser Cys.
DR PRINTS; PR00722; CHYMOTRYPSIN_GCP.
DR SMART; SM00020; TRYPSIN_1.
DR PROSITE; PS00923; SUSHI; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 417 AA; 46703 MW; 2546A52A3697C1C4 CRC64;

Query Match 53.68; Score 386; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 WSGKQPIKACREPKISDLVRRVLPQVQSRRTPLHQLYSAFSAKQLQSAFTKPKAL 394
DB 32 WSGKQPIKACREPKISDLVRRVLPQVQSRRTPLHQLYSAFSAKQLQSAFTKPKAL 91
QY 395 PFGDLPNGYQHLHTQLQYECISPFYRLGSRRTCLRTGWSGRAPSCIPICGKIENITA 454
DB 92 PFGDLPNGYQHLHTQLQYECISPFYRLGSRRTCLRTGWSGRAPSCIPICGKIENITA 151
QY 455 PKTQGLRWPNQAAIYRRTSGVHDSLHKGAWFLVCSGALVNRVTVAACHVTDLGKVTM 514
DB 152 PKTQGLRWPNQAAIYRRTSGVHDSLHKGAWFLVCSGALVNRVTVAACHVTDLGKVTM 211
QY 515 IKTDADLVVLGKGYRDDDEKTIQSIQISAILHPNYDPIILLDADIAILKLDKARIST 574
DB 212 IKTDADLVVLGKGYRDDDEKTIQSIQISAILHPNYDPIILLDADIAILKLDKARIST 271
QY 575 RVQPICLAAASRDLSSTFQESHITVAGNNVLADVRSPGFKNDTLRSQVSVVSDSLLCBQ 634
DB 272 RVQPICLAAASRDLSSTFQESHITVAGNNVLADVRSPGFKNDTLRSQVSVVSDSLLCBQ 331
QY 635 EDHGIPVSVTDNMFCAWEPTAPSDICTAETGGIAAVSFGRASPEPRHMLGLVSVSYD 694
DB 332 EDHGIPVSVTDNMFCAWEPTAPSDICTAETGGIAAVSFGRASPEPRHMLGLVSVSYD 391
QY 695 KTCSHRLSTAFKVLPPFKDWIERNMK 720
DB 392 KTCSHRLSTAFKVLPPFKDWIERNMK 417

RESULT 5
QY432 ID QY432 PRELIMINARY; PRT; 181 AA.
AC QY432;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp586H2123 (Fragment).
GN Name=DKFZp586H2123;
OS Homo sapiens (Human).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ansoerge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050214; CAB43317.1; -.
DR PIR; T08805; T08805.
DR HSSP; P00736; 1MD7.
DR MEROPS; S01.998; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR009003; Pept Ser Cys.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
KW Hydrolase; Hypothetical protein; Protease; Serine protease.
FT NON_TER 1
SQ SEQUENCE 181 AA; 19962 MW; ABC793BE8682D439 CRC64;

Query Match 24.7%; Score 178; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 2.5e-181;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 543 ISAILHPNYDPIILLDADIAILKLDKARISTRVQPICLAAASRDLSSTFQESHITVAGNN 602
DB 4 ISAILHPNYDPIILLDADIAILKLDKARISTRVQPICLAAASRDLSSTFQESHITVAGNN 63
QY 603 VLADVRSPGFKNDTLRSQVSVVSDSLLCBQEDHGIPVSVTDNMFCAWEPTAPSDICT 662
DB 64 VLADVRSPGFKNDTLRSQVSVVSDSLLCBQEDHGIPVSVTDNMFCAWEPTAPSDICT 123
QY 663 AETGGIAAVSFGRASPEPRHMLGLVSVSYDKTCSHRLSTAFKVLPPFKDWIERNMK 720
DB 124 AETGGIAAVSFGRASPEPRHMLGLVSVSYDKTCSHRLSTAFKVLPPFKDWIERNMK 181

RESULT 6
QY432 ID QY432 PRELIMINARY; PRT; 720 AA.
AC QY432;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:B430002G05 product:hypothetical EGF-like domain, CUB domain, Sushi domain / SCR repeat / CCP module and Serine protease, trypsin family domain containing protein, full insert sequence.
GN Name=E430002G05Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Thymus;
RA MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Thymus;
RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
```



```

DR InterPro: IPR006209; EGF like.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR009003; Pept Ser Cys.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00008; EGF; 1.
DR Pfam: PF00084; Sushi; 1.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00026; EGF_3; 1.
DR PROSITE: PS50923; SUSHI; 2.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 720 AA; 80377 MW; 7172B7F1E690FD0E CRC64;

Query Match 5.7%; Score 41; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 4.2e-34;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FLQLLISSIPREYTVINEACPGAEWNIMCRCEYDQIEC 53
Db 13 FLQLLISSIPREYTVINEACPGAEWNIMCRCEYDQIEC 53

RESULT 8
Q6DIV5 Q6DIV5 PRELIMINARY; PRT; 722 AA.
AC Q6DIV5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC89196 protein.
GN Name=MGC89196;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; BC075430; AAH75430.1; -.

```

```

DR GO: 0005509; F:calcium ion binding; IEA.
DR GO: 0004295; F:trypsin activity; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00008; EGF; 1.
DR Pfam: PF00084; Sushi; 2.
DR SMART: SM00032; CCP; 2.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00181; EGF; 2.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00020; TRYPSIN_DOM; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS50026; EGF_3; 1.
DR PROSITE: PS50923; SUSHI; 2.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 722 AA; 80366 MW; F173563206D1AE82 CRC64;

Query Match 3.3%; Score 24; DB 2; Length 722;
Best Local Similarity 100.0%; Pred. No. 6.7e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 VGYTIFFCRNEECDSCLIHPGC 85
Db 64 VGYTIFFCRNEECDSCLIHPGC 87

RESULT 9
Q91WZ0 Q91WZ0 PRELIMINARY; PRT; 222 AA.
AC Q91WZ0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bone morphogenetic protein 1 (Fragment).
GN Name=Bmp-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=E18 whole embryo;
RA Kataoka H., Enomoto K.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073100; BAB69961.1; -.
DR HSP; Q9UCV4; INZI.
DR GO: 0008533; F:astacin activity; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR Pfam: PF01400; Astacin; 1.
DR Pfam: PF00431; CUB; 2.
DR PROSITE: PS01180; CUB; 2.
FT NON_TER 1
FT NON_TER 222
SQ SEQUENCE 222 AA; 25426 MW; F6A9052DA98BB57A CRC64;

Query Match 1.2%; Score 9; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187

```

Db 80 YDYEVRDG 88

RESULT 10

Y836 AQUAE STANDARD; PRT; 232 AA.

AC O67008

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Hypothetical protein AQ_836.

GN OrderedLocusNames=AQ_836;

OS Aquifex aeolicus.

OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.

OC NCBI_TaxID=63363;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VF5;

RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;

RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,

RA Graham D.E., Overbeek R., Snead M.A., Keller M., AuJay M., Huber R.,

RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;

RT "The complete genome of the hyperthermophilic bacterium Aquifex

RT aeolicus";

RL Nature 392:353-358 (1998).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

EMBL; AB000709; AAC06970.1; --

DR F1R; E70372; E70372.

KW Complete proteome; Hypothetical protein; Transmembrane.

FT TRANSMEM 4 24 Potential.

FT TRANSMEM 42 62 Potential.

FT TRANSMEM 100 120 Potential.

FT TRANSMEM 145 165 Potential.

FT TRANSMEM 171 191 Potential.

FT TRANSMEM 232 AA; 26317 MW; B934B56FEA35B183 CRC64;

SQ SEQUENCE 232 AA; 26317 MW; B934B56FEA35B183 CRC64;

Query Match 1.2%; Score 9; DB 1; Length 232;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 FENCKSCRN 96

DB 23 FENCKSCRN 31

RESULT 11

O86553 PRELIMINARY; PRT; 276 AA.

ID O86553

AC O86553

DT 01-NOV-1998 (TEMBLrel. 08, Created)

DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)

DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)

DE Putative dehydrogenase.

GN ORFNames=SC1F2.16c;

OS Streptomyces coelicolor.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomyces.

OC NCBI_TaxID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2) / M145;

RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;

RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,

RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,

RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,

RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces

RT coelicolor A3(2).";

RL Nature 417:141-147 (2002).

CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases

CC (SDR) family;

CC EMBL; AL939128; CAA20507.1; --

DR PIR; T29125; T29125.

DR HSP; P08074; 1CYD.

DR GO; GO:0016491; P:oxidoreductase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002198; ADH_short.

DR InterPro; IPR002347; Adh_short_C2.

DR Pfam; PF00106; adh_short; 1.

DR PRINTS; PR00081; GDRDH.

DR PRINTS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH_SHORT; 1.

KW Complete proteome; Oxidoreductase.

SQ SEQUENCE 276 AA; 29010 MW; 30F0038B70D637C CRC64;

Query Match 1.2%; Score 9; DB 2; Length 276;

Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 670 AVSFPGRAS 678

DB 225 AVSFPGRAS 233

RESULT 12

Q6FJNS PRELIMINARY; PRT; 593 AA.

ID Q6FJNS

AC Q6FJNS; 27, Created)

DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)

DE TLL2 protein (Fragment).

GN Names=TLL2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Blakesley M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013871; AAH13871.1; -
DR HSSP; P07584; 1AST.
DR GO; GO:0008533; F:astacin activity; IEA.
DR GO; GO:0008237; F:metalloproteinase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001506; Peptidase_M12A.
DR Pfam; PF01400; Astacin; 1.
DR PRINTS; PR00431; CUB; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00235; ZnMG; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium; Developmental protein; EGF-like domain; Embryo; Hydrolase;
FT NON TER 593 593
SQ SEQUENCE 593 AA; 66353 MW; D7483E48E8260C69 CRC64;

Query Match 1.2%; Score 9; DB 2; Length 593;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
DB 406 YDYVEVRDG 414
|||||

RESULT 13
BMFH STRPU STANDARD; PRT; 639 AA.
AC P98069;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Bone morphogenetic protein 1 homolog precursor (BC 3.4.24.-) (SUBMP).
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinozoa; Echinacea; Echinozoa; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94215496; PubMed=8162855;
RA Hwang S.P.L., Partin J.S., Lennarz W.J.;
RT "Characterization of a homolog of human bone morphogenetic protein 1
in the embryo of the sea urchin, Strongylocentrotus purpuratus.";
RL Development 120:559-568(1994).
CC -1- TISSUE SPECIFICITY: Ectodermal and primary mesenchym cells in
hatched blastula.
CC -1- DEVELOPMENTAL STAGE: Embryo; highest level before epiculogenesis.
CC -1- SIMILARITY: Belongs to the peptidase M12A family.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L23838; AAA30081.1; -
CC HSSP; P35555; 1EMN.
CC MEROPS; M12.005; 1.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.

DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001506; Peptidase_M12A.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00008; EGF; 1.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00235; ZnMG; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium; Developmental protein; EGF-like domain; Embryo; Hydrolase;
KW Metalloprotease; Protease; Signal; Zinc.
FT SIGNAL 1 23
FT CHAIN 24 109
FT CHAIN 110 639
FT DOMAIN 110 306
FT DOMAIN 307 419
FT DOMAIN 420 531
FT DOMAIN 532 573
FT METAL 197 197
FT METAL 198 198
FT ACT_SITE 201 201
FT METAL 207 207
FT METAL 536 548
FT DISULFID 544 557
FT DISULFID 559 572
FT CARBOHYD 122 122
FT CARBOHYD 140 140
FT CARBOHYD 317 317
FT CARBOHYD 455 455
SQ SEQUENCE 639 AA; 71893 MW; 59307B26B7894AD CRC64;

Query Match 1.2%; Score 9; DB 1; Length 639;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
DB 475 YDYVEVRDG 483
|||||

RESULT 14
OS7658 PRELIMINARY; PRT; 691 AA.
AC OS7658;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Bone morphogenetic protein 1 (Fragment).
GN Name=BMP1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20267865; PubMed=10806368; DOI=10.1016/S0378-1119(00)00114-1;
RA Reynolds S.D., Zhang D., Puzas J.E., O'Keefe R.J., Rosier R.N.,
RA Reynolds P.R.;
RT "Cloning of the chick BMP1/Tolloid cDNA and expression in skeletal
tissues.";
RL Gene 248:233-243(2000).

```

RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6; TISSUE=Mouse;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RA ENBL; BC063079; RAH63079.1; -.
DR HSSP; P00736; IAPQ.
DR GO; GO:0004222; F:metalloendopeptidase activity; TAS.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001981; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001506; Peptidase_M12A.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07645; EGF_CA; 1.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_CA; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
FT NON_TER 1 1
SQ SEQUENCE 775 AA; 87858 MW; 1BA59AF0F86EEBE7 CRC64;
Query Match 1.2%; Score 9; DB 2; Length 775;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 179 YDYVEVRDG 187
Db 166 YDYVEVRDG 174
|||||||
|||||||

Search completed: May 8, 2005, 16:13:12
Job time : 92 secs

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 8, 2005, 16:06:14 ; Search time 21 Seconds
(without alignments)
2559.396 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 720

Sequence: 1 MELGCWTQLGLTLQLLLIS.....LSTFTKVLFPKDIERNMK 720

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : Issued Patents AA:*

1: /cgn2_6/protdata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/protdata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/protdata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/protdata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/protdata/1/iaa/PCTUS_COMB.pep.*

6: /cgn2_6/protdata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	
1	355	49.3	570	4	US-10-067-422-9	
2	16	2.2	46	4	US-10-067-422-17	
3	12	1.7	12	4	US-10-067-422-16	
4	9	1.2	101	3	US-09-374-135-4	
5	9	1.2	110	4	US-09-341-461-28	
6	9	1.2	113	4	US-09-438-046-20	
7	9	1.2	730	3	US-08-872-757-2	
8	9	1.2	730	4	US-09-850-048A-2	
9	9	1.2	788	1	US-08-572-225-1	
10	9	1.2	986	4	US-09-285-385C-19	
11	9	1.2	986	4	US-09-349-016-6690	
12	9	1.2	1015	4	US-09-285-385C-2	
13	8	1.1	51	3	US-09-188-930-342	
14	8	1.1	51	4	US-09-312-283C-342	
15	8	1.1	96	4	US-09-472-087-99	
16	8	1.1	152	3	US-09-188-930-187	
17	8	1.1	152	4	US-09-312-283C-187	
18	8	1.1	155	4	US-09-472-087-20	
19	8	1.1	155	4	US-09-472-087-112	
20	8	1.1	290	4	US-09-270-767-33918	
21	8	1.1	290	4	US-09-270-767-49135	
22	8	1.1	309	4	US-09-248-796A-26183	
23	8	1.1	1019	1	US-08-296-014A-4	
24	8	1.1	1019	2	US-08-596-405-4	
25	8	1.1	1019	2	US-08-877-620-4	
26	8	1.1	1019	4	US-09-287-368-4	
27	8	1.1	1019	4	US-09-626-795-4	
28	28	8	1.1	1083	1	US-08-296-014A-2
29	30	8	1.1	1083	2	US-08-596-405-2
30	31	8	1.1	1083	2	US-08-877-620-2
31	32	8	1.1	1083	4	US-09-287-368-2
32	33	8	1.1	1083	4	US-09-626-795-2
33	34	8	1.1	3571	4	US-09-911-842A-2
34	35	7	1.0	11	4	US-09-192-854-170
35	36	7	1.0	42	1	US-08-293-778-11
36	37	7	1.0	80	4	US-09-621-976-4542
37	38	7	1.0	83	4	US-09-543-681A-5389
38	39	7	1.0	99	4	US-09-270-767-62399
39	40	7	1.0	103	4	US-09-513-999C-7881
40	41	7	1.0	105	3	US-09-187-859-18
41	42	7	1.0	105	4	US-09-839-542B-18
42	43	7	1.0	105	4	US-09-535-852-18
43	44	7	1.0	111	4	US-09-252-991A-23343
44	45	7	1.0	121	4	US-09-252-991A-22436
45	46	7	1.0	123	4	US-09-621-976-5058
46	47	7	1.0	142	4	US-08-906-769-153
47	48	7	1.0	144	3	US-08-906-616-153
48	49	7	1.0	144	3	US-08-639-075A-153
49	50	7	1.0	144	3	US-09-004-731-81
50	51	7	1.0	144	3	US-09-012-431-153
51	52	7	1.0	144	3	US-08-749-699-81
52	53	7	1.0	144	3	US-09-012-692-153
53	54	7	1.0	144	3	US-08-906-613-153
54	55	7	1.0	144	4	US-09-004-729-81
55	56	7	1.0	164	4	US-09-248-796A-19751
56	57	7	1.0	172	4	US-09-198-452A-368
57	58	7	1.0	172	4	US-09-438-185A-352
58	59	7	1.0	187	4	US-09-107-532A-6736
59	60	7	1.0	210	4	US-09-198-452A-869
60	61	7	1.0	214	4	US-09-543-681A-4600
61	62	7	1.0	220	4	US-09-248-796A-17809
62	63	7	1.0	222	4	US-09-270-767-34290
63	64	7	1.0	222	4	US-09-270-767-49507
64	65	7	1.0	226	4	US-09-489-039A-7662
65	66	7	1.0	233	3	US-09-004-731-27
66	67	7	1.0	233	3	US-08-749-699-27
67	68	7	1.0	233	3	US-09-004-729-27
68	69	7	1.0	242	4	US-09-438-185A-813
69	70	7	1.0	245	4	US-09-252-991A-28491
70	71	7	1.0	255	4	US-09-540-236-2829
71	72	7	1.0	257	4	US-09-328-352-7049
72	73	7	1.0	259	3	US-08-944-483-52
73	74	7	1.0	259	4	US-10-165-442-2
74	75	7	1.0	259	4	US-10-165-442-4
75	76	7	1.0	265	4	US-09-050-739-16
76	77	7	1.0	266	3	US-09-004-731-24
77	78	7	1.0	266	3	US-08-749-699-24
78	79	7	1.0	266	4	US-09-004-729-24
79	80	7	1.0	268	3	US-09-032-215-42
80	81	7	1.0	295	3	US-08-338-368-2
81	82	7	1.0	295	4	US-10-165-442-1
82	83	7	1.0	295	4	US-10-165-442-3
83	84	7	1.0	310	4	US-09-107-532A-4185
84	85	7	1.0	312	4	US-09-538-092-742
85	86	7	1.0	314	4	US-09-636-382A-2
86	87	7	1.0	376	2	US-08-558-269-10
87	88	7	1.0	376	3	US-09-410-882-10
88	89	7	1.0	399	4	US-09-252-991A-28974
89	90	7	1.0	418	4	US-09-248-796A-18870
90	91	7	1.0	422	4	US-09-489-039A-12443
91	92	7	1.0	422	4	US-09-248-796A-14435
92	93	7	1.0	437	4	US-09-489-039A-14612
93	94	7	1.0	462	4	US-09-328-352-5694
94	95	7	1.0	468	4	US-09-949-016-9566
95	96	7	1.0	476	4	US-09-949-016-9566
96	97	7	1.0	503	4	US-09-071-035-360
97	98	7	1.0	525	4	US-09-252-991A-23870
98	99	7	1.0	553	4	US-09-583-110-5306
99	100	7	1.0	556	4	US-09-795-691-2

Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 170, Appl
Sequence 11, Appl
Sequence 4542, Ap
Sequence 5389, Ap
Sequence 62399, A
Sequence 7881, Ap
Sequence 18, Appl
Sequence 18, Appl
Sequence 23343, A
Sequence 22436, A
Sequence 5058, Ap
Sequence 10461, A
Sequence 153, App
Sequence 153, App
Sequence 153, App
Sequence 81, Appl
Sequence 81, Appl
Sequence 15751, A
Sequence 368, App
Sequence 352, App
Sequence 6736, Ap
Sequence 869, App
Sequence 4600, Ap
Sequence 17809, A
Sequence 34290, A
Sequence 49507, A
Sequence 7662, Ap
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 813, App
Sequence 28491, A
Sequence 7049, Ap
Sequence 52, Appl
Sequence 2, Appli
Sequence 4, Appli
Sequence 16, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 42, Appl
Sequence 2, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 4185, Ap
Sequence 742, App
Sequence 2, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 28974, A
Sequence 18870, A
Sequence 12443, A
Sequence 14435, A
Sequence 1612, Ap
Sequence 5694, Ap
Sequence 8272, Ap
Sequence 9566, Ap
Sequence 360, App
Sequence 23870, A
Sequence 5306, Ap
Sequence 2, Appli

101	7	1.0	558	4	US-09-107-433-4472	Sequence 4472, Ap	174	6	0.8	44	3	US-09-220-528-85	Sequence 85, Appl
102	7	1.0	579	1	US-08-295-411-4	Sequence 4, Appli	175	6	0.8	44	4	US-09-270-767-39906	Sequence 39906, A
103	7	1.0	579	2	US-08-955-471-4	Sequence 4, Appli	176	6	0.8	44	4	US-09-270-767-55123	Sequence 55123, A
104	7	1.0	579	3	US-09-117-708-14	Sequence 14, Appl	177	6	0.8	44	4	US-09-270-767-58106	Sequence 58106, A
105	7	1.0	579	4	US-09-270-767-42996	Sequence 42996, A	178	6	0.8	45	3	US-08-899-437-13	Sequence 13, Appl
106	7	1.0	579	5	PCT-US92-10245-4	Sequence 4, Appli	179	6	0.8	45	3	US-09-126-121-13	Sequence 13, Appl
107	7	1.0	615	1	US-07-998-9728-3	Sequence 3, Appli	180	6	0.8	46	3	US-08-753-007A-16	Sequence 16, Appl
108	7	1.0	615	1	US-08-463-953-3	Sequence 3, Appli	181	6	0.8	46	3	US-09-398-496-16	Sequence 16, Appl
109	7	1.0	615	1	US-08-462-261-3	Sequence 3, Appli	182	6	0.8	46	3	US-09-083-541-4	Sequence 4, Appli
110	7	1.0	615	5	PCT-US92-11357-3	Sequence 3, Appli	183	6	0.8	48	4	US-09-097-681-13	Sequence 13, Appl
111	7	1.0	616	1	US-09-949-016-6889	Sequence 6889, Ap	184	6	0.8	48	4	US-09-640-211A-1162	Sequence 1162, Ap
112	7	1.0	616	4	US-09-949-016-7740	Sequence 7740, Ap	185	6	0.8	50	3	US-09-004-406C-11	Sequence 10, Appl
113	7	1.0	622	3	US-08-952-967-8	Sequence 8, Appli	186	6	0.8	50	3	US-09-004-406C-11	Sequence 11, Appl
114	7	1.0	622	4	US-09-054-272-42	Sequence 42, Appl	187	6	0.8	52	1	US-08-294-189-17	Sequence 17, Appl
115	7	1.0	660	4	US-09-270-767-46777	Sequence 46777, A	188	6	0.8	56	3	US-09-055-075C-48	Sequence 48, Appl
116	7	1.0	805	4	US-09-252-991A-17822	Sequence 17822, A	189	6	0.8	56	4	US-09-519-124-48	Sequence 48, Appl
117	7	1.0	808	4	US-09-565-909-2	Sequence 2, Appli	190	6	0.8	56	4	US-09-765-815-9	Sequence 9, Appli
118	7	1.0	811	4	US-09-248-796A-18641	Sequence 18641, A	191	6	0.8	59	4	US-09-800-729-163	Sequence 163, App
119	7	1.0	859	4	US-09-538-092-717	Sequence 717, App	192	6	0.8	62	4	US-09-107-532A-5665	Sequence 5665, Ap
120	7	1.0	886	3	US-08-872-757-4	Sequence 4, Appli	193	6	0.8	62	4	US-09-497-491-27	Sequence 27, Appl
121	7	1.0	986	4	US-09-850-048A-4	Sequence 4, Appli	194	6	0.8	64	4	US-09-482-273-117	Sequence 117, App
122	7	1.0	1074	4	US-09-071-035-358	Sequence 358, App	195	6	0.8	64	4	US-09-252-991A-17573	Sequence 17573, A
123	7	1.0	1074	4	US-09-071-035-394	Sequence 394, App	196	6	0.8	68	4	US-09-248-796A-24682	Sequence 24682, A
124	7	1.0	1096	4	US-09-134-000C-5764	Sequence 5764, Ap	197	6	0.8	69	4	US-08-302-756B-20	Sequence 20, Appl
125	7	1.0	1346	3	US-09-320-878-4	Sequence 4, Appli	198	6	0.8	70	4	US-09-732-210-883	Sequence 883, App
126	7	1.0	1346	3	US-09-105-537-37	Sequence 37, Appl	199	6	0.8	72	4	US-09-540-236-2199	Sequence 2199, Ap
127	7	1.0	1346	4	US-09-141-908-5	Sequence 5, Appli	200	6	0.8	74	4	US-09-543-681A-8341	Sequence 8341, Ap
128	7	1.0	1346	4	US-09-657-440-4	Sequence 4, Appli	201	6	0.8	74	4	US-09-134-000C-6316	Sequence 6316, Ap
129	7	1.0	11877	3	US-09-105-537-6	Sequence 6, Appli	202	6	0.8	76	4	US-09-328-352-4331	Sequence 4331, Ap
130	6	0.8	11	2	US-08-464-961-2	Sequence 2, Appli	203	6	0.8	77	3	US-08-718-904-6	Sequence 6, Appli
131	6	0.8	11	3	US-08-957-130-17	Sequence 17, Appl	204	6	0.8	77	4	US-09-449-249-6	Sequence 6, Appli
132	6	0.8	11	3	US-08-369-315-2	Sequence 2, Appli	205	6	0.8	77	4	US-09-107-433-3411	Sequence 3411, Ap
133	6	0.8	11	5	PCT-US96-08233-2	Sequence 2, Appli	206	6	0.8	80	4	US-09-583-110-2844	Sequence 2844, Ap
134	6	0.8	12	1	US-09-205-258-304	Sequence 304, App	207	6	0.8	81	4	US-09-270-767-46160	Sequence 46160, A
135	6	0.8	13	1	US-08-179-481-87	Sequence 87, Appl	208	6	0.8	84	4	US-09-248-796A-23422	Sequence 23422, A
136	6	0.8	17	5	US-08-205-918A-14	Sequence 14, Appl	209	6	0.8	85	4	US-09-732-210-1467	Sequence 1467, Ap
137	6	0.8	17	5	PCT-US95-02626-14	Sequence 14, Appl	210	6	0.8	86	1	US-07-847-743B-19	Sequence 19, Appl
138	6	0.8	20	1	US-08-205-338A-13	Sequence 13, Appl	211	6	0.8	86	2	US-08-456-201-19	Sequence 17, Appl
139	6	0.8	20	5	PCT-US95-02626-13	Sequence 13, Appl	212	6	0.8	86	2	US-08-330-161-17	Sequence 19, Appl
140	6	0.8	25	3	US-09-660-587-28	Sequence 28, Appl	213	6	0.8	86	2	US-08-456-241-19	Sequence 17, Appl
141	6	0.8	25	4	US-09-261-358A-28	Sequence 28, Appl	214	6	0.8	86	2	US-08-440-401-17	Sequence 17, Appl
142	6	0.8	25	4	US-09-201-458-20	Sequence 20, Appl	215	6	0.8	86	2	US-08-419-878B-17	Sequence 17, Appl
143	6	0.8	25	4	US-09-811-007A-28	Sequence 28, Appl	216	6	0.8	86	3	US-09-134-001C-3359	Sequence 3359, Ap
144	6	0.8	31	4	US-08-437-943D-14	Sequence 14, Appl	217	6	0.8	86	3	US-09-173-480-17	Sequence 17, Appl
145	6	0.8	35	1	US-08-145-708A-15	Sequence 15, Appl	218	6	0.8	86	4	US-09-252-991A-29383	Sequence 29383, A
146	6	0.8	35	2	US-08-331-454-15	Sequence 15, Appl	219	6	0.8	86	5	PCT-US92-04295A-19	Sequence 19, Appl
147	6	0.8	37	2	US-09-066-074-14	Sequence 14, Appl	220	6	0.8	87	4	US-09-252-991A-28740	Sequence 28740, A
148	6	0.8	37	2	US-08-555-912A-14	Sequence 14, Appl	221	6	0.8	90	4	US-09-252-991A-24074	Sequence 24074, A
149	6	0.8	37	3	US-08-348-518C-24	Sequence 24, Appl	222	6	0.8	91	4	US-09-107-433-4244	Sequence 4244, Ap
150	6	0.8	37	3	US-08-476-509B-24	Sequence 24, Appl	223	6	0.8	93	4	US-09-252-991A-17535	Sequence 17535, A
151	6	0.8	37	4	US-09-252-404A-39	Sequence 39, Appl	224	6	0.8	93	4	US-09-270-767-39947	Sequence 39947, A
152	6	0.8	37	4	US-09-275-900-14	Sequence 14, Appl	225	6	0.8	93	4	US-09-270-767-55164	Sequence 55164, A
153	6	0.8	38	1	US-08-821-861-16	Sequence 16, Appl	226	6	0.8	94	3	US-08-946-329A-79	Sequence 79, Appl
154	6	0.8	38	1	US-08-145-708A-14	Sequence 14, Appl	227	6	0.8	94	3	US-08-466-368-5	Sequence 5, Appli
155	6	0.8	38	2	US-08-331-454-14	Sequence 14, Appl	228	6	0.8	94	4	US-08-470-998-2	Sequence 2, Appli
156	6	0.8	40	3	US-08-766-344C-19	Sequence 19, Appl	229	6	0.8	94	4	US-08-328-500-10	Sequence 10, Appl
157	6	0.8	40	4	US-08-469-260A-467	Sequence 467, App	230	6	0.8	94	4	US-09-270-767-33056	Sequence 33056, A
158	6	0.8	40	4	US-08-488-446-467	Sequence 467, App	231	6	0.8	94	4	Sequence 48273, A	Sequence 48273, A
159	6	0.8	40	4	US-08-467-344A-467	Sequence 467, App	232	6	0.8	95	4	US-09-270-767-46409	Sequence 46409, A
160	6	0.8	40	4	US-09-270-767-40577	Sequence 40577, A	233	6	0.8	95	4	US-09-248-796A-25418	Sequence 25418, A
161	6	0.8	40	4	US-09-270-767-55793	Sequence 55793, A	234	6	0.8	96	3	US-09-230-637-44	Sequence 44, Appl
162	6	0.8	40	4	US-08-424-550B-467	Sequence 467, App	235	6	0.8	99	4	US-09-270-767-32481	Sequence 32481, A
163	6	0.8	41	1	US-08-168-091A-41	Sequence 41, Appl	236	6	0.8	99	4	US-09-270-767-47698	Sequence 47698, A
164	6	0.8	42	4	US-09-066-330-3	Sequence 3, Appli	237	6	0.8	100	4	Sequence 35703, A	Sequence 35703, A
165	6	0.8	43	1	US-07-998-003A-73	Sequence 73, Appl	238	6	0.8	100	4	Sequence 5020, A	Sequence 5020, A
166	6	0.8	43	1	US-08-453-274B-73	Sequence 73, Appl	239	6	0.8	100	4	Sequence 832, App	Sequence 832, App
167	6	0.8	43	1	US-08-453-695A-73	Sequence 73, Appl	240	6	0.8	101	4	Sequence 58844, A	Sequence 58844, A
168	6	0.8	43	1	US-08-268-161A-73	Sequence 73, Appl	241	6	0.8	102	4	Sequence 271, App	Sequence 271, App
169	6	0.8	43	2	US-08-453-702A-73	Sequence 73, Appl	242	6	0.8	103	3	Sequence 32642, A	Sequence 32642, A
170	6	0.8	43	2	US-08-751-305-4	Sequence 4, Appli	243	6	0.8	103	4	Sequence 8322, Ap	Sequence 8322, Ap
171	6	0.8	43	3	US-09-099-639-73	Sequence 73, Appl	244	6	0.8	103	4	Sequence 4109, Ap	Sequence 4109, Ap
172	6	0.8	43	5	PCT-US93-13588-73	Sequence 73, Appl	245	6	0.8	103	4	US-09-621-976-4109	Sequence 5560, Ap
173	6	0.8	43	5	PCT-US95-08071-73	Sequence 73, Appl	246	6	0.8	103	4	US-09-513-999C-5560	

247	6	0.8	106	4	US-09-087-031E-13	Sequence 13, Appl	320	6	0.8	151	3	US-08-679-493A-74	Sequence 74, Appl
248	6	0.8	106	4	US-09-248-796A-14519	Sequence 14519, A	321	6	0.8	152	4	US-09-885-723-11	Sequence 11, Appl
249	6	0.8	107	4	US-09-732-210-230	Sequence 230, App	322	6	0.8	153	4	US-09-288-143-123	Sequence 123, App
250	6	0.8	107	4	US-09-489-039A-9954	Sequence 9954, Ap	323	6	0.8	153	4	US-09-252-991A-23634	Sequence 23634, A
251	6	0.8	107	4	US-09-710-279-1586	Sequence 1586, Ap	324	6	0.8	154	4	US-09-134-000C-5186	Sequence 5186, Ap
252	6	0.8	108	4	US-09-489-039A-9192	Sequence 9192, Ap	325	6	0.8	154	3	US-09-387-418A-8	Sequence 8, Appl
253	6	0.8	108	4	US-09-489-039A-11679	Sequence 11679, A	326	6	0.8	156	1	US-08-469-667-20	Sequence 20, Appl
254	6	0.8	109	4	US-09-134-000C-6718	Sequence 6718, Ap	327	6	0.8	156	3	US-09-224-110-20	Sequence 20, Appl
255	6	0.8	109	4	US-09-270-767-60583	Sequence 60583, A	328	6	0.8	156	4	US-09-252-991A-24413	Sequence 24413, A
256	6	0.8	110	3	US-09-376-330-24	Sequence 24, Appl	329	6	0.8	156	4	US-09-988-292A-20	Sequence 20, Appl
257	6	0.8	111	4	US-09-252-991A-17096	Sequence 17096, A	330	6	0.8	156	5	PCT-US95-07289-20	Sequence 20, Appl
258	6	0.8	111	4	US-09-294-298A-12	Sequence 12, Appl	331	6	0.8	157	2	US-08-811-949-41	Sequence 41, Appl
259	6	0.8	112	4	US-09-107-532A-7068	Sequence 7068, Ap	332	6	0.8	157	3	US-08-872-855-6	Sequence 6, Appl
260	6	0.8	112	4	US-09-270-767-34754	Sequence 34754, A	333	6	0.8	157	3	US-08-981-392-68	Sequence 68, Appl
261	6	0.8	112	4	US-09-270-767-49971	Sequence 49971, A	334	6	0.8	157	4	US-09-071-035-446	Sequence 446, App
262	6	0.8	112	4	US-09-902-540-9940	Sequence 9940, Ap	335	6	0.8	157	4	US-09-908-323-68	Sequence 68, Appl
263	6	0.8	113	4	US-09-438-046-23	Sequence 23, Appl	336	6	0.8	159	3	US-08-796-792-2	Sequence 2, Appl
264	6	0.8	115	4	US-09-270-767-47912	Sequence 47912, A	337	6	0.8	159	4	US-09-491-795-2	Sequence 2, Appl
265	6	0.8	115	4	US-09-902-540-10750	Sequence 10750, A	338	6	0.8	162	1	US-08-266-451B-29	Sequence 29, Appl
266	6	0.8	120	4	US-09-583-110-5022	Sequence 5022, Ap	339	6	0.8	162	2	US-08-748-725-29	Sequence 29, Appl
267	6	0.8	121	1	US-08-307-499-7	Sequence 7, Appl	340	6	0.8	162	4	US-09-540-236-2636	Sequence 2636, Ap
268	6	0.8	121	3	US-09-299-268-7	Sequence 7, Appl	341	6	0.8	164	4	US-09-489-039A-11750	Sequence 11750, A
269	6	0.8	121	4	US-10-101-464A-683	Sequence 683, App	342	6	0.8	167	4	US-09-270-767-41274	Sequence 41274, A
270	6	0.8	122	4	US-09-732-210-598	Sequence 598, App	343	6	0.8	167	4	US-09-270-767-56490	Sequence 56490, A
271	6	0.8	122	4	US-09-732-210-600	Sequence 600, App	344	6	0.8	170	4	US-09-252-991A-22362	Sequence 22362, A
272	6	0.8	122	4	US-10-101-464A-712	Sequence 712, App	345	6	0.8	172	4	US-09-252-991A-29480	Sequence 29480, A
273	6	0.8	122	4	US-09-424-840B-14	Sequence 14, Appl	346	6	0.8	172	4	US-09-328-352-5691	Sequence 5691, Ap
274	6	0.8	122	4	US-09-107-433-3697	Sequence 3697, Ap	347	6	0.8	175	4	US-09-902-540-11425	Sequence 11425, A
275	6	0.8	123	3	US-09-124-900-10	Sequence 10, Appl	348	6	0.8	176	4	US-09-252-991A-24281	Sequence 24281, A
276	6	0.8	123	3	US-09-134-001C-3283	Sequence 3283, Ap	349	6	0.8	176	4	US-09-252-991A-24805	Sequence 24805, A
277	6	0.8	124	4	US-08-311-731A-202	Sequence 202, App	350	6	0.8	177	4	US-09-489-039A-12706	Sequence 12706, A
278	6	0.8	124	4	US-09-270-767-61747	Sequence 61747, A	351	6	0.8	177	2	US-08-770-544-20	Sequence 20, Appl
279	6	0.8	125	4	US-09-543-681A-7177	Sequence 7177, Ap	352	6	0.8	177	4	US-09-579-259-20	Sequence 20, Appl
280	6	0.8	126	4	US-09-902-540-12158	Sequence 12158, A	353	6	0.8	177	4	US-09-543-681A-5159	Sequence 5159, Ap
281	6	0.8	127	3	US-09-134-001C-2936	Sequence 2936, Ap	354	6	0.8	177	4	US-09-650-324A-20	Sequence 20, Appl
282	6	0.8	127	3	US-09-134-001C-2937	Sequence 2937, Ap	355	6	0.8	177	4	US-09-583-110-3692	Sequence 3692, Ap
283	6	0.8	127	4	US-09-809-739-10	Sequence 10, Appl	356	6	0.8	178	4	US-09-270-767-31704	Sequence 31704, A
284	6	0.8	128	3	US-09-134-001C-2881	Sequence 2881, Ap	357	6	0.8	178	4	US-09-270-767-46921	Sequence 46921, A
285	6	0.8	128	4	US-09-134-000C-3953	Sequence 3953, Ap	358	6	0.8	179	3	US-09-612-126-11	Sequence 11, Appl
286	6	0.8	128	4	US-09-513-999C-8084	Sequence 8084, Ap	359	6	0.8	179	4	US-09-248-796A-21646	Sequence 21646, A
287	6	0.8	129	4	US-09-513-999C-5740	Sequence 5740, Ap	360	6	0.8	180	4	US-09-543-681A-7669	Sequence 7669, Ap
288	6	0.8	130	4	US-09-902-540-11601	Sequence 11601, A	361	6	0.8	180	4	US-09-270-767-37167	Sequence 37167, A
289	6	0.8	132	4	US-09-252-991A-29618	Sequence 29618, A	362	6	0.8	180	4	US-09-270-767-52384	Sequence 52384, A
290	6	0.8	132	4	US-09-311-021-162	Sequence 162, App	363	6	0.8	180	4	US-09-878-281A-14	Sequence 14, Appl
291	6	0.8	133	4	US-09-252-991A-32343	Sequence 32343, A	364	6	0.8	180	4	US-09-878-281A-16	Sequence 16, Appl
292	6	0.8	133	3	US-09-134-001C-3817	Sequence 3817, Ap	365	6	0.8	180	4	US-09-878-281A-18	Sequence 18, Appl
293	6	0.8	134	4	US-09-252-991A-24835	Sequence 24835, A	366	6	0.8	180	4	US-09-878-281A-20	Sequence 20, Appl
294	6	0.8	134	4	US-09-513-999C-8169	Sequence 8169, Ap	367	6	0.8	180	4	US-09-878-281A-22	Sequence 22, Appl
295	6	0.8	136	4	US-09-252-991A-24892	Sequence 24892, A	368	6	0.8	180	4	US-09-878-281A-24	Sequence 24, Appl
296	6	0.8	138	3	US-08-630-172-1	Sequence 1, Appl	369	6	0.8	180	4	US-09-878-281A-26	Sequence 26, Appl
297	6	0.8	138	3	US-09-375-419-1	Sequence 174, Appl	370	6	0.8	180	4	US-09-878-281A-28	Sequence 28, Appl
298	6	0.8	139	3	US-08-444-818-174	Sequence 174, App	371	6	0.8	180	4	US-09-902-540-10368	Sequence 10368, A
299	6	0.8	139	4	US-09-270-767-44805	Sequence 44805, A	372	6	0.8	181	4	US-09-252-991A-17818	Sequence 17818, A
300	6	0.8	140	4	US-09-252-991A-31623	Sequence 31623, A	373	6	0.8	181	4	US-09-134-000C-4533	Sequence 4533, Ap
301	6	0.8	140	4	US-09-270-767-31800	Sequence 31800, App	374	6	0.8	181	4	US-09-640-211A-1033	Sequence 1033, Ap
302	6	0.8	141	3	US-08-906-769-135	Sequence 135, App	375	6	0.8	183	4	US-09-621-976-4025	Sequence 4025, Ap
303	6	0.8	141	3	US-08-906-616-135	Sequence 135, App	376	6	0.8	183	4	US-09-976-451-2	Sequence 2, Appl
304	6	0.8	141	3	US-08-639-075A-135	Sequence 135, App	377	6	0.8	184	3	US-08-907-800A-2	Sequence 2, Appl
305	6	0.8	141	3	US-09-012-431-135	Sequence 135, App	378	6	0.8	184	3	US-08-969-317-2	Sequence 2, Appl
306	6	0.8	141	3	US-09-012-692-135	Sequence 135, App	379	6	0.8	184	4	US-09-270-767-44233	Sequence 44233, A
307	6	0.8	141	3	US-08-906-613-135	Sequence 135, App	380	6	0.8	184	4	US-09-107-433-4306	Sequence 4306, Ap
308	6	0.8	141	4	US-09-270-767-60471	Sequence 60471, A	381	6	0.8	185	3	US-08-975-762-11	Sequence 11, Appl
309	6	0.8	143	4	US-09-538-092-237	Sequence 237, App	382	6	0.8	185	3	US-08-821-324-11	Sequence 11, Appl
310	6	0.8	144	3	US-09-199-637A-17	Sequence 17, Appl	383	6	0.8	185	3	US-09-295-028-11	Sequence 11, Appl
311	6	0.8	144	3	US-09-134-001C-4218	Sequence 4218, Ap	384	6	0.8	185	3	US-09-106-582-11	Sequence 11, Appl
312	6	0.8	145	4	US-09-252-991A-21532	Sequence 21532, A	385	6	0.8	185	4	US-09-159-463-11	Sequence 11, Appl
313	6	0.8	146	4	US-09-252-991A-18563	Sequence 18563, A	386	6	0.8	185	4	US-09-693-542-11	Sequence 11, Appl
314	6	0.8	146	4	US-09-270-767-39779	Sequence 39779, A	387	6	0.8	186	3	US-09-612-126-8	Sequence 8, Appl
315	6	0.8	146	4	US-09-270-767-54996	Sequence 54996, A	388	6	0.8	187	4	US-08-635-886C-208	Sequence 208, App
316	6	0.8	146	4	US-09-248-796A-26332	Sequence 26332, A	389	6	0.8	187	4	US-08-635-886C-209	Sequence 209, App
317	6	0.8	149	2	US-08-039-364-18	Sequence 18, Appl	390	6	0.8	187	4	US-08-974-690C-207	Sequence 207, App
318	6	0.8	149	3	US-09-158-710-18	Sequence 18, Appl	391	6	0.8	187	4	US-08-974-690C-208	Sequence 208, App
319	6	0.8	150	4	US-09-252-991A-17720	Sequence 17720, A	392	6	0.8	187	4	US-08-974-690C-208	Sequence 208, App

393	6	0.8	187	4	US-08-974-690C-209	Sequence 209, App	466	6	0.8	209	4	US-09-693-542-71	Sequence 71, Appl
394	6	0.8	187	4	US-09-248-796A-14589	Sequence 14589, A	467	6	0.8	209	4	US-09-438-185A-949	Sequence 949, App
395	6	0.8	187	4	US-09-248-796A-16267	Sequence 16267, A	468	6	0.8	210	3	US-09-162-184-33	Sequence 33, Appl
396	6	0.8	188	4	US-09-248-796A-18153	Sequence 18153, A	469	6	0.8	210	3	US-09-489-777A-33	Sequence 27171, A
397	6	0.8	188	4	US-10-101-464A-540	Sequence 540, App	470	6	0.8	210	4	US-09-252-991A-27171	Sequence 28553, A
398	6	0.8	189	4	US-09-270-767-46721	Sequence 46721, A	471	6	0.8	211	4	US-09-252-991A-28553	Sequence 9913, Ap
399	6	0.8	191	2	US-08-290-665A-187	Sequence 187, App	472	6	0.8	211	4	US-09-949-016-9913	Sequence 22, Appl
400	6	0.8	191	2	US-08-290-665A-189	Sequence 189, App	473	6	0.8	212	3	US-08-861-774E-22	Sequence 34, Appl
401	6	0.8	191	2	US-08-290-665A-190	Sequence 190, App	474	6	0.8	212	3	US-08-861-774E-34	Sequence 500, App
402	6	0.8	191	5	PCT-US95-10398-187	Sequence 187, App	475	6	0.8	212	4	US-09-538-092-500	Sequence 60, Appl
403	6	0.8	191	5	PCT-US95-10398-189	Sequence 189, App	476	6	0.8	213	3	US-08-861-774E-60	Sequence 44, Appl
404	6	0.8	191	5	PCT-US95-10398-190	Sequence 190, App	477	6	0.8	213	3	US-08-861-774E-62	Sequence 72, Appl
405	6	0.8	192	4	US-09-198-452A-276	Sequence 276, App	478	6	0.8	213	3	US-08-861-774E-77	Sequence 64, Appl
406	6	0.8	192	4	US-09-248-796A-22528	Sequence 22528, A	479	6	0.8	213	4	US-09-902-540-13705	Sequence 13705, A
407	6	0.8	192	4	US-09-438-185A-266	Sequence 266, App	480	6	0.8	214	3	US-08-861-774E-30	Sequence 30, Appl
408	6	0.8	193	1	US-08-248-466B-14	Sequence 14, Appl	481	6	0.8	214	3	US-08-861-774E-32	Sequence 32, Appl
409	6	0.8	193	3	US-09-041-889-5	Sequence 5, Appli	482	6	0.8	214	3	US-08-861-774E-44	Sequence 44, Appl
410	6	0.8	193	3	US-08-837-058-5	Sequence 5, Appli	483	6	0.8	214	3	US-08-861-774E-48	Sequence 48, Appl
411	6	0.8	193	4	US-09-417-264-5	Sequence 5, Appli	484	6	0.8	214	3	US-08-861-774E-54	Sequence 54, Appl
412	6	0.8	193	4	US-08-635-886C-210	Sequence 210, App	485	6	0.8	214	3	US-08-861-774E-66	Sequence 66, Appl
413	6	0.8	193	4	US-08-974-690C-210	Sequence 210, App	486	6	0.8	214	3	US-08-861-774E-76	Sequence 76, Appl
414	6	0.8	194	3	US-09-516-914-9	Sequence 9, Appli	487	6	0.8	214	3	US-08-861-774E-78	Sequence 78, Appl
415	6	0.8	194	4	US-09-489-039A-8286	Sequence 8286, Ap	488	6	0.8	214	5	PCT-US96-08950-2	Sequence 2, Appli
416	6	0.8	194	4	US-09-248-796A-16995	Sequence 16995, A	489	6	0.8	215	1	US-08-266-451B-27	Sequence 27, Appl
417	6	0.8	196	3	US-08-981-392-35	Sequence 35, Appl	490	6	0.8	215	2	US-08-748-725-27	Sequence 27, Appl
418	6	0.8	196	4	US-09-308-322-35	Sequence 35, Appl	491	6	0.8	215	2	US-08-861-774E-40	Sequence 40, Appl
419	6	0.8	198	4	US-09-252-991A-22691	Sequence 22691, A	492	6	0.8	215	3	US-09-270-767-45086	Sequence 45086, A
420	6	0.8	199	4	US-09-252-991A-31135	Sequence 31135, A	493	6	0.8	215	4	US-09-270-767-45086	Sequence 45086, A
421	6	0.8	200	4	US-09-101-272C-73	Sequence 73, Appl	494	6	0.8	216	3	US-08-861-774E-58	Sequence 58, Appl
422	6	0.8	200	4	US-09-252-991A-28054	Sequence 28054, A	495	6	0.8	216	3	US-08-861-774E-62	Sequence 62, Appl
423	6	0.8	200	4	US-09-489-039A-7526	Sequence 7526, Ap	496	6	0.8	218	3	US-08-861-774E-46	Sequence 46, Appl
424	6	0.8	201	3	US-08-679-493A-190	Sequence 190, App	497	6	0.8	218	3	US-08-861-774E-50	Sequence 50, Appl
425	6	0.8	202	4	US-09-252-991A-28505	Sequence 28505, A	498	6	0.8	218	4	US-09-134-000C-3898	Sequence 3898, Ap
426	6	0.8	202	4	US-09-252-991A-27017	Sequence 27017, A	499	6	0.8	218	4	US-09-828-303-23	Sequence 23, Appl
427	6	0.8	203	2	US-08-284-391B-31	Sequence 31, Appl	500	6	0.8	219	3	US-08-861-774E-70	Sequence 70, Appl
428	6	0.8	203	3	US-09-218-950-31	Sequence 31, Appl	501	6	0.8	219	4	US-09-252-991A-28228	Sequence 28228, A
429	6	0.8	203	4	US-09-543-681A-4329	Sequence 4329, Ap	502	6	0.8	219	4	US-09-198-452A-634	Sequence 634, App
430	6	0.8	203	4	US-08-394-388A-31	Sequence 31, Appl	503	6	0.8	219	4	US-09-270-767-33084	Sequence 33084, A
431	6	0.8	203	4	US-10-101-464A-537	Sequence 537, App	504	6	0.8	219	4	US-09-270-767-48301	Sequence 48301, A
432	6	0.8	203	4	US-10-101-464A-658	Sequence 658, App	505	6	0.8	219	4	US-09-438-185A-593	Sequence 593, App
433	6	0.8	204	4	US-09-252-991A-29225	Sequence 29225, A	506	6	0.8	221	4	US-09-874-926-2	Sequence 2, Appli
434	6	0.8	204	4	US-09-543-681A-8020	Sequence 8020, Ap	507	6	0.8	222	4	US-09-252-991A-24147	Sequence 24147, A
435	6	0.8	205	3	US-09-134-001C-4766	Sequence 4766, Ap	508	6	0.8	223	4	US-09-252-991A-19065	Sequence 19065, A
436	6	0.8	205	4	US-09-252-991A-29334	Sequence 29334, A	509	6	0.8	224	4	US-09-198-452A-683	Sequence 683, App
437	6	0.8	205	4	US-09-134-000C-3913	Sequence 3913, Ap	510	6	0.8	229	3	US-08-630-915A-221	Sequence 221, App
438	6	0.8	206	3	US-08-679-493A-75	Sequence 75, Appl	511	6	0.8	229	4	US-09-879-957-221	Sequence 221, App
439	6	0.8	206	4	US-09-543-681A-4763	Sequence 4763, Ap	512	6	0.8	229	4	US-09-438-185A-648	Sequence 648, App
440	6	0.8	206	4	US-09-270-767-35977	Sequence 35977, A	513	6	0.8	230	3	US-09-516-143A-6	Sequence 6, Appli
441	6	0.8	206	4	US-09-270-767-51194	Sequence 51194, A	514	6	0.8	230	4	US-09-984-205-6	Sequence 36, Appl
442	6	0.8	207	4	US-09-198-452A-1020	Sequence 1020, Ap	515	6	0.8	231	4	US-09-543-681A-6357	Sequence 6357, Ap
443	6	0.8	208	1	US-07-935-309-2	Sequence 2, Appli	516	6	0.8	231	4	US-09-069-023-36	Sequence 36462, A
444	6	0.8	208	1	US-08-884-682-1	Sequence 1, Appli	517	6	0.8	233	4	US-09-270-767-36462	Sequence 51679, A
445	6	0.8	208	2	US-08-039-364-2	Sequence 2, Appli	518	6	0.8	233	4	US-09-270-767-51679	Sequence 52, Appl
446	6	0.8	208	2	US-08-766-551-9	Sequence 9, Appli	519	6	0.8	234	3	US-08-861-774E-52	Sequence 8, Appli
447	6	0.8	208	2	US-09-096-082-1	Sequence 1, Appli	520	6	0.8	235	1	US-08-287-959-8	Sequence 879, Ap
448	6	0.8	208	3	US-08-718-904-5	Sequence 5, Appli	521	6	0.8	235	4	US-09-107-532A-6979	Sequence 4199, Ap
449	6	0.8	208	3	US-08-718-904-7	Sequence 7, Appli	522	6	0.8	235	4	US-09-583-110-4199	Sequence 3326, Ap
450	6	0.8	208	3	US-08-612-973-30	Sequence 30, Appl	523	6	0.8	236	4	US-09-107-433-3386	Sequence 4896, App
451	6	0.8	208	3	US-09-181-974-2	Sequence 2, Appli	524	6	0.8	236	4	US-09-134-000C-4896	Sequence 68, Appl
452	6	0.8	208	3	US-09-158-710-2	Sequence 2, Appli	525	6	0.8	237	3	US-08-861-774E-68	Sequence 29406, A
453	6	0.8	208	3	US-08-927-597-30	Sequence 30, Appl	526	6	0.8	238	4	US-09-252-991A-29406	Sequence 13083, A
454	6	0.8	208	3	US-09-518-950-2	Sequence 2, Appli	527	6	0.8	238	4	US-09-902-540-13083	Sequence 44, Appl
455	6	0.8	208	4	US-09-449-249-5	Sequence 5, Appli	528	6	0.8	239	3	US-09-004-731-44	Sequence 44, Appl
456	6	0.8	208	4	US-09-449-249-7	Sequence 7, Appli	529	6	0.8	239	3	US-08-749-699-44	Sequence 76, Appl
457	6	0.8	208	4	US-09-252-991A-22641	Sequence 22641, A	530	6	0.8	239	3	US-08-679-493A-76	Sequence 44, Appl
458	6	0.8	208	4	US-10-138-158-18	Sequence 18, Appl	531	6	0.8	239	4	US-09-004-729-44	Sequence 7253, Ap
459	6	0.8	208	4	US-09-949-016-6149	Sequence 6149, Ap	532	6	0.8	239	4	US-09-328-352-7328	Sequence 41, Appl
460	6	0.8	209	3	US-08-975-762-71	Sequence 71, Appl	533	6	0.8	240	3	US-09-328-352-7253	Sequence 47, Appl
461	6	0.8	209	3	US-09-295-028-71	Sequence 71, Appl	534	6	0.8	242	3	US-09-004-731-41	Sequence 41, Appl
462	6	0.8	209	3	US-09-106-582-71	Sequence 71, Appl	535	6	0.8	242	3	US-09-032-215-47	Sequence 47, Appl
463	6	0.8	209	3	US-09-311-311C-20	Sequence 20, Appl	536	6	0.8	242	3	US-08-749-699-41	Sequence 41, Appl
464	6	0.8	209	4	US-09-252-991A-29571	Sequence 29571, A	537	6	0.8	242	4	US-09-004-729-41	Sequence 41, Appl
465	6	0.8	209	4	US-09-159-469-71	Sequence 71, Appl	538	6	0.8	242	4	US-09-252-991A-19021	Sequence 19021, A

539	6	0.8	242	4	US-09-107-532A-6244	Sequence 6244, Ap	612	6	0.8	281	4	US-09-270-767-43839	Sequence 43839, A
540	6	0.8	243	4	US-09-583-110-3522	Sequence 3522, Ap	613	6	0.8	282	4	US-09-252-991A-25948	Sequence 25948, A
541	6	0.8	244	4	US-09-543-681A-7356	Sequence 7356, Ap	614	6	0.8	284	4	US-08-976-063E-2	Sequence 2, Appli
542	6	0.8	245	4	US-09-461-325-463	Sequence 463, App	615	6	0.8	285	3	US-09-027-137-3	Sequence 3, Appli
543	6	0.8	246	4	US-09-252-991A-29762	Sequence 29762, A	616	6	0.8	285	3	US-09-344-441-3	Sequence 3, Appli
544	6	0.8	247	4	US-10-012-542-463	Sequence 463, App	617	6	0.8	285	4	US-09-248-796A-16474	Sequence 16474, A
545	6	0.8	248	4	US-10-115-123-463	Sequence 463, App	618	6	0.8	285	4	US-09-248-796A-20009	Sequence 20009, A
546	6	0.8	249	4	US-08-356-171E-5222	Sequence 5222, Ap	619	6	0.8	287	3	US-08-549-515-10	Sequence 10, Appl
547	6	0.8	250	4	US-08-781-986A-5222	Sequence 5222, Ap	620	6	0.8	288	4	US-09-489-039A-8919	Sequence 8919, Ap
548	6	0.8	245	4	US-09-640-211A-8333	Sequence 833, App	621	6	0.8	288	4	US-09-248-796A-16494	Sequence 16494, A
549	6	0.8	248	1	US-08-366-451B-2	Sequence 2, Appli	622	6	0.8	289	4	US-09-071-035-72	Sequence 72, Appl
550	6	0.8	248	2	US-08-748-725-2	Sequence 2, Appli	623	6	0.8	289	4	US-09-252-991A-22483	Sequence 22483, A
551	6	0.8	248	3	US-08-944-483-71	Sequence 71, Appl	624	6	0.8	292	3	US-09-027-137-1	Sequence 1, Appli
552	6	0.8	248	4	US-09-252-991A-17358	Sequence 17358, A	625	6	0.8	292	3	US-09-344-441-1	Sequence 1, Appli
553	6	0.8	249	3	US-09-010-809-21	Sequence 21, Appl	626	6	0.8	292	4	US-09-328-352-6642	Sequence 6642, Ap
554	6	0.8	250	3	US-09-010-809-3	Sequence 3, Appli	627	6	0.8	292	4	US-09-543-681A-7918	Sequence 7918, Ap
555	6	0.8	250	4	US-09-538-092-355	Sequence 355, App	628	6	0.8	295	6	5223394-9	Patent No. 5223394
556	6	0.8	251	3	US-08-630-915A-8	Sequence 8, Appli	629	6	0.8	295	6	5223394-9	Patent No. 5223394
557	6	0.8	251	4	US-09-270-767-4493	Sequence 4493, A	630	6	0.8	296	6	5223394-9	Patent No. 5223394
558	6	0.8	251	4	US-09-879-957-8	Sequence 8, Appli	631	6	0.8	296	4	US-09-252-991A-17385	Sequence 17385, A
559	6	0.8	252	3	US-08-944-483-72	Sequence 72, Appl	632	6	0.8	296	4	US-09-949-016-9495	Sequence 9495, Ap
560	6	0.8	253	2	US-09-027-337-8	Sequence 8, Appli	633	6	0.8	297	4	US-09-543-681A-7800	Sequence 7800, Ap
561	6	0.8	253	3	US-08-975-762-52	Sequence 52, Appl	634	6	0.8	298	4	US-09-252-991A-25360	Sequence 25360, A
562	6	0.8	253	3	US-08-944-483-73	Sequence 73, Appl	635	6	0.8	298	4	US-09-270-767-41439	Sequence 41439, A
563	6	0.8	253	3	US-09-295-028-52	Sequence 52, Appl	636	6	0.8	299	4	US-09-270-767-41683	Sequence 41683, A
564	6	0.8	253	3	US-09-106-582-52	Sequence 52, Appl	637	6	0.8	300	1	US-08-148-910-1	Sequence 1, Appli
565	6	0.8	253	4	US-09-644-600-8	Sequence 8, Appli	638	6	0.8	300	1	US-08-448-937A-1	Sequence 1, Appli
566	6	0.8	253	4	US-09-159-469-52	Sequence 52, Appl	639	6	0.8	301	4	US-09-252-991A-20115	Sequence 20115, A
567	6	0.8	253	4	US-09-489-039A-13739	Sequence 13739, A	640	6	0.8	301	4	US-09-252-991A-25396	Sequence 25396, A
568	6	0.8	253	4	US-09-654-600A-8	Sequence 8, Appli	641	6	0.8	301	4	US-09-134-000C-6014	Sequence 6014, Ap
569	6	0.8	253	4	US-09-631-542-52	Sequence 52, Appl	642	6	0.8	302	4	US-09-252-991A-21231	Sequence 21231, A
570	6	0.8	254	2	US-08-560-098A-49	Sequence 49, Appl	643	6	0.8	302	4	US-09-328-352-4508	Sequence 4508, Ap
571	6	0.8	254	4	US-09-270-767-46094	Sequence 46094, A	644	6	0.8	302	4	US-09-540-236-2119	Sequence 2119, Ap
572	6	0.8	254	4	US-09-248-796A-19272	Sequence 19272, A	645	6	0.8	303	4	US-09-107-532A-5585	Sequence 5585, Ap
573	6	0.8	255	3	US-09-612-126-1	Sequence 1, Appli	646	6	0.8	303	4	US-09-949-016-10112	Sequence 10112, A
574	6	0.8	256	3	US-09-230-637-29	Sequence 29, Appl	647	6	0.8	304	4	US-09-902-540-11322	Sequence 11322, A
575	6	0.8	256	4	US-09-489-039A-8774	Sequence 8774, Ap	648	6	0.8	304	4	US-09-489-039A-9424	Sequence 9424, Ap
576	6	0.8	257	2	US-08-467-265-16	Sequence 16, Appl	649	6	0.8	304	4	US-09-902-540-15483	Sequence 15483, A
577	6	0.8	257	3	US-08-467-265-16	Sequence 16, Appl	650	6	0.8	306	2	US-08-560-098A-45	Sequence 45, Appl
578	6	0.8	257	3	US-09-407-891-16	Sequence 16, Appl	651	6	0.8	306	4	US-09-252-991A-27054	Sequence 27054, A
579	6	0.8	257	4	US-09-375-907-5	Sequence 5, Appli	652	6	0.8	306	4	US-09-328-352-5398	Sequence 5398, Ap
580	6	0.8	257	4	US-09-828-447-14	Sequence 14, Appl	653	6	0.8	306	4	US-09-602-787A-572	Sequence 572, App
581	6	0.8	257	4	US-09-248-796A-24697	Sequence 24697, A	654	6	0.8	307	4	US-09-393-634-53	Sequence 53, Appl
582	6	0.8	258	3	US-09-227-357-198	Sequence 198, App	655	6	0.8	308	4	US-09-107-532A-6023	Sequence 6023, Ap
583	6	0.8	258	4	US-09-252-991A-33929	Sequence 32929, A	656	6	0.8	308	4	US-09-248-796A-18392	Sequence 18392, A
584	6	0.8	261	4	US-09-252-991A-29007	Sequence 29007, A	657	6	0.8	309	2	US-08-849-480A-6	Sequence 6, Appli
585	6	0.8	262	4	US-09-270-767-45003	Sequence 45003, A	658	6	0.8	310	3	US-08-477-460B-6	Sequence 6, Appli
586	6	0.8	263	4	US-09-270-767-32374	Sequence 32374, A	659	6	0.8	310	3	US-08-379-516-6	Sequence 6, Appli
587	6	0.8	263	4	US-09-270-767-47591	Sequence 47591, A	660	6	0.8	310	3	US-09-329-916-6	Sequence 6, Appli
588	6	0.8	264	2	US-08-484-905-120	Sequence 120, App	661	6	0.8	310	3	US-08-485-372A-6	Sequence 6, Appli
589	6	0.8	264	3	US-08-370-476-120	Sequence 120, App	662	6	0.8	310	3	US-09-409-006A-6	Sequence 6, Appli
590	6	0.8	264	3	US-09-949-016-11038	Sequence 120, App	663	6	0.8	310	4	US-08-484-681-6	Sequence 6, Appli
591	6	0.8	270	4	US-09-252-991A-27911	Sequence 11038, A	664	6	0.8	310	4	US-09-766-995-6	Sequence 6, Appli
592	6	0.8	272	4	US-09-270-767-40695	Sequence 27911, A	665	6	0.8	310	5	PCT-US93-07422-6	Sequence 6, Appli
593	6	0.8	274	4	US-09-270-767-55911	Sequence 40695, A	666	6	0.8	311	4	US-09-543-681A-5602	Sequence 5602, Ap
594	6	0.8	274	4	US-08-953-326-18	Sequence 55911, A	667	6	0.8	311	4	US-09-489-039A-13013	Sequence 13013, A
595	6	0.8	276	3	US-08-553-662-18	Sequence 18, Appl	668	6	0.8	312	4	US-09-071-035-70	Sequence 70, Appl
596	6	0.8	276	4	US-10-062-994-18	Sequence 18, Appl	669	6	0.8	312	4	US-09-351-150A-11	Sequence 11, Appl
597	6	0.8	276	4	US-09-880-503-5	Sequence 5, Appli	670	6	0.8	312	4	US-09-599-360B-96	Sequence 96, Appl
598	6	0.8	276	4	US-09-252-991A-17567	Sequence 17567, A	671	6	0.8	313	4	US-09-148-545-233	Sequence 233, App
599	6	0.8	277	4	US-09-328-352-5824	Sequence 28712, A	672	6	0.8	313	4	US-09-248-796A-17016	Sequence 17016, A
600	6	0.8	278	4	US-09-328-352-5824	Sequence 5824, Ap	673	6	0.8	315	4	US-09-270-767-42766	Sequence 42766, A
601	6	0.8	278	4	US-09-107-532A-6088	Sequence 11962, A	674	6	0.8	315	4	US-09-270-767-43483	Sequence 43483, A
602	6	0.8	280	4	US-09-270-767-40154	Sequence 4088, Ap	675	6	0.8	315	4	US-09-603-208A-212	Sequence 212, App
603	6	0.8	280	4	US-10-101-464A-511	Sequence 511, App	676	6	0.8	317	4	US-09-583-110-5279	Sequence 5279, Ap
604	6	0.8	280	4	US-09-261-358A-9	Sequence 9, Appli	677	6	0.8	317	4	US-09-270-767-42690	Sequence 42690, A
605	6	0.8	280	4	US-09-201-458-5	Sequence 5, Appli	678	6	0.8	318	4	US-09-252-991A-25243	Sequence 25243, A
606	6	0.8	281	3	US-09-660-587-9	Sequence 9, Appli	679	6	0.8	318	6	5223394-11	Patent No. 5223394
607	6	0.8	281	4	US-09-314-701-2	Sequence 2, Appli	680	6	0.8	318	6	5223394-11	Patent No. 5223394
608	6	0.8	281	4	US-09-811-007A-9	Sequence 9, Appli	681	6	0.8	320	3	US-09-134-001C-3522	Sequence 3522, Ap
609	6	0.8	281	4			682	6	0.8	320	3	US-09-134-001C-3823	Sequence 3823, Ap
610	6	0.8	281	4			683	6	0.8	320	4	US-09-489-039A-10349	Sequence 10349, A
611	6	0.8	281	4			684	6	0.8				

685	6	0.8	320	4	US-09-489-039A-13881	Sequence 13881, A	758	6	0.8	359	4	US-09-583-110-3909	Sequence 3909, Ap
686	6	0.8	320	4	US-09-134-000C-5021	Sequence 5021, Ap	759	6	0.8	362	4	US-09-252-991A-18494	Sequence 18494, A
687	6	0.8	322	4	US-09-252-991A-29347	Sequence 29347, A	760	6	0.8	363	4	US-09-107-433-3869	Sequence 3869, Ap
688	6	0.8	322	4	US-09-949-016-8007	Sequence 8007, Ap	761	6	0.8	364	4	US-09-252-991A-19037	Sequence 19037, A
689	6	0.8	323	4	US-09-270-767-61011	Sequence 61011, A	762	6	0.8	364	4	US-09-438-185A-815	Sequence 815, Appl
690	6	0.8	323	4	US-09-880-503-7	Sequence 7, Appli	763	6	0.8	365	1	US-08-093-741-83	Sequence 83, Appl
691	6	0.8	324	4	US-09-270-767-44986	Sequence 44986, A	764	6	0.8	365	1	US-08-720-013-83	Sequence 3, Appli
692	6	0.8	325	4	US-08-311-731A-249	Sequence 249, App	765	6	0.8	365	3	US-09-231-529-3	Sequence 3, Appli
693	6	0.8	325	4	US-09-248-796A-14929	Sequence 14929, A	766	6	0.8	365	3	US-08-977-816-3	Sequence 24466, A
694	6	0.8	326	3	US-09-066-046-29	Sequence 29, Appl	767	6	0.8	366	4	US-09-252-991A-15482	Sequence 15482, A
695	6	0.8	326	3	US-09-066-047-15	Sequence 15, Appl	768	6	0.8	366	4	US-08-895-707-6	Sequence 6, Appli
696	6	0.8	326	3	US-09-411-977-3	Sequence 3, Appli	769	6	0.8	367	3	US-09-252-991A-17240	Sequence 17240, A
697	6	0.8	326	4	US-09-543-681A-7709	Sequence 7709, Ap	770	6	0.8	367	4	US-09-328-352-7662	Sequence 7662, Ap
698	6	0.8	326	4	US-10-057-951-3	Sequence 3, Appli	771	6	0.8	367	4	US-09-902-540-9972	Sequence 9972, Ap
699	6	0.8	327	4	US-09-252-991A-33067	Sequence 33067, A	772	6	0.8	369	4	US-09-248-796A-14930	Sequence 14930, A
700	6	0.8	331	2	US-09-107-433-3331	Sequence 3331, Ap	773	6	0.8	370	4	US-09-252-991A-28586	Sequence 28586, A
701	6	0.8	332	4	US-09-248-796A-20663	Sequence 20663, A	774	6	0.8	372	4	US-09-973-963-4	Sequence 4, Appli
702	6	0.8	332	4	US-09-710-279-2476	Sequence 2476, Ap	775	6	0.8	372	4	US-09-949-016-6463	Sequence 6463, Ap
703	6	0.8	330	4	US-09-710-279-2734	Sequence 2734, Ap	776	6	0.8	372	4	US-09-404-296B-4	Sequence 4, Appli
704	6	0.8	331	2	US-08-560-098A-46	Sequence 46, Appl	777	6	0.8	373	4	US-08-820-170A-25	Sequence 25, Appl
705	6	0.8	332	3	US-09-134-001C-4323	Sequence 4323, Ap	778	6	0.8	374	2	US-09-055-699-25	Sequence 25, Appl
706	6	0.8	333	4	US-09-328-352-7516	Sequence 7516, Ap	779	6	0.8	374	3	US-09-273-565-25	Sequence 25, Appl
707	6	0.8	334	3	US-09-218-363-11	Sequence 11, Appl	780	6	0.8	374	3	US-09-565-538-25	Sequence 25, Appl
708	6	0.8	336	1	US-07-904-073-2	Sequence 2, Appli	781	6	0.8	374	3	US-09-661-468-25	Sequence 25, Appl
709	6	0.8	336	1	US-07-904-071-2	Sequence 2, Appli	782	6	0.8	374	4	US-09-976-165-25	Sequence 25, Appli
710	6	0.8	336	1	US-08-442-043A-16	Sequence 16, Appl	783	6	0.8	374	4	US-09-227-853A-2	Sequence 2, Appli
711	6	0.8	336	4	US-08-441-893A-16	Sequence 16, Appl	784	6	0.8	374	4	US-09-540-236-2230	Sequence 2230, Ap
712	6	0.8	337	4	US-09-252-991A-26757	Sequence 26757, A	785	6	0.8	374	5	PCT-US95-06385-2	Sequence 2, Appli
713	6	0.8	337	4	US-09-252-991A-30261	Sequence 30261, A	786	6	0.8	375	3	US-08-872-979-3	Sequence 3, Appli
714	6	0.8	338	4	US-09-107-532A-5819	Sequence 5819, Ap	787	6	0.8	375	4	US-09-328-352-6191	Sequence 6191, Ap
715	6	0.8	340	4	US-09-543-681A-7850	Sequence 7850, Ap	788	6	0.8	375	4	US-09-489-039A-11560	Sequence 11560, A
716	6	0.8	340	4	US-09-816-248-15	Sequence 15, Appl	789	6	0.8	377	4	US-09-679-279-3	Sequence 3, Appli
717	6	0.8	341	4	US-09-543-681A-4713	Sequence 4713, Ap	790	6	0.8	377	4	US-09-489-039A-12546	Sequence 12546, A
718	6	0.8	341	4	US-09-248-796A-17051	Sequence 17051, A	791	6	0.8	377	4	US-09-553-439-10	Sequence 10, Appl
719	6	0.8	341	4	US-09-902-540-13921	Sequence 13921, A	792	6	0.8	378	3	US-09-618-869-10	Sequence 10, Appl
720	6	0.8	342	4	US-09-252-991A-30257	Sequence 30257, A	793	6	0.8	378	4	US-09-673-395A-618	Sequence 618, App
721	6	0.8	342	4	US-09-902-540-10704	Sequence 10704, A	794	6	0.8	378	4	US-09-252-991A-17472	Sequence 17472, A
722	6	0.8	343	4	US-09-252-991A-22307	Sequence 22307, A	795	6	0.8	379	4	US-09-673-395A-441	Sequence 441, App
723	6	0.8	345	3	US-09-027-900-11	Sequence 11, Appl	796	6	0.8	381	4	US-09-270-767-46183	Sequence 46183, A
724	6	0.8	345	4	US-09-489-039A-10740	Sequence 10740, A	797	6	0.8	383	1	US-08-486-037B-2	Sequence 2, Appli
725	6	0.8	346	4	US-09-252-991A-21487	Sequence 21487, A	798	6	0.8	383	2	US-08-558-269-6	Sequence 2, Appli
726	6	0.8	347	2	US-08-811-949-1	Sequence 1, Appli	799	6	0.8	383	3	US-09-410-882-6	Sequence 6, Appli
727	6	0.8	347	4	US-09-636-215-590	Sequence 590, App	800	6	0.8	385	3	US-09-071-224-19	Sequence 19, Appl
728	6	0.8	347	4	US-09-685-166A-590	Sequence 590, App	801	6	0.8	385	3	US-08-895-707-7	Sequence 7, Appli
729	6	0.8	347	4	US-09-679-426-590	Sequence 590, App	802	6	0.8	386	3	US-09-045-284A-2	Sequence 2, Appli
730	6	0.8	347	4	US-09-759-143-590	Sequence 590, App	803	6	0.8	386	3	US-09-190-911-1	Sequence 1, Appli
731	6	0.8	347	4	US-09-651-236-590	Sequence 590, App	804	6	0.8	386	4	US-09-786-240-11	Sequence 11, Appl
732	6	0.8	348	4	US-09-360-376-13	Sequence 13, Appl	805	6	0.8	386	4	US-09-489-039A-7410	Sequence 7410, Ap
733	6	0.8	349	4	US-09-489-039A-7582	Sequence 7582, Ap	806	6	0.8	386	4	US-09-248-796A-15757	Sequence 15757, A
734	6	0.8	351	1	US-08-324-483-2	Sequence 2, Appli	807	6	0.8	389	2	US-08-811-949-67	Sequence 67, Appl
735	6	0.8	351	4	US-09-902-540-12944	Sequence 12944, A	808	6	0.8	389	3	US-09-071-224-27	Sequence 27, Appl
736	6	0.8	354	2	US-08-811-949-61	Sequence 61, Appl	809	6	0.8	389	3	US-107-532A-6185	Sequence 6185, Ap
737	6	0.8	355	1	US-08-137-116-1	Sequence 1, Appli	810	6	0.8	389	4	US-09-252-991A-26543	Sequence 26543, A
738	6	0.8	355	1	US-08-217-618-1	Sequence 1, Appli	811	6	0.8	390	4	US-09-543-681A-7029	Sequence 9, Appli
739	6	0.8	355	1	US-08-427-640-2	Sequence 2, Appli	812	6	0.8	391	2	US-08-706-539-9	Sequence 9, Appli
740	6	0.8	355	1	US-08-427-640-6	Sequence 6, Appli	813	6	0.8	392	3	US-09-027-007-9	Sequence 2794, Ap
741	6	0.8	355	1	US-08-217-617A-1	Sequence 1, Appli	814	6	0.8	392	4	US-09-710-279-2794	Sequence 2794, Ap
742	6	0.8	355	1	US-08-217-616-1	Sequence 1, Appli	815	6	0.8	392	4	US-09-710-279-2874	Sequence 8786, Ap
743	6	0.8	355	2	US-08-811-949-45	Sequence 45, Appl	816	6	0.8	392	4	US-09-949-016-8786	Sequence 8787, Ap
744	6	0.8	355	2	US-08-811-949-47	Sequence 47, Appl	817	6	0.8	392	4	US-09-949-016-8787	Sequence 44, Appl
745	6	0.8	355	2	US-08-811-949-53	Sequence 53, Appl	818	6	0.8	393	2	US-08-560-098A-44	Sequence 24, Appl
746	6	0.8	355	2	US-08-811-949-59	Sequence 59, Appl	819	6	0.8	393	3	US-08-967-024C-24	Sequence 25, Appl
747	6	0.8	355	3	US-08-794-528-1	Sequence 1, Appli	820	6	0.8	393	3	US-08-967-024C-25	Sequence 42793, A
748	6	0.8	355	4	US-09-252-991A-22326	Sequence 22326, A	821	6	0.8	393	4	US-09-270-767-42793	Sequence 2, Appli
749	6	0.8	355	4	US-09-198-452A-871	Sequence 871, App	822	6	0.8	394	3	US-08-466-368-2	Sequence 4, Appli
750	6	0.8	355	4	US-09-902-540-11796	Sequence 11796, A	823	6	0.8	394	3	US-09-144-914-4	Sequence 18502, A
751	6	0.8	355	6	5223256-1	Patent No. 5223256	824	6	0.8	394	4	US-08-328-500-2	Sequence 2, Appli
752	6	0.8	355	6	5223256-1	Patent No. 5223256	825	6	0.8	394	4	US-08-328-500-2	Patent No. 5223418
753	6	0.8	356	1	US-08-427-640-4	Sequence 4, Appli	826	6	0.8	394	6	5223418-2	Patent No. 5223418
754	6	0.8	356	1	US-08-427-640-8	Sequence 8, Appli	827	6	0.8	394	6	5223418-2	Sequence 2, Appli
755	6	0.8	356	4	US-09-252-991A-30030	Sequence 30030, A	828	6	0.8	395	1	US-08-485-859-2	Sequence 11, Appl
756	6	0.8	356	4	US-09-902-540-12881	Sequence 12881, A	829	6	0.8	395	1	US-08-706-539-11	
757	6	0.8	358	4	US-09-248-796A-19081	Sequence 19081, A	830	6	0.8	395	1		

831	6	0.8	395	1	US-08-522-166-2	Sequence 2, Appli	904	4	US-09-107-532A-5459	Sequence 5459, Ap
832	6	0.8	395	1	US-08-488-382A-2	Sequence 2, Appli	905	4	US-09-248-796A-18949	Sequence 18949, A
833	6	0.8	395	2	US-08-480-912-2	Sequence 2, Appli	906	4	US-10-027-450-45	Sequence 45, Appl
834	6	0.8	395	3	US-09-027-007-11	Sequence 11, Appl	907	6	US-09-071-224-6	Sequence 6, Appli
835	6	0.8	396	4	US-09-252-991A-18619	Sequence 18619, A	908	6	US-09-134-001C-5619	Sequence 5619, Ap
836	6	0.8	397	1	US-08-647-928-8	Sequence 8, Appli	909	6	US-09-540-236-3465	Sequence 3466, Ap
837	6	0.8	397	4	US-09-489-039A-13498	Sequence 13498, A	910	6	US-09-252-991A-25192	Sequence 25192, A
838	6	0.8	397	4	US-09-949-016-10639	Sequence 10639, A	911	6	US-09-198-452A-31	Sequence 31, Appl
839	6	0.8	397	4	US-09-949-016-10640	Sequence 10640, A	912	6	US-09-328-352-5205	Sequence 5205, Ap
840	6	0.8	398	2	US-08-284-391B-29	Sequence 29, Appl	913	6	US-08-570-157-5	Sequence 5, Appli
841	6	0.8	398	4	US-09-218-905-29	Sequence 29, Appl	914	6	US-08-029-170-31	Sequence 31, Appl
842	6	0.8	398	4	US-08-394-388A-29	Sequence 29, Appl	915	6	US-08-403-797-2	Sequence 2, Appli
843	6	0.8	399	4	US-09-489-039A-8859	Sequence 8859, Ap	916	6	US-09-076-510-5	Sequence 5, Appli
844	6	0.8	399	4	US-09-270-767-45921	Sequence 45921, A	917	6	US-09-004-349-5	Sequence 5, Appli
845	6	0.8	399	4	US-09-710-279-2576	Sequence 2576, Ap	918	6	US-09-443-745-31	Sequence 31, Appl
846	6	0.8	400	3	US-09-134-001C-4785	Sequence 4785, Ap	919	6	US-09-949-016-10965	Sequence 10965, A
847	6	0.8	400	4	US-09-252-991A-31296	Sequence 31296, A	920	6	US-09-252-991A-28788	Sequence 28788, A
848	6	0.8	400	4	US-09-248-796A-15785	Sequence 15785, A	921	6	US-09-854-133-391	Sequence 391, App
849	6	0.8	401	4	US-09-489-847-202	Sequence 202, App	922	6	US-07-942-157A-3	Sequence 3, Appli
850	6	0.8	401	4	US-09-252-991A-17090	Sequence 17090, A	923	6	5219569-2	Patent No. 5219569
851	6	0.8	401	4	US-09-902-540-10491	Sequence 10491, A	924	6	5219569-2	Patent No. 5219569
852	6	0.8	402	1	US-08-236-311-1	Sequence 1, Appli	925	6	US-09-376-689-4	Sequence 4, Appli
853	6	0.8	402	3	US-08-457-918-1	Sequence 1, Appli	926	6	US-09-101-272G-1	Sequence 1, Appli
854	6	0.8	402	4	US-10-157-408-1	Sequence 1, Appli	927	6	US-09-540-236-3536	Sequence 3536, Ap
855	6	0.8	403	4	US-09-802-213-5	Sequence 5, Appli	928	6	US-09-270-767-45503	Sequence 45503, A
856	6	0.8	403	4	US-09-880-503-6	Sequence 6, Appli	929	6	US-09-248-796A-18354	Sequence 18354, A
857	6	0.8	405	3	US-09-144-914-5	Sequence 5, Appli	930	6	5188829-1	Patent No. 5188829
858	6	0.8	405	4	US-09-252-991A-23838	Sequence 23838, A	931	6	5188829-1	Patent No. 5188829
859	6	0.8	405	4	US-09-134-000C-5465	Sequence 5465, Ap	932	6	US-08-560-098A-47	Sequence 47, Appl
860	6	0.8	408	4	US-09-252-991A-21303	Sequence 21303, A	933	6	US-08-477-460B-2	Sequence 2, Appli
861	6	0.8	408	4	US-09-138-452A-141	Sequence 141, App	934	6	US-08-379-516-2	Sequence 2, Appli
862	6	0.8	408	4	US-09-583-110-3016	Sequence 3016, Ap	935	6	US-09-329-916-2	Sequence 2, Appli
863	6	0.8	408	4	US-09-902-540-11436	Sequence 11436, A	936	6	US-08-485-372A-2	Sequence 2, Appli
864	6	0.8	409	4	US-09-710-279-2002	Sequence 2002, Ap	937	6	US-09-409-006A-2	Sequence 2, Appli
865	6	0.8	409	4	US-09-710-279-2306	Sequence 2306, Ap	938	6	US-08-484-681-2	Sequence 2, Appli
866	6	0.8	410	1	US-08-732-283A-9	Sequence 9, Appli	939	6	US-09-766-995-2	Sequence 2, Appli
867	6	0.8	410	2	US-09-105-508-9	Sequence 9, Appli	940	6	PCT-US93-07422-2	Sequence 2, Appli
868	6	0.8	410	3	US-08-630-172-17	Sequence 17, Appl	941	6	US-08-867-149-1	Sequence 1, Appli
869	6	0.8	410	3	US-09-271-713-9	Sequence 9, Appli	942	6	US-08-808-374-1	Sequence 1, Appli
870	6	0.8	410	3	US-09-375-419-17	Sequence 17, Appl	943	6	US-09-100-409A-1	Sequence 1, Appli
871	6	0.8	410	4	US-09-252-991A-25812	Sequence 25812, A	944	6	US-09-364-230-14	Sequence 14, Appl
872	6	0.8	410	4	US-09-252-991A-31937	Sequence 31937, A	945	6	US-09-792-024-78	Sequence 78, Appl
873	6	0.8	410	4	US-09-489-039A-10283	Sequence 10283, A	946	6	5171838-13	Patent No. 5171838
874	6	0.8	411	1	US-08-087-163-1	Sequence 1, Appli	947	6	5171838-13	Patent No. 5171838
875	6	0.8	411	1	US-08-286-748B-18	Sequence 18, Appl	948	6	US-08-236-311-4	Sequence 4, Appli
876	6	0.8	411	1	US-08-153-799-18	Sequence 18, Appl	949	6	US-08-457-918-4	Sequence 4, Appli
877	6	0.8	411	2	US-08-560-098A-48	Sequence 48, Appl	950	6	US-09-252-991A-23131	Sequence 23131, A
878	6	0.8	411	3	US-09-376-689-2	Sequence 2, Appli	951	6	US-09-543-681A-7154	Sequence 7154, Ap
879	6	0.8	411	3	US-09-181-816-1	Sequence 1, Appli	952	6	US-10-157-408-4	Sequence 4, Appli
880	6	0.8	411	4	US-09-403-736-2	Sequence 2, Appli	953	6	US-09-949-016-11448	Sequence 11448, A
881	6	0.8	411	4	US-09-880-503-3	Sequence 3, Appli	954	6	US-08-811-949-49	Sequence 49, Appl
882	6	0.8	412	4	US-09-902-540-13518	Sequence 13518, A	955	6	US-08-811-949-51	Sequence 51, Appl
883	6	0.8	413	4	US-09-949-016-10736	Sequence 10736, A	956	6	US-08-811-949-55	Sequence 55, Appl
884	6	0.8	413	4	US-09-949-016-10737	Sequence 10737, A	957	6	US-08-811-949-57	Sequence 57, Appl
885	6	0.8	414	4	US-09-252-991A-27828	Sequence 27828, A	958	6	US-09-710-279-2960	Sequence 2960, Ap
886	6	0.8	415	1	US-08-110-286A-6	Sequence 6, Appli	959	6	US-09-252-991A-28398	Sequence 28398, A
887	6	0.8	415	3	US-08-981-189B-10	Sequence 10, Appl	960	6	Sequence 8464, Ap	Sequence 8464, Ap
888	6	0.8	415	3	US-08-482-746-6	Sequence 6, Appli	961	6	Sequence 1277, A	Sequence 1277, A
889	6	0.8	415	4	US-09-180-109A-9	Sequence 9, Appli	962	6	Sequence 9, Appli	Sequence 9, Appli
890	6	0.8	415	4	US-09-180-109A-12	Sequence 12, Appl	963	6	Sequence 7293, Ap	Sequence 7293, Ap
891	6	0.8	415	4	US-09-580-734-6	Sequence 6, Appli	964	6	Sequence 10782, A	Sequence 10782, A
892	6	0.8	415	4	US-08-374-009-6	Sequence 6, Appli	965	6	Sequence 54, Appl	Sequence 54, Appl
893	6	0.8	415	4	US-09-191-724-6	Sequence 6, Appli	966	6	Sequence 11, Appl	Sequence 11, Appl
894	6	0.8	415	4	US-09-799-978-16	Sequence 16, Appl	967	6	Sequence 10792, A	Sequence 10792, A
895	6	0.8	418	4	US-09-591-279A-42	Sequence 42, Appl	968	6	Sequence 54, Appl	Sequence 54, Appl
896	6	0.8	419	4	US-09-270-767-41700	Sequence 41700, A	969	6	Sequence 6, Appli	Sequence 6, Appli
897	6	0.8	419	4	US-09-902-540-13149	Sequence 13149, A	970	6	Sequence 6, Appli	Sequence 6, Appli
898	6	0.8	420	4	US-09-252-991A-17500	Sequence 17500, A	971	6	Sequence 14, Appl	Sequence 14, Appl
899	6	0.8	420	4	US-09-583-110-5061	Sequence 5061, Ap	972	6	Sequence 14, Appl	Sequence 14, Appl
900	6	0.8	420	4	US-09-107-433-3919	Sequence 3919, Ap	973	6	Sequence 28809, A	Sequence 28809, A
901	6	0.8	422	4	US-09-489-847-357	Sequence 357, App	974	6	Sequence 43807, A	Sequence 43807, A
902	6	0.8	424	3	US-09-134-001C-5009	Sequence 5009, Ap	975	6	Sequence 14, Appl	Sequence 14, Appl
903	6	0.8	424	4	US-09-173-300-45	Sequence 45, Appl	976	6		

977	6	0.8	445	4	US-09-710-279-2858	Sequence 2858, Ap	1050	492	4	US-09-248-796A-17174	Sequence 17174, A
978	6	0.8	451	4	US-09-328-352-7659	Sequence 7659, Ap	1051	493	4	US-09-543-681A-7006	Sequence 7006, Ap
979	6	0.8	451	4	US-09-134-000C-3849	Sequence 3849, Ap	1052	494	4	US-09-517-773-2	Sequence 2, Appli
980	6	0.8	454	3	US-09-134-001C-4438	Sequence 4438, Ap	1053	495	4	US-08-311-731A-3	Sequence 3, Appli
981	6	0.8	454	4	US-09-302-540-12501	Sequence 12501, A	1054	497	1	US-08-278-635B-5	Sequence 5, Appli
982	6	0.8	456	1	US-08-205-719-4	Sequence 4, Appli	1055	497	3	US-08-464-258B-5	Sequence 5, Appli
983	6	0.8	456	3	US-08-431-517F-6	Sequence 6, Appli	1056	497	3	US-08-471-961-5	Sequence 5, Appli
984	6	0.8	456	4	US-09-328-352-5446	Sequence 5446, Ap	1057	497	4	US-09-345-109C-5	Sequence 5, Appli
985	6	0.8	456	4	US-09-919-172-31	Sequence 31, Appli	1058	497	4	US-09-270-767-62287	Sequence 62287, A
986	6	0.8	457	4	US-08-328-500-9	Sequence 9, Appli	1059	497	6	US-09-949-016-6616	Sequence 6616, Ap
987	6	0.8	457	4	US-08-328-500-9	Sequence 9, Appli	1060	497	6	5486473-4	Patent No. 5486473
988	6	0.8	458	3	US-08-466-268-4	Sequence 4, Appli	1061	497	6	5486473-4	Patent No. 5486473
989	6	0.8	458	3	US-09-517-605-3	Sequence 3, Appli	1062	497	6	US-09-949-016-7370	Sequence 7370, Ap
990	6	0.8	458	4	US-09-252-991A-30535	Sequence 30535, A	1063	499	4	US-09-902-540-16496	Sequence 16496, A
991	6	0.8	458	4	US-09-489-039A-8987	Sequence 8987, Ap	1064	501	3	US-08-906-791-2	Sequence 2, Appli
992	6	0.8	458	4	US-09-612-402B-36	Sequence 36, Appli	1065	501	3	US-09-111-730-1	Sequence 1, Appli
993	6	0.8	458	4	US-10-092-138A-25	Sequence 25, Appli	1066	502	3	US-09-499-302A-7	Sequence 7, Appli
994	6	0.8	458	6	5223394-7	Sequence 25, Appli	1067	503	4	US-09-949-016-6578	Sequence 6578, Ap
995	6	0.8	458	6	5223394-7	Patent No. 5223394	1068	504	2	US-08-466-589-4	Sequence 4, Appli
996	6	0.8	459	3	US-09-491-785-2	Sequence 20, Appli	1069	504	2	US-08-700-636-4	Sequence 4, Appli
997	6	0.8	459	3	US-09-364-230-20	Sequence 20, Appli	1070	504	3	US-08-467-574-4	Sequence 4, Appli
998	6	0.8	459	4	US-09-252-991A-29528	Sequence 29528, A	1071	504	3	US-09-217-345-4	Sequence 4, Appli
999	6	0.8	459	4	US-09-710-279-2462	Sequence 2462, Ap	1072	504	3	US-08-487-596-4	Sequence 4, Appli
1000	6	0.8	460	4	US-09-543-681A-5773	Sequence 5773, Ap	1073	504	4	US-08-660-451A-4	Sequence 4, Appli
1001	6	0.8	461	4	US-09-248-796A-16479	Sequence 16479, A	1074	504	4	US-09-892-985-4	Sequence 4, Appli
1002	6	0.8	461	4	US-09-302-540-12101	Sequence 12101, A	1075	505	4	US-09-612-402B-17	Sequence 17, Appli
1003	6	0.8	462	2	US-08-417-495-5	Sequence 5, Appli	1076	505	4	US-09-949-016-6538	Sequence 6538, Ap
1004	6	0.8	462	2	US-08-384-391B-5	Sequence 5, Appli	1077	509	4	US-09-270-767-43544	Sequence 43544, A
1005	6	0.8	462	3	US-09-218-950-5	Sequence 5, Appli	1078	510	3	US-09-291-922-22	Sequence 22, Appli
1006	6	0.8	462	5	PCT-US92-0178B-5	Sequence 5, Appli	1079	511	3	US-09-949-016-6034	Sequence 6034, Ap
1007	6	0.8	462	5	PCT-US95-0045A-5	Sequence 5, Appli	1080	513	4	US-09-248-796A-20548	Sequence 20548, A
1008	6	0.8	462	5	PCT-US95-0045A-5	Sequence 5, Appli	1081	514	4	US-09-252-991A-30600	Sequence 30600, A
1009	6	0.8	463	2	US-08-679-635A-4	Sequence 4, Appli	1082	514	4	US-09-270-767-59153	Sequence 59153, A
1010	6	0.8	463	3	US-09-419-163-4	Sequence 4, Appli	1083	514	4	US-09-270-767-62396	Sequence 62396, A
1011	6	0.8	463	4	US-09-902-540-14193	Sequence 14193, A	1084	518	4	US-09-248-796A-15232	Sequence 15232, A
1012	6	0.8	464	3	US-09-134-001C-4562	Sequence 4562, Ap	1085	518	4	US-09-816-248-17	Sequence 17, Appli
1013	6	0.8	465	4	US-09-328-352-5222	Sequence 5222, Ap	1086	519	4	US-09-540-236-3050	Sequence 3050, Ap
1014	6	0.8	465	4	US-09-710-279-1676	Sequence 1676, Ap	1087	520	3	US-09-668-740B-3	Sequence 3, Appli
1015	6	0.8	466	4	US-09-252-991A-16891	Sequence 16891, A	1088	520	4	US-09-949-016-8026	Sequence 8026, Ap
1016	6	0.8	466	4	US-09-252-991A-21778	Sequence 21778, A	1089	521	4	US-09-540-236-3722	Sequence 3722, Ap
1017	6	0.8	467	4	US-09-489-039A-9899	Sequence 9899, Ap	1090	521	4	US-09-949-016-8809	Sequence 8809, Ap
1018	6	0.8	468	4	US-09-710-279-1648	Sequence 1648, Ap	1091	522	4	US-09-134-000C-4946	Sequence 4946, Ap
1019	6	0.8	468	4	US-09-248-796A-17456	Sequence 17456, A	1092	523	3	US-09-550-338-2	Sequence 2, Appli
1020	6	0.8	469	4	US-09-583-110-4480	Sequence 4480, Ap	1093	523	3	US-09-767-878-2	Sequence 2, Appli
1021	6	0.8	470	2	US-08-724-394A-10	Sequence 10, Appli	1094	525	3	US-09-369-364A-21	Sequence 21, Appli
1022	6	0.8	470	3	US-09-328-352-7348	Sequence 7348, Ap	1095	525	4	US-09-540-236-2855	Sequence 2855, Ap
1023	6	0.8	471	3	US-09-134-001C-4125	Sequence 4125, Ap	1096	525	4	US-10-101-464A-613	Sequence 613, App
1024	6	0.8	471	4	US-09-645-337A-4	Sequence 4, Appli	1097	526	2	US-08-852-401-3	Sequence 3, Appli
1025	6	0.8	472	2	US-08-811-949-63	Sequence 63, Appli	1098	527	1	US-07-609-510B-16	Sequence 16, Appli
1026	6	0.8	472	4	US-09-107-433-4609	Sequence 4609, Ap	1099	527	2	US-08-811-949-39	Sequence 39, Appli
1027	6	0.8	473	4	US-09-252-991A-22921	Sequence 22921, A	1100	527	4	US-09-600-985-1	Sequence 1, Appli
1028	6	0.8	473	4	US-09-252-991A-31406	Sequence 31406, A	1101	527	4	US-09-600-985-2	Sequence 2, Appli
1029	6	0.8	473	4	US-09-328-352-5279	Sequence 5279, Ap	1102	527	4	US-09-600-985-3	Sequence 3, Appli
1030	6	0.8	473	4	US-09-949-016-9481	Sequence 9481, Ap	1103	527	4	US-09-612-314A-51	Sequence 51, Appli
1031	6	0.8	476	4	US-09-675-018B-13	Sequence 13, Appli	1104	527	5	PCT-US91-01025A-2	Sequence 2, Appli
1032	6	0.8	476	4	US-09-675-018B-14	Sequence 14, Appli	1105	527	6	5185259-8	Patent No. 5185259
1033	6	0.8	477	2	US-08-560-098A-51	Sequence 51, Appli	1106	527	6	5520913-1	Patent No. 5520913
1034	6	0.8	478	4	US-09-252-991A-23438	Sequence 23438, A	1107	527	6	5185259-8	Patent No. 5185259
1035	6	0.8	478	4	US-09-134-000C-3709	Sequence 3709, Ap	1108	527	6	5520913-1	Patent No. 5520913
1036	6	0.8	480	4	US-09-252-991A-17687	Sequence 17687, A	1109	530	3	US-08-477-460B-4	Sequence 4, Appli
1037	6	0.8	480	4	US-09-252-991A-29770	Sequence 29770, A	1110	530	3	US-08-379-516-4	Sequence 4, Appli
1038	6	0.8	480	4	US-09-270-767-60056	Sequence 60056, A	1111	530	3	US-09-329-916-4	Sequence 4, Appli
1039	6	0.8	481	4	US-09-902-540-13111	Sequence 13111, A	1112	530	3	US-08-485-372A-4	Sequence 4, Appli
1040	6	0.8	482	3	US-08-431-517F-5	Sequence 5, Appli	1113	530	3	US-09-409-006A-4	Sequence 4, Appli
1041	6	0.8	482	6	5245013-2	Patent No. 5245013	1114	530	4	US-08-484-681-4	Sequence 4, Appli
1042	6	0.8	482	6	5245013-2	Patent No. 5245013	1115	530	4	US-09-766-995-4	Sequence 4, Appli
1043	6	0.8	483	4	US-09-603-208A-210	Sequence 210, App	1116	530	5	PCT-US93-07422-4	Sequence 4, Appli
1044	6	0.8	484	3	US-09-134-001C-5063	Sequence 5063, Ap	1117	531	4	US-09-949-016-7044	Sequence 6, Appli
1045	6	0.8	484	4	US-09-107-532A-4946	Sequence 4946, Ap	1118	532	2	US-08-417-495-6	Sequence 6, Appli
1046	6	0.8	487	4	US-09-248-796A-19788	Sequence 19788, A	1119	532	3	US-08-284-391B-6	Sequence 6, Appli
1047	6	0.8	489	4	US-09-986-536-2	Sequence 2, Appli	1120	532	3	US-09-218-950-6	Sequence 6, Appli
1048	6	0.8	489	4	US-09-252-991A-18918	Sequence 18918, A	1121	532	4	US-08-394-388A-6	Sequence 6, Appli
1049	6	0.8	491	4	US-09-248-796A-14421	Sequence 14421, A	1122	532	5	PCT-US92-01785-6	Sequence 6, Appli

1123	6	0.8	532	5	PCT-US95-00454-6	Sequence 6, Appli	1196	6	0.8	598	4	US-09-270-767-45253	Sequence 45253, A
1124	6	0.8	534	4	US-09-328-352-5713	Sequence 6713, Ap	1197	6	0.8	599	4	US-09-773-426A-7	Sequence 7, Appli
1125	6	0.8	534	4	US-09-270-767-45080	Sequence 45080, A	1198	6	0.8	599	4	US-10-314-881-7	Sequence 7, Appli
1126	6	0.8	535	4	US-09-312-762A-14	Sequence 14, Appl	1199	6	0.8	602	4	US-09-438-185A-18	Sequence 18, Appl
1127	6	0.8	542	4	US-09-489-039A-11757	Sequence 11757, A	1200	6	0.8	603	3	US-09-198-122-2	Sequence 2, Appli
1128	6	0.8	544	3	US-08-687-590-30	Sequence 30, Appl	1201	6	0.8	603	3	US-09-311-111C-26	Sequence 26, Appl
1129	6	0.8	545	4	US-09-489-039A-11980	Sequence 11980, A	1202	6	0.8	603	3	US-09-134-001C-5226	Sequence 5226, Ap
1130	6	0.8	546	4	US-09-270-767-33916	Sequence 33916, A	1203	6	0.8	603	3	US-09-110-279-1684	Sequence 1684, Ap
1131	6	0.8	546	4	US-09-270-767-49133	Sequence 49133, A	1204	6	0.8	605	3	US-09-134-001C-4425	Sequence 4425, Ap
1132	6	0.8	546	4	US-09-949-016-7169	Sequence 7169, Ap	1205	6	0.8	607	4	US-09-248-796A-14958	Sequence 14958, A
1133	6	0.8	550	4	US-09-455-823-7	Sequence 7, Appli	1206	6	0.8	609	4	US-09-248-796A-19292	Sequence 19292, A
1134	6	0.8	556	4	US-09-252-991A-22670	Sequence 22670, A	1207	6	0.8	610	4	US-09-800-170-22	Sequence 22, Appl
1135	6	0.8	556	4	US-09-489-039A-12775	Sequence 12775, A	1208	6	0.8	612	1	US-08-344-695-2	Sequence 2, Appli
1136	6	0.8	556	4	US-09-275-252A-8	Sequence 8, Appli	1209	6	0.8	614	3	US-09-252-991A-31412	Sequence 31412, A
1137	6	0.8	557	4	US-09-252-991A-17260	Sequence 17260, A	1210	6	0.8	616	3	US-08-895-707-2	Sequence 2, Appli
1138	6	0.8	558	2	US-09-256-177A-2	Sequence 2, Appli	1211	6	0.8	621	3	US-09-311-626B-2	Sequence 2, Appli
1139	6	0.8	558	3	US-09-256-797-2	Sequence 2, Appli	1212	6	0.8	621	3	US-09-252-991A-30689	Sequence 30689, A
1140	6	0.8	560	4	US-09-919-016-6458	Sequence 6458, Ap	1213	6	0.8	621	4	US-09-248-796A-14463	Sequence 14463, A
1141	6	0.8	560	4	US-09-912-559-3	Sequence 3, Appli	1214	6	0.8	623	4	US-09-538-092-802	Sequence 802, App
1142	6	0.8	560	4	US-09-912-559-4	Sequence 4, Appli	1215	6	0.8	625	4	US-09-949-016-11531	Sequence 11531, A
1143	6	0.8	562	2	US-08-811-949-43	Sequence 43, Appl	1216	6	0.8	627	4	US-08-851-567B-28	Sequence 28, Appl
1144	6	0.8	562	2	US-08-560-098A-50	Sequence 50, Appl	1217	6	0.8	628	4	US-09-252-991A-24741	Sequence 24741, A
1145	6	0.8	562	2	US-08-883-795A-38	Sequence 38, Appl	1218	6	0.8	628	4	US-09-841-786-5	Sequence 5, Appli
1146	6	0.8	562	4	US-09-703-695A-4	Sequence 4, Appli	1219	6	0.8	630	4	US-09-252-991A-19822	Sequence 19822, A
1147	6	0.8	562	4	US-09-879-792-12	Sequence 12, Appl	1220	6	0.8	630	4	US-08-472-888A-6	Sequence 6, Appli
1148	6	0.8	562	4	US-10-443-701-4	Sequence 4, Appli	1221	6	0.8	632	4	US-09-976-594-41	Sequence 41, Appl
1149	6	0.8	562	6	5185259-3	Patent No. 5185259	1222	6	0.8	632	4	US-09-949-016-6976	Sequence 6976, Ap
1150	6	0.8	562	6	5200340-2	Patent No. 5200340	1223	6	0.8	634	4	US-09-816-248-13	Sequence 13, Appl
1151	6	0.8	562	6	5244676-5	Patent No. 5244676	1224	6	0.8	634	4	US-09-949-016-10571	Sequence 10571, A
1152	6	0.8	562	6	5344773-2	Patent No. 5344773	1225	6	0.8	635	4	US-09-270-767-44609	Sequence 44609, A
1153	6	0.8	562	6	5185259-3	Patent No. 5185259	1226	6	0.8	638	4	US-09-811-469-9	Sequence 9, Appli
1154	6	0.8	562	6	5200340-2	Patent No. 5200340	1227	6	0.8	638	4	US-10-370-659-9	Sequence 9, Appli
1155	6	0.8	562	6	5244676-5	Patent No. 5244676	1228	6	0.8	640	4	US-09-252-991A-20343	Sequence 20343, A
1156	6	0.8	562	6	5344773-2	Patent No. 5344773	1229	6	0.8	641	4	US-09-252-991A-26329	Sequence 26329, A
1157	6	0.8	563	4	US-09-252-991A-28458	Sequence 28458, A	1230	6	0.8	649	4	US-09-252-991A-31187	Sequence 31187, A
1158	6	0.8	563	4	US-09-252-991A-29210	Sequence 29210, A	1231	6	0.8	649	4	US-09-107-532A-5832	Sequence 5832, Ap
1159	6	0.8	563	4	US-09-583-110-4195	Sequence 1195, Ap	1232	6	0.8	650	4	US-09-252-991A-22234	Sequence 22234, A
1160	6	0.8	564	4	US-09-107-532A-5248	Sequence 5248, Ap	1233	6	0.8	652	2	US-08-751-305-2	Sequence 2, Appli
1161	6	0.8	565	4	US-09-248-796A-20098	Sequence 20098, A	1234	6	0.8	653	3	US-09-443-184-50	Sequence 50, Appl
1162	6	0.8	566	4	US-09-543-681A-4544	Sequence 4544, Ap	1235	6	0.8	655	1	US-08-148-910-12	Sequence 12, Appl
1163	6	0.8	569	1	US-07-821-716-2	Sequence 2, Appli	1236	6	0.8	655	1	US-08-448-937A-12	Sequence 12, Appl
1164	6	0.8	569	2	US-08-381-603-2	Sequence 2, Appli	1237	6	0.8	656	4	US-09-252-991A-30630	Sequence 30630, A
1165	6	0.8	569	3	US-08-924-376-2	Sequence 2, Appli	1238	6	0.8	657	4	US-09-949-016-11365	Sequence 11365, A
1166	6	0.8	569	3	US-08-685-212-2	Sequence 2, Appli	1239	6	0.8	657	4	US-09-949-016-11366	Sequence 11366, A
1167	6	0.8	569	3	US-09-173-151A-31	Sequence 31, Appl	1240	6	0.8	657	4	US-09-949-016-11367	Sequence 11367, A
1168	6	0.8	569	4	US-08-466-932A-2	Sequence 2, Appli	1241	6	0.8	657	4	US-09-949-016-11368	Sequence 11368, A
1169	6	0.8	569	4	US-08-406-824A-6	Sequence 6, Appli	1242	6	0.8	659	4	US-09-252-991A-31126	Sequence 31126, A
1170	6	0.8	569	4	US-09-949-016-6000	Sequence 6000, Ap	1243	6	0.8	661	4	US-09-949-016-6157	Sequence 6157, Ap
1171	6	0.8	569	5	PCT-US94-02414-2	Sequence 2, Appli	1244	6	0.8	665	4	US-09-949-016-10776	Sequence 10776, A
1172	6	0.8	569	5	PCT-US96-08899-2	Sequence 2, Appli	1245	6	0.8	666	4	US-09-489-039A-12388	Sequence 12388, A
1173	6	0.8	572	4	US-09-252-991A-23996	Sequence 23996, A	1246	6	0.8	668	4	US-09-930-181-2	Sequence 2, Appli
1174	6	0.8	573	3	US-09-134-001C-4813	Sequence 4813, Ap	1247	6	0.8	669	2	US-07-861-800-2	Sequence 2, Appli
1175	6	0.8	575	1	US-07-683-957B-2	Sequence 2, Appli	1248	6	0.8	670	4	US-09-252-991A-24930	Sequence 24930, A
1176	6	0.8	575	2	US-08-417-495-4	Sequence 4, Appli	1249	6	0.8	673	3	US-09-192-104-2	Sequence 2, Appli
1177	6	0.8	575	2	US-08-284-391B-4	Sequence 4, Appli	1250	6	0.8	673	3	US-09-543-446-2	Sequence 2, Appli
1178	6	0.8	575	3	US-09-218-950-4	Sequence 4, Appli	1251	6	0.8	673	4	US-09-079-955-11	Sequence 11, Appl
1179	6	0.8	575	4	US-08-394-388A-4	Sequence 4, Appli	1252	6	0.8	673	4	US-09-957-189-2	Sequence 2, Appli
1180	6	0.8	575	4	US-09-949-016-11264	Sequence 11264, A	1253	6	0.8	675	4	US-09-252-991A-29650	Sequence 29650, A
1181	6	0.8	575	4	US-09-949-016-11265	Sequence 11265, A	1254	6	0.8	676	4	US-09-134-000C-6050	Sequence 6050, Ap
1182	6	0.8	575	4	US-09-949-016-11266	Sequence 11266, A	1255	6	0.8	677	4	US-09-540-236-3700	Sequence 3700, Ap
1183	6	0.8	575	4	US-09-949-016-11267	Sequence 11267, A	1256	6	0.8	677	4	US-09-949-016-11369	Sequence 11369, A
1184	6	0.8	575	5	PCT-US92-01785-4	Sequence 4, Appli	1257	6	0.8	677	4	US-09-949-016-11370	Sequence 11370, A
1185	6	0.8	575	5	PCT-US95-00454-6	Sequence 4, Appli	1258	6	0.8	677	4	US-09-949-016-11371	Sequence 11371, A
1186	6	0.8	577	4	US-09-107-433-3424	Sequence 3424, Ap	1259	6	0.8	677	4	US-09-949-016-11372	Sequence 11372, A
1187	6	0.8	579	4	US-09-744-852-2	Sequence 2, Appli	1260	6	0.8	678	4	US-09-902-540-16113	Sequence 16113, A
1188	6	0.8	580	4	US-09-328-352-7656	Sequence 7656, Ap	1261	6	0.8	678	4	US-09-252-991A-26693	Sequence 20693, A
1189	6	0.8	583	4	US-09-489-039A-7653	Sequence 7653, Ap	1262	6	0.8	681	4	US-09-248-796A-17097	Sequence 17097, A
1190	6	0.8	587	4	US-09-328-352-8096	Sequence 8096, Ap	1263	6	0.8	682	4	US-09-252-991A-22929	Sequence 22929, A
1191	6	0.8	587	4	US-09-949-016-11501	Sequence 11501, A	1264	6	0.8	683	4	US-09-620-412C-357	Sequence 357, App
1192	6	0.8	588	4	US-09-949-016-8572	Sequence 8572, Ap	1265	6	0.8	683	4	US-09-598-419-357	Sequence 357, App
1193	6	0.8	593	4	US-09-538-092-919	Sequence 919, App	1266	6	0.8	685	2	US-08-878-989-1	Sequence 1, Appli
1194	6	0.8	595	4	US-09-248-796A-14562	Sequence 14562, A	1267	6	0.8	685	3	US-09-136-282-2	Sequence 2, Appli
1195	6	0.8	597	4	US-09-252-991A-17139	Sequence 17139, A	1268	6	0.8	685	3	US-09-272-796-1	Sequence 1, Appli

1269	6	0.8	685	3	US-09-505-744-2	Sequence 2, Appli	1342	770	3	US-08-956-653A-12	Sequence 12, Appli
1270	6	0.8	686	4	US-09-252-991A-26437	Sequence 26437, A	1343	770	3	US-09-526-542-2	Sequence 2, Appli
1271	6	0.8	686	4	US-09-540-236-3611	Sequence 3611, Ap	1344	770	4	US-09-972-800A-6	Sequence 6, Appli
1272	6	0.8	686	4	US-09-270-767-36547	Sequence 36547, A	1345	770	4	US-09-252-991A-25267	Sequence 25267, A
1273	6	0.8	686	4	US-09-270-767-51764	Sequence 51764, A	1346	770	4	US-08-212-185-12	Sequence 12, Appli
1274	6	0.8	687	2	US-08-449-645A-29	Sequence 29, Appl	1347	770	4	US-10-117-087-2	Sequence 2, Appli
1275	6	0.8	687	2	US-08-702-367A-29	Sequence 29, Appl	1348	770	5	PCT-US95-17025-12	Sequence 12, Appli
1276	6	0.8	687	4	US-09-489-039A-9868	Sequence 9868, Ap	1349	771	1	US-08-276-098A-14	Sequence 14, Appli
1277	6	0.8	687	4	US-09-252-991A-16715	Sequence 16715, A	1350	771	1	US-08-781-890-14	Sequence 2, Appli
1278	6	0.8	690	4	US-09-886-319A-36	Sequence 36, Appl	1351	771	4	US-09-214-916A-2	Sequence 4, Appli
1279	6	0.8	696	1	US-08-765-081-5	Sequence 5, Appli	1352	775	4	US-09-214-916A-4	Sequence 4, Appli
1280	6	0.8	696	3	US-09-098-082-5	Sequence 5, Appli	1353	775	4	US-09-252-991A-23591	Sequence 4, Appli
1281	6	0.8	696	5	PCT-US95-06994-5	Sequence 5, Appli	1354	778	2	US-08-906-925-4	Sequence 2, Appli
1282	6	0.8	698	4	US-09-270-767-42292	Sequence 42292, A	1355	778	4	US-10-116-326-2	Sequence 2, Appli
1283	6	0.8	702	3	US-09-068-740A-4	Sequence 4, Appli	1356	778	4	US-10-003-690-2	Sequence 2, Appli
1284	6	0.8	703	4	US-10-116-326-6	Sequence 6, Appli	1357	779	1	US-08-375-134-12	Sequence 12, Appli
1285	6	0.8	703	5	PCT-US95-06994-8	Sequence 8, Appli	1358	779	5	PCT-US95-15263-12	Sequence 12, Appli
1286	6	0.8	704	4	US-09-543-681A-7274	Sequence 7274, Ap	1359	780	1	US-08-188-228-50	Sequence 50, Appli
1287	6	0.8	707	4	US-09-902-540-16063	Sequence 16063, A	1360	780	1	US-08-332-643-44	Sequence 44, Appli
1288	6	0.8	713	3	US-08-872-855-5	Sequence 5, Appli	1361	780	1	US-08-332-638-50	Sequence 50, Appli
1289	6	0.8	714	4	US-09-252-991A-31209	Sequence 31209, A	1362	782	4	US-09-270-767-46675	Sequence 46675, A
1290	6	0.8	718	5	PCT-US95-06994-6	Sequence 6, Appli	1363	784	3	US-09-004-838-12	Sequence 12, Appli
1291	6	0.8	720	3	US-09-257-799-48	Sequence 48, Appl	1364	791	4	US-09-252-991A-23201	Sequence 2, Appli
1292	6	0.8	720	3	US-08-920-919A-48	Sequence 48, Appl	1365	802	4	US-09-634-955B-2	Sequence 2, Appli
1293	6	0.8	723	3	US-09-068-740A-9	Sequence 9, Appli	1366	802	4	US-09-816-760-2	Sequence 2, Appli
1294	6	0.8	723	4	US-09-423-753-27	Sequence 27, Appl	1367	802	4	US-09-838-561-2	Sequence 2, Appli
1295	6	0.8	723	4	US-09-976-594-503	Sequence 503, App	1368	803	4	US-09-252-991A-28469	Sequence 28469, A
1296	6	0.8	723	4	US-09-641-612-6	Sequence 6, Appli	1369	805	4	US-09-252-991A-32752	Sequence 32752, A
1297	6	0.8	724	4	US-09-562-737-22	Sequence 22, Appl	1370	806	1	US-08-270-076A-11	Sequence 11, Appli
1298	6	0.8	728	3	US-08-981-392-2	Sequence 2, Appli	1371	808	4	US-09-543-681A-4995	Sequence 4995, Ap
1299	6	0.8	728	3	US-09-908-322-2	Sequence 2, Appli	1372	810	4	US-09-198-452A-20	Sequence 20, Appli
1300	6	0.8	729	3	US-08-872-855-8	Sequence 8, Appli	1373	810	4	US-09-198-452A-1128	Sequence 1128, Ap
1301	6	0.8	732	4	US-10-160-748-6	Sequence 6, Appli	1374	812	4	US-09-248-796A-20875	Sequence 20875, A
1302	6	0.8	734	4	US-09-336-115C-4	Sequence 4, Appli	1375	819	4	US-09-438-185A-1055	Sequence 1055, Ap
1303	6	0.8	734	4	US-09-438-185A-125	Sequence 125, App	1376	821	4	US-09-252-991A-30347	Sequence 30347, A
1304	6	0.8	740	4	US-09-489-039A-11157	Sequence 11157, A	1377	822	4	US-09-248-796A-14728	Sequence 14728, A
1305	6	0.8	744	4	US-09-252-991A-19290	Sequence 19290, A	1378	823	4	US-09-252-991A-17457	Sequence 17457, A
1306	6	0.8	744	4	US-09-252-991A-30945	Sequence 30945, A	1379	824	4	US-09-252-991A-17457	Sequence 17457, A
1307	6	0.8	749	4	US-09-562-737-94	Sequence 94, Appl	1380	837	3	US-09-270-767-45676	Sequence 45676, A
1308	6	0.8	753	4	US-09-252-991A-17987	Sequence 17987, A	1381	841	3	US-09-564-805-228	Sequence 228, App
1309	6	0.8	756	2	US-08-887-518-4	Sequence 4, Appli	1382	843	4	US-09-252-991A-32609	Sequence 32609, A
1310	6	0.8	756	2	US-08-023-321-4	Sequence 2, Appli	1383	844	4	US-09-902-540-12865	Sequence 12865, A
1311	6	0.8	756	2	US-08-890-853-2	Sequence 2, Appli	1384	846	1	US-08-149-103-3	Sequence 3, Appli
1312	6	0.8	756	2	US-09-032-475-4	Sequence 4, Appli	1385	846	1	US-08-451-883-3	Sequence 3, Appli
1313	6	0.8	756	2	US-09-099-125A-2	Sequence 2, Appli	1386	846	1	US-08-451-883-4	Sequence 4, Appli
1314	6	0.8	756	2	US-09-099-124A-2	Sequence 2, Appli	1387	846	1	US-08-369-796-2	Sequence 2, Appli
1315	6	0.8	756	3	US-09-032-476-2	Sequence 2, Appli	1388	851	1	US-08-852-091-2	Sequence 2, Appli
1316	6	0.8	756	3	US-08-890-854-2	Sequence 2, Appli	1389	851	2	US-08-830-754-2	Sequence 2, Appli
1317	6	0.8	756	3	US-09-023-324-2	Sequence 2, Appli	1390	851	3	US-08-856-652-2	Sequence 2, Appli
1318	6	0.8	756	3	US-09-168-629-15	Sequence 15, Appl	1391	851	3	US-08-956-869-2	Sequence 2, Appli
1319	6	0.8	756	3	US-08-910-820-9	Sequence 9, Appli	1392	851	3	US-09-012-710-2	Sequence 2, Appli
1320	6	0.8	756	4	US-09-109-986-2	Sequence 2, Appli	1393	851	3	US-09-087-465-4	Sequence 4, Appli
1321	6	0.8	756	4	US-09-844-908-9	Sequence 9, Appli	1394	851	3	US-09-087-465-4	Sequence 4, Appli
1322	6	0.8	756	4	US-09-868-758-4	Sequence 4, Appli	1395	851	3	US-09-364-970-2	Sequence 2, Appli
1323	6	0.8	756	4	US-09-796-872-15	Sequence 15, Appl	1396	851	3	US-09-556-273-2	Sequence 2, Appli
1324	6	0.8	760	4	US-09-489-039A-8055	Sequence 8055, Ap	1397	851	3	US-08-956-653A-2	Sequence 2, Appli
1325	6	0.8	765	4	US-09-724-653-2	Sequence 2, Appli	1398	851	4	US-09-972-800A-4	Sequence 4, Appli
1326	6	0.8	766	4	US-09-724-653-14	Sequence 14, Appl	1399	851	4	US-08-212-185-2	Sequence 2, Appli
1327	6	0.8	766	4	US-09-724-653-15	Sequence 15, Appl	1400	851	5	PCT-US95-17025-2	Sequence 2, Appli
1328	6	0.8	770	1	US-08-369-796-12	Sequence 12, Appl	1401	851	5	US-08-276-099A-13	Sequence 13, Appli
1329	6	0.8	770	1	US-08-416-581B-1	Sequence 1, Appli	1402	852	1	US-08-781-890-13	Sequence 2, Appli
1330	6	0.8	770	1	US-08-416-581B-5	Sequence 5, Appli	1403	852	1	US-09-483-253-2	Sequence 2, Appli
1331	6	0.8	770	1	US-08-416-581B-9	Sequence 9, Appli	1404	859	3	US-09-543-681A-6315	Sequence 6315, Ap
1332	6	0.8	770	2	US-08-852-091-12	Sequence 12, Appl	1405	862	4	US-09-328-352-6730	Sequence 2, Appli
1333	6	0.8	770	2	US-08-820-754-12	Sequence 12, Appl	1406	863	4	US-08-620-694A-2	Sequence 2, Appli
1334	6	0.8	770	3	US-08-956-652-12	Sequence 12, Appl	1407	864	3	US-09-022-255-2	Sequence 2, Appli
1335	6	0.8	770	3	US-08-956-869-12	Sequence 12, Appl	1408	864	3	US-09-022-255-2	Sequence 2, Appli
1336	6	0.8	770	3	US-08-956-869-12	Sequence 12, Appl	1409	864	3	US-08-978-773-2	Sequence 2, Appli
1337	6	0.8	770	3	US-08-948-547-12	Sequence 18, Appl	1410	864	3	US-09-022-253-2	Sequence 2, Appli
1338	6	0.8	770	3	US-09-087-465-6	Sequence 6, Appli	1411	864	3	US-09-022-253-2	Sequence 2, Appli
1339	6	0.8	770	3	US-09-364-970-3	Sequence 3, Appli	1412	864	3	US-09-022-257-2	Sequence 2, Appli
1340	6	0.8	770	3	US-09-364-970-5	Sequence 5, Appli	1413	864	3	US-09-022-257-2	Sequence 2, Appli
1341	6	0.8	770	3	US-09-556-273-8	Sequence 8, Appli	1414	864	3		


```
1415 6 0.8 864 4 US-09-549-679-2 Sequence 2, Appli
1416 6 0.8 864 4 US-09-248-796A-20612 Sequence 20612, A
1417 6 0.8 865 4 US-09-248-796A-17692 Sequence 17692, A
1418 6 0.8 873 1 US-08-393-734-2 Sequence 2, Appli
1419 6 0.8 873 3 US-08-894-489-2 Sequence 2, Appli
1420 6 0.8 874 3 US-09-369-364A-15 Sequence 15, Appli
1421 6 0.8 875 4 US-09-489-039A-10917 Sequence 10917, A
1422 6 0.8 888 4 US-09-697-022-4 Sequence 4, Appli
1423 6 0.8 896 4 US-09-252-991A-19758 Sequence 19758, A
1424 6 0.8 898 4 US-09-248-796A-15853 Sequence 15853, A
1425 6 0.8 899 4 US-09-538-092-27 Sequence 27, Appli
1426 6 0.8 900 4 US-09-252-991A-25011 Sequence 25011, A
1427 6 0.8 901 4 US-09-248-796A-14747 Sequence 14747, A
1428 6 0.8 901 4 US-09-538-092-115 Sequence 115, App
1429 6 0.8 903 1 US-08-021-601-12 Sequence 12, Appli
1430 6 0.8 903 1 US-08-082-849B-12 Sequence 12, Appli
1431 6 0.8 903 5 PCT-US94-01624-12 Sequence 12, Appli
1432 6 0.8 904 4 US-09-949-016-9528 Sequence 9528, Ap
1433 6 0.8 905 3 US-09-074-658-70 Sequence 70, Appli
1434 6 0.8 905 4 US-09-248-796A-16333 Sequence 16333, A
1435 6 0.8 911 4 US-09-489-039A-13537 Sequence 13537, A
1436 6 0.8 913 4 US-09-134-000C-6040 Sequence 6040, Ap
1437 6 0.8 920 4 US-09-919-039-76 Sequence 76, Appli
1438 6 0.8 920 4 US-09-248-796A-17529 Sequence 17529, A
1439 6 0.8 921 1 US-07-872-644-39 Sequence 39, Appli
1440 6 0.8 921 1 US-08-297-494-39 Sequence 39, Appli
1441 6 0.8 921 1 US-08-297-510-39 Sequence 39, Appli
1442 6 0.8 921 1 US-08-479-532-39 Sequence 39, Appli
1443 6 0.8 921 1 US-08-455-526-39 Sequence 39, Appli
1444 6 0.8 921 1 US-08-455-525-39 Sequence 39, Appli
1445 6 0.8 921 3 US-09-139-491-39 Sequence 39, Appli
1446 6 0.8 921 3 US-09-754-250-5 Sequence 5, Appli
1447 6 0.8 921 4 US-09-439-711C-4 Sequence 4, Appli
1448 6 0.8 921 4 US-09-883-825-39 Sequence 39, Appli
1449 6 0.8 921 5 PCT-US92-03222-39 Sequence 39, Appli
1450 6 0.8 922 4 US-09-116-473-4 Sequence 4, Appli
1451 6 0.8 923 3 US-08-936-135-6 Sequence 6, Appli
1452 6 0.8 923 4 US-09-439-711C-2 Sequence 2, Appli
1453 6 0.8 923 4 US-09-439-711C-6 Sequence 6, Appli
1454 6 0.8 923 4 US-09-583-638-2 Sequence 2, Appli
1455 6 0.8 930 4 US-09-198-452A-470 Sequence 470, App
1456 6 0.8 934 4 US-09-949-016-8012 Sequence 8012, Ap
1457 6 0.8 934 4 US-09-949-016-8013 Sequence 8013, Ap
1458 6 0.8 938 4 US-09-438-185A-448 Sequence 448, App
1459 6 0.8 939 4 US-09-134-000C-5584 Sequence 5584, Ap
1460 6 0.8 941 4 US-09-390-134B-31 Sequence 31, Appli
1461 6 0.8 941 4 US-09-719-085A-2 Sequence 2, Appli
1462 6 0.8 942 4 US-08-685-852-3 Sequence 3, Appli
1463 6 0.8 943 2 US-08-469-537A-107 Sequence 107, App
1464 6 0.8 945 4 US-09-252-991A-30699 Sequence 30699, A
1465 6 0.8 946 4 US-09-538-092-1230 Sequence 1230, Ap
1466 6 0.8 946 4 US-09-949-016-6105 Sequence 6105, Ap
1467 6 0.8 948 4 US-09-556-877-194 Sequence 194, App
1468 6 0.8 948 4 US-09-620-412C-194 Sequence 194, App
1469 6 0.8 948 4 US-09-598-419-194 Sequence 194, App
1470 6 0.8 949 4 US-09-902-540-15712 Sequence 15712, A
1471 6 0.8 957 4 US-09-107-532A-4021 Sequence 4021, Ap
1472 6 0.8 960 4 US-09-949-016-10492 Sequence 10492, A
1473 6 0.8 961 4 US-09-328-352-4182 Sequence 4182, Ap
1474 6 0.8 968 4 US-09-107-532A-5970 Sequence 5970, Ap
1475 6 0.8 973 4 US-09-392-714-24 Sequence 24, Appli
1476 6 0.8 976 3 US-09-104-324B-4 Sequence 4, Appli
1477 6 0.8 976 4 US-09-538-092-1339 Sequence 1339, Ap
1478 6 0.8 982 4 US-09-556-877-176 Sequence 176, App
1479 6 0.8 982 4 US-09-620-412C-176 Sequence 176, App
1480 6 0.8 982 4 US-09-598-419-176 Sequence 176, App
1481 6 0.8 984 4 US-09-612-402B-43 Sequence 43, Appli
1482 6 0.8 987 4 US-09-252-991A-27483 Sequence 27483, A
1483 6 0.8 989 4 US-09-540-236-2137 Sequence 2137, Ap
1484 6 0.8 990 4 US-09-252-991A-22792 Sequence 22792, A
1485 6 0.8 994 3 US-08-699-103B-3 Sequence 3, Appli
1486 6 0.8 994 3 US-09-229-059-3 Sequence 3, Appli
1487 6 0.8 994 4 US-09-628-133-3 Sequence 3, Appli
```

```
1488 6 0.8 995 4 US-08-747-562-15 Sequence 15, Appli
1489 6 0.8 996 4 US-10-101-464A-889 Sequence 889, App
1490 6 0.8 996 4 US-10-101-464A-933 Sequence 933, App
1491 6 0.8 998 4 US-10-101-464A-914 Sequence 914, App
1492 6 0.8 1006 4 US-09-556-877-190 Sequence 190, App
1493 6 0.8 1006 4 US-09-620-412C-190 Sequence 190, App
1494 6 0.8 1006 4 US-09-598-419-190 Sequence 190, App
1495 6 0.8 1012 4 US-09-612-402B-2 Sequence 2, Appli
1496 6 0.8 1013 2 US-08-866-650-3 Sequence 3, Appli
1497 6 0.8 1013 2 US-09-021-287-3 Sequence 3, Appli
1498 6 0.8 1013 3 US-09-240-473-3 Sequence 3, Appli
1499 6 0.8 1013 4 US-09-612-402B-15 Sequence 15, Appli
1500 6 0.8 1013 4 US-09-612-402B-16 Sequence 16, Appli
```

ALIGNMENTS

RESULT 1

```
US-10-067-422-9
; Sequence 9, Application US/10067422
; Patent No. 6743613
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, an
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: FT004P1
; CURRENT APPLICATION NUMBER: US/10/067,422
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/685,899
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: PCT/US00/09028
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/152,933
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/147,020
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/131,672
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/130,693
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 9
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-422-9
```

```
Query Match 49.3%; Score 355; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 LEERNCSDPGPNVQKITGGFGLNGRHAQITGVVSPFCNNNSYVLSGNEKRTCCQNGE 334
Db 125 LEERNCSDPGPNVQKITGGFGLNGRHAQITGVVSPFCNNNSYVLSGNEKRTCCQNGE 184
QY 335 WSGKQPTICACREPKISDLVRRRVLPMQVSRTPHLQLYSAAFSKOKLSQAPTCKPAL 394
Db 185 WSGKQPTICACREPKISDLVRRRVLPMQVSRTPHLQLYSAAFSKOKLSQAPTCKPAL 244
QY 395 PFQDLPMGVOHLLTQYECISPFYRRRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITA 454
Db 245 PFQDLPMGVOHLLTQYECISPFYRRRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITA 304
QY 455 PTKQGLRWPMQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNRVTVVAAHCVTLGKVTM 514
Db 305 PTKQGLRWPMQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNRVTVVAAHCVTLGKVTM 364
QY 515 IKTADLVVLGKGYRDRDDREKTIQSIQISAIILHPNYDPIILDADITAILKLDKARIST 574
Db 365 IKTADLVVLGKGYRDRDDREKTIQSIQISAIILHPNYDPIILDADITAILKLDKARIST 424
```

QY 575 RVQPCIAASRDLSFQESHITVAGWNVLDVRSFGFKNDTLRSVGWSVDSLL 629
DB 425 RVQPCIAASRDLSFQESHITVAGWNVLDVRSFGFKNDTLRSVGWSVDSLL 479

RESULT 2
US-10-067-422-17
; Sequence 17, Application US/10067422
; Patent No. 6743613
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT004PI
; CURRENT APPLICATION NUMBER: US/10/067,422
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/685,899
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: PCT/US00/09028
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/152,933
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/147,020
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/131,672
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/130,693
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-422-17

Query Match 2.2%; Score 16; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 LEERNCSDFGPGVNGY 290
DB 31 LEERNCSDFGPGVNGY 46

RESULT 3
US-10-067-422-16
; Sequence 16, Application US/10067422
; Patent No. 6743613
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT004PI
; CURRENT APPLICATION NUMBER: US/10/067,422
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/685,899
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: PCT/US00/09028
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/152,933
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/147,020
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/131,672
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/130,693
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-067-422-16

Query Match 1.7%; Score 12; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 CACLAGYTGRC 271
DB 1 CACLAGYTGRC 12

RESULT 4
US-09-374-135-4
; Sequence 4, Application US/09374135
; Patent No. 6277972
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel E.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saifran, Douglas C.
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: BPC-1: A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND SECRETED BY PROSTATE AND BLADDER CANCER CELLS
; FILE REFERENCE: 1703-017 US1
; CURRENT APPLICATION NUMBER: US/09/374,135
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/095,982
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Mouse
US-09-374-135-4

Query Match 1.2%; Score 9; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
DB 47 YDYVEVRDG 55

RESULT 5
US-09-341-461-28
; Sequence 28, Application US/09341461
; Patent No. 6586389
; GENERAL INFORMATION:
; APPLICANT: Hammond, Timothy G.
; APPLICANT: Verroust, Pierre J.
; TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin and Uses Thereof
; FILE REFERENCE: D6148
; CURRENT APPLICATION NUMBER: US/09/341,461
; CURRENT FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: PCT/US99/01259
; PRIOR FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 28
; LENGTH: 110
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: amino acid sequence of Bmp-1 CUB1 domain
US-09-341-461-28

Query Match 1.2%; Score 9; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
| | | | |
Db 56 YDYVEVRDG 64

RESULT 6

US-09-438-046-20
; Sequence 20, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 20
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-20

Query Match 1.2%; Score 9; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
| | | | |
Db 56 YDYVEVRDG 64

RESULT 7

US-08-872-757-2
; Sequence 2, Application US/08872757
; Patent No. 6258584
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Hojima, Yoshio
; APPLICANT: Li, Shi-Wu
; APPLICANT: Sieron, Aleksander
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
; TITLE OF INVENTION: PROCESSES, METHODS AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/850,048A
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,187
; FILING DATE: 1996-03-01
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-028-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,757
; FILING DATE: 10-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,187
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-028-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-872-757-2
Query Match 1.2%; Score 9; DB 3; Length 730;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 179 YDYVEVRDG 187
| | | | |
Db 377 YDYVEVRDG 385
RESULT 8
US-09-850-048A-2
; Sequence 2, Application US/09850048A
; Patent No. 6562613
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Hojima, Yoshio
; APPLICANT: Li, Shi-Wu
; APPLICANT: Sieron, Aleksander
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
; TITLE OF INVENTION: PROCESSES, METHODS AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/850,048A
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,187
; FILING DATE: 1996-03-01
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-028-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE

```
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 730 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-850-048A-2

Query Match          1.2%; Score 9; DB 4; Length 730;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      179 YDYVEVRDG 187
Db      377 YDYVEVRDG 385

RESULT 9
US-08-572-225-1
; Sequence 1, Application US/08572225
; Patent No. 5807981
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Hojima, Yoshio
; APPLICANT: Li, Shi-Wu
; APPLICANT: Sieron, Aleksander
; APPLICANT: Brenner, Mitch
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND ITS USE FOR
; TITLE OF INVENTION: DRUG DEVELOPMENT FOR THE TREATMENT OF DISEASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/572,225
; APPLICATION NUMBER: US/08/572,225
; FILING DATE: 13-DEC-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 788 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: unknown
;   TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-572-225-1

Query Match          1.2%; Score 9; DB 1; Length 788;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      179 YDYVEVRDG 187
Db      179 YDYVEVRDG 187
```

```
RESULT 10
US-09-285-385C-19
; Sequence 19, Application US/09285385C
; Patent No. 6579702
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S.
; APPLICANT: Scott, Ian C.
; APPLICANT: Thomas, Christina L.
; TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN
; FILE REFERENCE: 960296.96111
; CURRENT APPLICATION NUMBER: US/09/285,385C
; CURRENT FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/111873
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 60/080550
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 986
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-285-385C-19

Query Match          1.2%; Score 9; DB 4; Length 986;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      179 YDYVEVRDG 187
Db      377 YDYVEVRDG 385

RESULT 11
US-09-949-016-6690
; Sequence 6690, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6690
; LENGTH: 986
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6690

Query Match          1.2%; Score 9; DB 4; Length 986;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      179 YDYVEVRDG 187
Db      377 YDYVEVRDG 385

RESULT 12
US-09-285-385C-2
; Sequence 2, Application US/09285385C
; Patent No. 6579702
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S.
```

; APPLICANT: Scott, Ian C.
; APPLICANT: Thomas, Christina L.
; TITLE OF INVENTION: MAMMALIAN TOLLID-LIKE GENE AND PROTEIN
; FILE REFERENCE: 960296.96111
; CURRENT APPLICATION NUMBER: US/09/285.385C
; CURRENT FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/111873
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 60/080550
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1015
; TYPE: PRT
; ORGANISM: human
US-09-285-385C-2

Query Match 1.2%; Score 9; DB 4; Length 1015;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDVEVRDG 187
Db 406 YDVEVRDG 414

RESULT 13
US-09-188-930-342
; Sequence 342, Application US/09188930A
; Patent No. 6150502

; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Mouse
US-09-188-930-342

Query Match 1.1%; Score 8; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 GYTGORCE 272
Db 36 GYTGORCE 43

RESULT 14
US-09-312-283C-342
; Sequence 342, Application US/09312283C
; Patent No. 6573095

; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2

; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 342
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-342

Query Match 1.1%; Score 8; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 GYTGORCE 272
Db 36 GYTGORCE 43

RESULT 15

US-09-472-087-99
; Sequence 99, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-99

Query Match 1.1%; Score 8; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 QSIGSSLH 215
Db 27 QSIGSSLH 34

Search completed: May 8, 2005, 16:11:18
Job time : 35 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 8, 2005, 16:11:24 ; Search time 42 Seconds
(without alignments)
5718.837 Million cell updates/sec

Perfect score: 720

Sequence: 1 MELGCWTQLGLTFIQLLLIS.....LSTAFKVLFPKDIERNMK 720

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1428581 seqs, 333598853 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : Published Applications AA:*

- 1: /cgn2_5/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
27	720	100.0	720	10	US-09-997-428-231
562	720	100.0	720	14	US-10-174-587-170
626	720	100.0	720	14	US-10-063-742-38
741	720	100.0	720	17	US-10-972-317-38
742	556	77.2	567	14	US-10-004-551-2
743	518	71.9	720	14	US-10-004-551-4
744	518	71.9	720	14	US-10-098-871-26
745	446	61.9	737	16	US-10-408-765A-1796
746	375	52.1	649	15	US-10-274-639-17
747	375	52.1	649	15	US-10-333-574-17
748	355	49.3	570	13	US-10-067-422-9
749	277	38.5	455	11	US-09-833-245-1401
750	276	38.3	323	11	US-09-833-243-1402
751	16	2.2	46	13	US-10-067-422-17

752	12	1.7	12	13	US-10-067-422-16	Sequence 16, Appl
753	9	1.2	101	9	US-09-887-593-4	Sequence 4, Appl
754	9	1.2	113	9	US-09-852-209A-20	Sequence 20, Appl
755	9	1.2	113	13	US-10-086-623-20	Sequence 20, Appl
756	9	1.2	113	14	US-10-260-539-20	Sequence 20, Appl
757	9	1.2	113	14	US-10-131-600-20	Sequence 20, Appl
758	9	1.2	113	15	US-10-303-997B-20	Sequence 20, Appl
759	9	1.2	113	15	US-10-439-337A-20	Sequence 20, Appl
760	9	1.2	730	9	US-09-850-048A-2	Sequence 2, Appl
761	9	1.2	823	15	US-10-016-248-98	Sequence 98, Appl
762	9	1.2	823	15	US-10-112-944-309	Sequence 309, Appl
763	9	1.2	870	15	US-10-016-248-42	Sequence 42, Appl
764	9	1.2	986	9	US-09-285-385C-19	Sequence 19, Appl
765	9	1.2	986	10	US-09-918-715-242	Sequence 242, Appl
766	9	1.2	986	15	US-10-366-345-33	Sequence 33, Appl
767	9	1.2	992	15	US-10-016-248-40	Sequence 40, Appl
768	9	1.2	1015	9	US-09-285-385C-2	Sequence 2, Appl
769	9	1.2	1015	15	US-10-016-248-97	Sequence 97, Appl
770	9	1.2	1579	16	US-10-437-963-196551	Sequence 196551, Appl
771	8	1.1	11	15	US-10-443-466A-8	Sequence 8, Appl
772	8	1.1	11	15	US-10-656-769-71	Sequence 71, Appl
773	8	1.1	51	10	US-09-866-050A-342	Sequence 342, Appl
774	8	1.1	88	9	US-09-905-243-30	Sequence 30, Appl
775	8	1.1	95	14	US-10-194-975-91	Sequence 91, Appl
776	8	1.1	95	14	US-10-194-975-92	Sequence 92, Appl
777	8	1.1	95	15	US-10-308-817-38	Sequence 38, Appl
778	8	1.1	95	15	US-10-308-817-39	Sequence 39, Appl
779	8	1.1	95	15	US-10-453-698-38	Sequence 38, Appl
780	8	1.1	95	15	US-10-453-698-39	Sequence 39, Appl
781	8	1.1	95	16	US-10-379-392-105	Sequence 105, Appl
782	8	1.1	95	16	US-10-379-392-106	Sequence 106, Appl
783	8	1.1	96	14	US-10-153-382-34	Sequence 34, Appl
784	8	1.1	108	17	US-10-805-177-67	Sequence 67, Appl
785	8	1.1	108	17	US-10-805-177-67	Sequence 71, Appl
786	8	1.1	124	9	US-09-764-877-1346	Sequence 1346, Ap
787	8	1.1	124	15	US-10-242-515-1346	Sequence 1346, Ap
788	8	1.1	126	15	US-10-362-082-2	Sequence 2, Appl
789	8	1.1	126	15	US-10-656-769-18	Sequence 18, Appl
790	8	1.1	128	15	US-10-443-466A-2	Sequence 2, Appl
791	8	1.1	128	15	US-10-443-466A-41	Sequence 41, Appl
792	8	1.1	128	15	US-10-443-466A-43	Sequence 43, Appl
793	8	1.1	128	15	US-10-443-466A-72	Sequence 72, Appl
794	8	1.1	128	15	US-10-443-466A-74	Sequence 74, Appl
795	8	1.1	128	15	US-10-443-466A-76	Sequence 76, Appl
796	8	1.1	128	15	US-10-443-466A-78	Sequence 78, Appl
797	8	1.1	151	16	US-10-437-963-107837	Sequence 107837, Appl
798	8	1.1	152	10	US-09-866-050A-187	Sequence 187, Appl
799	8	1.1	152	15	US-10-099-322-57	Sequence 57, Appl
800	8	1.1	152	15	US-10-044-564-57	Sequence 57, Appl
801	8	1.1	155	14	US-10-153-382-35	Sequence 35, Appl
802	8	1.1	157	17	US-10-644-277-36	Sequence 36, Appl
803	8	1.1	233	15	US-10-656-769-40	Sequence 40, Appl
804	8	1.1	273	14	US-10-148-671-25	Sequence 25, Appl
805	8	1.1	302	15	US-10-369-493-6856	Sequence 6856, Ap
806	8	1.1	411	16	US-10-437-963-111499	Sequence 111499, A
807	8	1.1	425	15	US-10-425-114-68970	Sequence 68970, A
808	8	1.1	481	15	US-10-425-114-72031	Sequence 72031, A
809	8	1.1	596	15	US-10-282-122A-50055	Sequence 50055, A
810	8	1.1	675	16	US-10-437-963-166405	Sequence 166405, A
811	8	1.1	807	14	US-10-132-350-42	Sequence 42, Appl
812	8	1.1	807	14	US-10-132-350-44	Sequence 44, Appl
813	8	1.1	967	16	US-10-437-963-118384	Sequence 118384, A
814	8	1.1	1019	14	US-10-183-992-4	Sequence 4, Appl
815	8	1.1	1019	14	US-10-183-992-8	Sequence 8, Appl
816	8	1.1	1019	16	US-10-638-125-4	Sequence 4, Appl
817	8	1.1	1068	16	US-10-437-963-195653	Sequence 195653, A
818	8	1.1	1083	14	US-10-183-992-6	Sequence 6, Appl
819	8	1.1	1083	16	US-10-638-125-2	Sequence 2, Appl
820	8	1.1	1316	15	US-10-028-248A-48	Sequence 48, Appl
821	8	1.1	1316	15	US-10-107-782-48	Sequence 48, Appl
822	8	1.1	3557	15	US-10-295-027-430	Sequence 430, Appl
823	8	1.1	3557	15	US-10-295-027-1297	Sequence 1297, Ap
824	8	1.1	3571	9	US-09-911-842-2	Sequence 2, Appl

825	8	1.1	3571	13	US-10-150-821-2	Sequence 2, Appli	898	7	1.0	227	15	US-10-282-122A-68048	Sequence 68048, A
826	8	1.1	3571	16	US-10-603-283-2	Sequence 2, Appli	899	7	1.0	227	16	US-10-437-963-141622	Sequence 141622, A
827	7	1.0	11	9	US-09-192-854-170	Sequence 170, App	900	7	1.0	228	15	US-10-282-122A-69437	Sequence 69437, A
828	7	1.0	11	9	US-09-968-561A-298	Sequence 298, App	901	7	1.0	230	16	US-10-437-963-178045	Sequence 178045, A
829	7	1.0	11	10	US-09-968-744A-298	Sequence 298, App	902	7	1.0	231	15	US-10-282-122A-54986	Sequence 54986, A
830	7	1.0	11	11	US-09-968-561A-298	Sequence 298, App	903	7	1.0	232	9	US-09-815-242-5151	Sequence 5151, Ap
831	7	1.0	46	15	US-10-424-599-272809	Sequence 272809, A	904	7	1.0	232	15	US-10-282-122A-43430	Sequence 43430, A
832	7	1.0	47	16	US-10-437-963-141351	Sequence 141351, A	905	7	1.0	239	15	US-10-282-122A-77383	Sequence 77383, A
833	7	1.0	54	9	US-09-738-626-5214	Sequence 5214, Ap	906	7	1.0	244	16	US-10-437-963-153664	Sequence 153664, A
834	7	1.0	57	9	US-09-864-761-45299	Sequence 45299, A	907	7	1.0	248	15	US-10-424-599-270715	Sequence 270715, A
835	7	1.0	66	15	US-10-424-599-186581	Sequence 186581, A	908	7	1.0	250	10	US-09-898-837A-45	Sequence 45, Appl
836	7	1.0	69	15	US-10-424-599-223128	Sequence 223128, A	909	7	1.0	251	10	US-09-898-837A-41	Sequence 41, Appl
837	7	1.0	72	16	US-10-437-963-152234	Sequence 152234, A	910	7	1.0	254	16	US-10-437-963-178860	Sequence 178860, A
838	7	1.0	72	16	US-10-437-963-169418	Sequence 169418, A	911	7	1.0	259	11	US-09-815-242-13845	Sequence 13845, A
839	7	1.0	73	16	US-10-437-963-170815	Sequence 170815, A	912	7	1.0	259	15	US-10-165-442-2	Sequence 2, Appli
840	7	1.0	74	11	US-09-864-408A-8324	Sequence 8324, Ap	913	7	1.0	259	15	US-10-165-442-4	Sequence 4, Appli
841	7	1.0	75	15	US-10-424-599-148860	Sequence 148860, A	914	7	1.0	259	16	US-10-699-393-2	Sequence 2, Appli
842	7	1.0	79	11	US-09-833-245-1400	Sequence 1400, Ap	915	7	1.0	259	16	US-10-699-393-4	Sequence 4, Appli
843	7	1.0	85	15	US-10-424-599-275249	Sequence 275249, A	916	7	1.0	259	16	US-10-692-365-155	Sequence 5, Appli
844	7	1.0	85	16	US-10-767-701-59878	Sequence 59878, A	917	7	1.0	259	16	US-10-872-198-5	Sequence 5, Appli
845	7	1.0	105	14	US-10-006-869-18	Sequence 18, Appl	918	7	1.0	259	17	US-10-872-197A-5	Sequence 30, Appl
846	7	1.0	105	15	US-10-395-032-18	Sequence 18, Appl	919	7	1.0	263	16	US-10-822-613-30	Sequence 34, Appl
847	7	1.0	108	9	US-09-800-095A-86	Sequence 86, Appl	920	7	1.0	263	16	US-10-822-613-34	Sequence 36, Appl
848	7	1.0	108	15	US-10-424-599-253529	Sequence 253529, A	921	7	1.0	265	9	US-09-791-171-16	Sequence 16, Appl
849	7	1.0	115	15	US-10-425-114-41281	Sequence 41281, A	922	7	1.0	265	10	US-09-804-980-16	Sequence 16, Appl
850	7	1.0	115	15	US-10-424-599-218597	Sequence 218597, A	923	7	1.0	265	16	US-10-620-246-16	Sequence 16, Appl
851	7	1.0	124	15	US-10-425-114-60253	Sequence 60253, A	924	7	1.0	267	16	US-10-437-963-109889	Sequence 109889, A
852	7	1.0	125	15	US-10-424-599-147528	Sequence 147528, A	925	7	1.0	271	16	US-10-408-765A-1200	Sequence 1200, Ap
853	7	1.0	130	16	US-10-437-963-129837	Sequence 129837, A	926	7	1.0	285	16	US-10-437-963-134290	Sequence 134290, A
854	7	1.0	133	16	US-10-437-963-129837	Sequence 129837, A	927	7	1.0	285	16	US-10-767-701-35097	Sequence 35097, A
855	7	1.0	134	15	US-10-437-963-151149	Sequence 151149, A	928	7	1.0	292	16	US-10-437-963-161568	Sequence 161568, A
856	7	1.0	134	15	US-10-424-599-274398	Sequence 274398, A	929	7	1.0	295	15	US-10-165-442-1	Sequence 1, Appli
857	7	1.0	136	15	US-10-424-599-274378	Sequence 274378, A	930	7	1.0	295	15	US-10-165-442-3	Sequence 3, Appli
858	7	1.0	142	15	US-10-424-599-274613	Sequence 274613, A	931	7	1.0	295	16	US-10-699-393-1	Sequence 1, Appli
859	7	1.0	144	16	US-10-437-963-102869	Sequence 102869, A	932	7	1.0	295	16	US-10-699-393-3	Sequence 3, Appli
860	7	1.0	146	15	US-10-424-599-242899	Sequence 242899, A	933	7	1.0	306	16	US-10-437-963-182869	Sequence 182869, A
861	7	1.0	149	15	US-10-424-599-212242	Sequence 212242, A	934	7	1.0	308	10	US-09-510-332-155	Sequence 155, App
862	7	1.0	151	16	US-10-437-963-142354	Sequence 142354, A	935	7	1.0	308	17	US-10-962-365-135	Sequence 135, App
863	7	1.0	156	13	US-10-053-200-2	Sequence 2, Appli	936	7	1.0	314	14	US-10-261-845-2	Sequence 2, Appli
864	7	1.0	157	15	US-10-424-599-199827	Sequence 199827, A	937	7	1.0	324	15	US-10-264-049-2827	Sequence 2827, Ap
865	7	1.0	157	15	US-10-425-114-49725	Sequence 49725, A	938	7	1.0	330	15	US-10-369-493-15829	Sequence 15829, A
866	7	1.0	164	15	US-10-437-963-203623	Sequence 203623, A	939	7	1.0	330	15	US-10-369-493-16209	Sequence 16209, A
867	7	1.0	172	15	US-10-289-762-368	Sequence 368, App	940	7	1.0	331	15	US-10-425-114-52205	Sequence 52205, A
868	7	1.0	172	15	US-10-282-122A-67170	Sequence 67170, A	941	7	1.0	332	10	US-09-510-332-101	Sequence 101, App
869	7	1.0	172	16	US-10-437-963-160181	Sequence 160181, A	942	7	1.0	332	15	US-10-369-493-18461	Sequence 18461, A
870	7	1.0	187	16	US-10-437-963-193489	Sequence 193489, A	943	7	1.0	332	17	US-10-962-365-101	Sequence 101, App
871	7	1.0	186	15	US-10-425-114-62298	Sequence 62298, A	944	7	1.0	336	15	US-10-389-566-1548	Sequence 1548, Ap
872	7	1.0	186	15	US-10-425-114-62298	Sequence 62298, A	945	7	1.0	338	15	US-10-389-566-1565	Sequence 1565, Ap
873	7	1.0	192	16	US-10-437-963-104072	Sequence 104072, A	946	7	1.0	345	15	US-10-424-599-268634	Sequence 268634, A
874	7	1.0	194	10	US-09-791-932-104	Sequence 104, App	947	7	1.0	345	15	US-10-275-026A-94	Sequence 94, Appl
875	7	1.0	200	9	US-09-811-284-240	Sequence 240, App	948	7	1.0	375	15	US-10-424-599-160824	Sequence 160824, A
876	7	1.0	204	16	US-10-437-963-178632	Sequence 178632, A	949	7	1.0	383	15	US-10-425-114-50358	Sequence 50358, A
877	7	1.0	206	16	US-10-437-963-105498	Sequence 105498, A	950	7	1.0	386	15	US-10-425-114-50358	Sequence 50358, A
878	7	1.0	206	16	US-10-767-701-57306	Sequence 57306, A	951	7	1.0	409	15	US-10-282-122A-65178	Sequence 65178, A
879	7	1.0	209	15	US-10-425-114-65921	Sequence 65921, A	952	7	1.0	416	10	US-09-976-782-114	Sequence 114, App
880	7	1.0	210	15	US-10-289-762-869	Sequence 869, App	953	7	1.0	427	15	US-10-425-114-38905	Sequence 38905, A
881	7	1.0	210	15	US-10-289-762-869	Sequence 869, App	954	7	1.0	429	16	US-10-437-963-117075	Sequence 117075, A
882	7	1.0	211	15	US-10-282-122A-55523	Sequence 55523, A	955	7	1.0	433	15	US-10-282-122A-62604	Sequence 62604, A
883	7	1.0	211	15	US-10-282-122A-77886	Sequence 77886, A	956	7	1.0	443	16	US-10-437-963-180424	Sequence 180424, A
884	7	1.0	212	9	US-09-815-242-10149	Sequence 10149, A	957	7	1.0	448	15	US-10-424-599-199828	Sequence 199828, A
885	7	1.0	212	15	US-10-282-122A-42990	Sequence 42990, A	958	7	1.0	453	15	US-10-425-114-48669	Sequence 48669, A
886	7	1.0	212	15	US-10-282-122A-59410	Sequence 59410, A	959	7	1.0	456	10	US-09-932-227-64	Sequence 64, Appl
887	7	1.0	212	15	US-10-282-122A-73395	Sequence 73395, A	960	7	1.0	456	14	US-10-183-708-64	Sequence 64, Appl
888	7	1.0	212	15	US-10-282-122A-75987	Sequence 75987, A	961	7	1.0	461	15	US-10-282-122A-61657	Sequence 61657, A
889	7	1.0	213	15	US-10-282-122A-75987	Sequence 75987, A	962	7	1.0	461	15	US-10-282-122A-64914	Sequence 64914, A
890	7	1.0	213	15	US-10-282-122A-68483	Sequence 68483, A	963	7	1.0	462	16	US-10-437-963-185820	Sequence 185820, A
891	7	1.0	214	15	US-10-425-114-71387	Sequence 71387, A	964	7	1.0	463	17	US-10-959-539-8	Sequence 8, Appli
892	7	1.0	218	15	US-10-425-114-64477	Sequence 64477, A	965	7	1.0	464	16	US-10-437-963-109962	Sequence 109962, A
893	7	1.0	218	15	US-10-425-114-66277	Sequence 66277, A	966	7	1.0	465	15	US-10-389-566-2016	Sequence 2016, Ap
894	7	1.0	218	15	US-10-425-114-67294	Sequence 67294, A	967	7	1.0	467	15	US-10-369-493-3738	Sequence 3738, Ap
895	7	1.0	222	15	US-10-425-114-69657	Sequence 69657, A	968	7	1.0	470	14	US-10-355-430-34	Sequence 34, Appl
896	7	1.0	223	16	US-10-424-599-215367	Sequence 215367, A	969	7	1.0	471	16	US-10-437-963-118377	Sequence 118377, A
897	7	1.0	225	16	US-10-437-963-178810	Sequence 178810, A	970	7	1.0	477	15	US-10-425-114-65737	Sequence 65737, A
					Sequence 143960, A								

971	7	1.0	492	9	US-09-801-368-192	Sequence 192, App	1044	7	1.0	3972	14	US-10-156-761-8476	Sequence 8476, Ap
972	7	1.0	493	10	US-09-976-782-115	Sequence 115, App	1045	7	1.0	3972	16	US-10-204-862A-4	Sequence 4, Appli
973	7	1.0	494	10	US-09-820-843A-32	Sequence 32, Appl	1046	7	1.0	3972	16	US-10-204-862A-8	Sequence 8, Appli
974	7	1.0	498	9	US-09-764-864-1122	Sequence 1122, Ap	1047	7	1.0	11877	9	US-09-861-289-6	Sequence 6, Appli
975	7	1.0	500	15	US-10-369-493-20424	Sequence 20424, A	1048	7	1.0	11877	9	US-09-860-846-6	Sequence 6, Appli
976	7	1.0	502	16	US-10-474-776-295	Sequence 295, App	1049	7	1.0	11877	10	US-09-836-821-6	Sequence 6, Appli
977	7	1.0	502	17	US-10-472-928-1880	Sequence 1880, Ap	1050	7	1.0	11877	10	US-09-836-821-6	Sequence 6, Appli
978	7	1.0	503	9	US-09-071-035-360	Sequence 360, App	1051	7	1.0	12199	10	US-09-988-384B-6	Sequence 49, Appl
979	7	1.0	503	14	US-10-206-576-360	Sequence 360, App	1052	6	0.8	9	15	US-10-013-312-45	Sequence 6, Appli
980	7	1.0	503	17	US-10-912-362-360	Sequence 360, App	1053	6	0.8	9	15	US-10-013-312-111	Sequence 45, Appl
981	7	1.0	509	15	US-10-114-270-94	Sequence 94, Appl	1054	6	0.8	9	15	US-10-013-312-420	Sequence 111, App
982	7	1.0	513	15	US-10-369-493-11240	Sequence 11240, A	1055	6	0.8	9	15	US-10-013-312-523	Sequence 420, App
983	7	1.0	517	15	US-10-381-596A-4	Sequence 4, Appli	1056	6	0.8	9	15	US-10-013-312-523	Sequence 523, App
984	7	1.0	519	15	US-10-424-599-216138	Sequence 216138, A	1057	6	0.8	9	15	US-10-013-312-1328	Sequence 646, App
985	7	1.0	543	15	US-10-369-493-3712	Sequence 3712, Ap	1058	6	0.8	9	15	US-10-013-312-1353	Sequence 1328, Ap
986	7	1.0	553	9	US-09-815-242-13391	Sequence 13391, A	1059	6	0.8	9	15	US-10-013-312-1369	Sequence 1369, Ap
987	7	1.0	553	15	US-10-282-122A-73854	Sequence 73854, A	1060	6	0.8	9	15	US-10-013-312-1451	Sequence 1451, Ap
988	7	1.0	553	17	US-10-472-928-1116	Sequence 1116, Ap	1061	6	0.8	9	15	US-10-013-312-1495	Sequence 1495, Ap
989	7	1.0	556	9	US-09-795-691-2	Sequence 2, Appli	1062	6	0.8	9	15	US-10-013-312-1542	Sequence 1542, Ap
990	7	1.0	556	14	US-10-229-662-2	Sequence 2, Appli	1063	6	0.8	9	15	US-10-013-312-1590	Sequence 1590, Ap
991	7	1.0	556	15	US-10-426-776-2	Sequence 2, Appli	1064	6	0.8	9	15	US-10-013-312-1591	Sequence 1591, Ap
992	7	1.0	560	16	US-10-437-963-185707	Sequence 185707, A	1065	6	0.8	9	15	US-10-013-312-1591	Sequence 1650, Ap
993	7	1.0	571	16	US-10-437-963-111762	Sequence 111762, A	1066	6	0.8	9	15	US-10-013-312-1686	Sequence 1686, Ap
994	7	1.0	573	15	US-10-282-122A-46569	Sequence 46569, A	1067	6	0.8	9	15	US-10-013-312-1712	Sequence 1712, Ap
995	7	1.0	588	15	US-10-369-493-17841	Sequence 17841, A	1068	6	0.8	9	15	US-10-013-312-1731	Sequence 1731, Ap
996	7	1.0	593	16	US-10-437-963-122654	Sequence 122654, A	1069	6	0.8	9	15	US-10-013-312-1795	Sequence 1795, Ap
997	7	1.0	600	14	US-10-156-761-8406	Sequence 8406, Ap	1070	6	0.8	9	15	US-10-013-312-1821	Sequence 1821, Ap
998	7	1.0	622	14	US-10-020-141-8	Sequence 2, Appli	1071	6	0.8	9	15	US-10-013-312-1922	Sequence 1922, Ap
999	7	1.0	622	14	US-10-017-631-2	Sequence 2, Appli	1072	6	0.8	10	15	US-10-013-312-178	Sequence 178, App
1000	7	1.0	622	14	US-10-214-932-116	Sequence 116, App	1073	6	0.8	10	15	US-10-013-312-375	Sequence 375, App
1001	7	1.0	622	14	US-10-172-712-23	Sequence 29, Appl	1074	6	0.8	10	15	US-10-013-312-478	Sequence 478, App
1002	7	1.0	622	16	US-10-872-198-149	Sequence 149, App	1075	6	0.8	10	15	US-10-013-312-573	Sequence 573, App
1003	7	1.0	639	17	US-10-792-498-16	Sequence 16, Appl	1076	6	0.8	10	15	US-10-013-312-683	Sequence 683, App
1004	7	1.0	639	17	US-10-792-498-17	Sequence 17, Appl	1077	6	0.8	10	15	US-10-013-312-683	Sequence 2078, Ap
1005	7	1.0	713	15	US-10-282-122A-50120	Sequence 50120, A	1078	6	0.8	10	15	US-10-013-312-2091	Sequence 2091, Ap
1006	7	1.0	716	16	US-10-437-963-147102	Sequence 147102, A	1079	6	0.8	10	15	US-10-013-312-2098	Sequence 2098, Ap
1007	7	1.0	772	16	US-10-437-963-152918	Sequence 152918, A	1080	6	0.8	10	15	US-10-013-312-2183	Sequence 2183, Ap
1008	7	1.0	776	15	US-10-320-797-3397	Sequence 3297, Ap	1081	6	0.8	10	15	US-10-013-312-2200	Sequence 2200, Ap
1009	7	1.0	783	15	US-10-389-647-553	Sequence 553, App	1082	6	0.8	10	15	US-10-013-312-2280	Sequence 2280, Ap
1010	7	1.0	784	15	US-10-259-194A-178	Sequence 178, App	1083	6	0.8	10	15	US-10-013-312-2300	Sequence 2300, Ap
1011	7	1.0	790	14	US-10-174-677-17	Sequence 17, Appl	1084	6	0.8	10	15	US-10-013-312-2346	Sequence 2346, Ap
1012	7	1.0	799	9	US-09-738-626-4131	Sequence 4131, Ap	1085	6	0.8	10	15	US-10-013-312-2367	Sequence 2367, Ap
1013	7	1.0	799	16	US-10-494-672-142	Sequence 142, App	1086	6	0.8	10	15	US-10-013-312-2390	Sequence 2390, Ap
1014	7	1.0	859	8	US-08-945-749-1	Sequence 1, Appli	1087	6	0.8	11	9	US-09-987-844-2	Sequence 2, Appli
1015	7	1.0	859	16	US-10-437-963-166508	Sequence 166508, A	1088	6	0.8	11	14	US-10-062-710-168	Sequence 168, App
1016	7	1.0	878	16	US-10-437-963-158328	Sequence 158328, A	1089	6	0.8	12	14	US-09-933-767-304	Sequence 304, App
1017	7	1.0	950	16	US-10-437-963-115663	Sequence 115663, A	1090	6	0.8	12	14	US-10-004-860-304	Sequence 304, App
1018	7	1.0	984	17	US-10-211-028-25	Sequence 25, Appl	1091	6	0.8	12	14	US-10-023-282-304	Sequence 304, App
1019	7	1.0	986	9	US-09-850-048A-4	Sequence 4, Appli	1093	6	0.8	14	14	US-10-014-340-139	Sequence 139, App
1020	7	1.0	1074	9	US-09-071-035-358	Sequence 358, App	1094	6	0.8	14	16	US-10-712-447-162	Sequence 162, App
1021	7	1.0	1074	9	US-09-071-035-394	Sequence 394, App	1095	6	0.8	14	16	US-10-712-447-198	Sequence 198, App
1022	7	1.0	1074	14	US-10-206-576-358	Sequence 358, App	1096	6	0.8	15	14	US-10-062-710-167	Sequence 167, App
1023	7	1.0	1074	14	US-10-206-576-394	Sequence 394, App	1097	6	0.8	15	15	US-10-013-312-2625	Sequence 2625, Ap
1024	7	1.0	1074	17	US-10-912-362-358	Sequence 358, App	1098	6	0.8	15	15	US-10-013-312-2639	Sequence 2639, Ap
1025	7	1.0	1074	17	US-10-912-362-394	Sequence 394, App	1099	6	0.8	15	15	US-10-013-312-2658	Sequence 2658, Ap
1026	7	1.0	1141	16	US-10-437-963-156334	Sequence 156334, A	1100	6	0.8	15	15	US-10-013-312-2678	Sequence 2678, Ap
1027	7	1.0	1346	9	US-09-861-289-37	Sequence 37, Appl	1101	6	0.8	15	15	US-10-013-312-2711	Sequence 2711, Ap
1028	7	1.0	1346	9	US-09-860-846-37	Sequence 37, Appl	1102	6	0.8	15	15	US-10-013-312-2724	Sequence 2724, Ap
1029	7	1.0	1346	10	US-09-988-384B-37	Sequence 37, Appl	1103	6	0.8	15	15	US-10-013-312-2768	Sequence 2768, Ap
1030	7	1.0	1346	10	US-09-836-821-37	Sequence 37, Appl	1104	6	0.8	15	15	US-10-013-312-2828	Sequence 2828, Ap
1031	7	1.0	1346	10	US-09-793-708-4	Sequence 4, Appli	1105	6	0.8	15	15	US-10-013-312-2835	Sequence 2835, Ap
1032	7	1.0	1346	14	US-10-201-365-5	Sequence 5, Appli	1106	6	0.8	15	15	US-10-013-312-2836	Sequence 2836, Ap
1033	7	1.0	1346	14	US-10-160-539-4	Sequence 4, Appli	1107	6	0.8	15	15	US-10-013-312-2886	Sequence 2886, Ap
1034	7	1.0	1346	14	US-10-271-889-37	Sequence 37, Appl	1108	6	0.8	15	15	US-10-013-312-2900	Sequence 2900, Ap
1035	7	1.0	1346	17	US-10-468-828-4	Sequence 4, Appli	1109	6	0.8	15	15	US-10-013-312-2916	Sequence 2916, Ap
1036	7	1.0	1522	15	US-10-369-493-22058	Sequence 22058, A	1110	6	0.8	20	15	US-10-324-143-47	Sequence 147, App
1037	7	1.0	1592	16	US-10-437-963-188419	Sequence 188419, A	1111	6	0.8	20	15	US-10-414-583-67	Sequence 67, Appl
1038	7	1.0	2306	15	US-10-015-115-60	Sequence 60, Appl	1112	6	0.8	21	14	US-10-062-710-47	Sequence 47, Appl
1039	7	1.0	2910	16	US-10-322-696-18	Sequence 18, Appl	1113	6	0.8	21	14	US-10-062-710-169	Sequence 169, App
1040	7	1.0	2911	10	US-09-825-751A-68	Sequence 68, Appl	1114	6	0.8	21	14	US-10-084-813-286	Sequence 286, App
1041	7	1.0	2911	15	US-10-295-027-162	Sequence 162, App	1115	6	0.8	21	14	US-10-084-813-287	Sequence 287, App
1042	7	1.0	2911	16	US-10-408-765A-421	Sequence 421, App	1116	6	0.8	21	14	US-10-084-813-288	Sequence 288, App
1043	7	1.0	3564	15	US-10-016-248-45	Sequence 45, Appl	1117	6	0.8	22	9	US-09-864-761-37828	Sequence 37828, A

1118	6	0.8	22	14	US-10-073-118-36	Sequence 36, Appl	1191	6	0.8	50	16	US-10-437-963-178130	Sequence 178130,
1119	6	0.8	22	17	US-10-794-774-36	Sequence 36, Appl	1192	6	0.8	51	9	US-09-984-245-236	Sequence 236, App
1120	6	0.8	23	9	US-09-864-761-39777	Sequence 39777, A	1193	6	0.8	51	10	US-09-966-262-236	Sequence 236, App
1121	6	0.8	25	10	US-09-811-007-28	Sequence 28, Appl	1194	6	0.8	51	10	US-09-983-966-236	Sequence 236, App
1122	6	0.8	25	13	US-10-062-624-28	Sequence 28, Appl	1195	6	0.8	51	14	US-10-059-395-236	Sequence 236, App
1123	6	0.8	25	14	US-10-062-051-28	Sequence 28, Appl	1196	6	0.8	51	14	US-10-143-090-236	Sequence 236, App
1124	6	0.8	25	14	US-10-062-920-28	Sequence 28, Appl	1197	6	0.8	51	15	US-10-424-599-215530	Sequence 215530,
1125	6	0.8	25	16	US-10-060-349-28	Sequence 28, Appl	1198	6	0.8	51	15	US-10-424-599-110596	Sequence 110596,
1126	6	0.8	31	8	US-08-438-182-14	Sequence 14, Appl	1199	6	0.8	51	16	US-10-437-963-113279	Sequence 113279,
1127	6	0.8	31	9	US-08-438-182-14	Sequence 14, Appl	1200	6	0.8	51	16	US-10-437-963-113279	Sequence 113279,
1128	6	0.8	32	14	US-10-073-118-35	Sequence 35, Appl	1201	6	0.8	51	16	US-10-437-963-113279	Sequence 113279,
1129	6	0.8	32	15	US-10-424-599-232939	Sequence 232939	1202	6	0.8	51	16	US-10-437-963-113279	Sequence 113279,
1130	6	0.8	32	17	US-10-794-774-35	Sequence 35, Appl	1203	6	0.8	51	16	US-10-437-963-113279	Sequence 113279,
1131	6	0.8	33	17	US-10-794-774-35	Sequence 35, Appl	1204	6	0.8	51	16	US-10-437-963-113279	Sequence 113279,
1132	6	0.8	33	15	US-10-424-599-153198	Sequence 153198	1205	6	0.8	51	16	US-10-437-963-113279	Sequence 113279,
1133	6	0.8	35	14	US-10-073-118-33	Sequence 33, Appl	1206	6	0.8	51	15	US-10-424-599-259440	Sequence 259440,
1134	6	0.8	35	14	US-10-133-128-62	Sequence 62, Appl	1207	6	0.8	51	15	US-10-424-599-259440	Sequence 259440,
1135	6	0.8	35	14	US-10-289-660-62	Sequence 62, Appl	1208	6	0.8	51	15	US-10-424-599-158899	Sequence 158899,
1136	6	0.8	35	16	US-10-437-963-115252	Sequence 115252	1209	6	0.8	51	15	US-10-424-599-171307	Sequence 171307,
1137	6	0.8	35	16	US-10-693-057-62	Sequence 62, Appl	1210	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1138	6	0.8	35	17	US-10-693-056-62	Sequence 62, Appl	1211	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1139	6	0.8	35	17	US-10-794-774-33	Sequence 33, Appl	1212	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1140	6	0.8	35	17	US-10-840-723-62	Sequence 62, Appl	1213	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1141	6	0.8	35	17	US-10-871-602-62	Sequence 62, Appl	1214	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1142	6	0.8	37	10	US-09-821-861-16	Sequence 16, Appl	1215	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1143	6	0.8	37	14	US-10-256-865-39	Sequence 39, Appl	1216	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1144	6	0.8	37	14	US-10-266-325-16	Sequence 16, Appl	1217	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1145	6	0.8	37	16	US-10-687-361-14	Sequence 14, Appl	1218	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1146	6	0.8	37	17	US-10-716-379-14	Sequence 14, Appl	1219	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1147	6	0.8	37	17	US-10-616-410-14	Sequence 14, Appl	1220	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1148	6	0.8	37	17	US-10-648-631-14	Sequence 14, Appl	1221	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1149	6	0.8	38	14	US-10-029-386-31904	Sequence 31904, A	1222	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1150	6	0.8	38	15	US-10-424-599-282337	Sequence 282337	1223	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1151	6	0.8	39	14	US-10-431-577-55	Sequence 55, Appl	1224	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1152	6	0.8	39	14	US-10-112-589-22	Sequence 22, Appl	1225	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1153	6	0.8	40	8	US-08-424-5508-467	Sequence 467, App	1226	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1154	6	0.8	40	9	US-09-785-474-19	Sequence 19, Appl	1227	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1155	6	0.8	40	15	US-10-131-487A-102	Sequence 102, App	1228	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1156	6	0.8	40	15	US-10-424-599-177896	Sequence 177896	1229	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1157	6	0.8	41	15	US-10-424-599-179384	Sequence 179384	1230	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1158	6	0.8	42	4	US-09-275-805-11	Sequence 11, Appl	1231	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1159	6	0.8	42	14	US-10-229-066-3	Sequence 3, Appl	1232	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1160	6	0.8	42	14	US-10-029-386-34230	Sequence 34230, A	1233	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1161	6	0.8	42	15	US-10-424-599-153117	Sequence 153117	1234	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1162	6	0.8	43	10	US-09-880-573-73	Sequence 73, Appl	1235	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1163	6	0.8	43	15	US-10-424-599-270343	Sequence 270343	1236	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1164	6	0.8	44	9	US-09-230-920-85	Sequence 85, Appl	1237	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1165	6	0.8	44	15	US-10-424-599-143791	Sequence 143791	1238	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1166	6	0.8	44	17	US-10-884-358A-48	Sequence 48, Appl	1239	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1167	6	0.8	45	9	US-09-864-761-33941	Sequence 33941, A	1240	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1168	6	0.8	45	9	US-09-817-647-13	Sequence 13, Appl	1241	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1169	6	0.8	45	9	US-09-877-665-13	Sequence 13, Appl	1242	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1170	6	0.8	45	13	US-10-136-573A-13	Sequence 13, Appl	1243	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1171	6	0.8	45	14	US-10-215-862-13	Sequence 13, Appl	1244	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1172	6	0.8	45	15	US-10-424-599-204077	Sequence 204077	1245	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1173	6	0.8	45	15	US-10-424-599-243998	Sequence 243998	1246	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1174	6	0.8	45	17	US-10-944-116-13	Sequence 13, Appl	1247	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1175	6	0.8	46	9	US-09-764-877-1274	Sequence 1274, Ap	1248	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1176	6	0.8	46	13	US-10-096-241-16	Sequence 16, Appl	1249	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1177	6	0.8	46	14	US-10-083-357-1050	Sequence 1050, Ap	1250	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1178	6	0.8	46	15	US-10-242-515-1274	Sequence 1274, Ap	1251	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1179	6	0.8	46	15	US-10-424-599-211167	Sequence 211167	1252	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1180	6	0.8	46	16	US-10-437-963-192681	Sequence 192681	1253	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1181	6	0.8	47	15	US-10-424-599-229505	Sequence 229505	1254	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1182	6	0.8	47	16	US-10-313-972-44	Sequence 44, Appl	1255	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1183	6	0.8	47	16	US-10-767-701-54607	Sequence 54607, A	1256	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1184	6	0.8	48	15	US-10-424-599-208062	Sequence 208062	1257	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1185	6	0.8	48	15	US-10-609-370-13	Sequence 13, Appl	1258	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1186	6	0.8	48	16	US-10-437-963-143488	Sequence 143488	1259	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1187	6	0.8	49	9	US-09-864-761-43525	Sequence 43525, A	1260	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1188	6	0.8	50	9	US-09-864-761-37527	Sequence 37527, A	1261	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1189	6	0.8	50	15	US-10-424-599-262647	Sequence 262647	1262	6	0.8	51	15	US-10-424-599-268702	Sequence 268702,
1190	6	0.8	50	16	US-10-437-963-176586	Sequence 176586	1263	6	0.8	51	15	US-10-437-963-176586	Sequence 176586,

1264	6	0.8	66	9	US-09-796-692-780	Sequence 780, App	1337	6	0.8	72	15	US-10-424-599-269108	Sequence 269108,
1265	6	0.8	66	9	US-09-796-692-1109	Sequence 1109, App	1338	6	0.8	73	15	US-10-424-599-199780	Sequence 199780,
1266	6	0.8	66	9	US-09-796-692-1122	Sequence 1122, App	1339	6	0.8	73	15	US-10-424-599-231235	Sequence 231235,
1267	6	0.8	66	9	US-09-796-692-1426	Sequence 1426, App	1340	6	0.8	73	15	US-10-424-599-279252	Sequence 279252,
1268	6	0.8	66	9	US-09-796-692-1575	Sequence 1575, App	1341	6	0.8	73	15	US-10-424-599-279252	Sequence 279252,
1269	6	0.8	66	10	US-09-826-734-76	Sequence 76, App1	1342	6	0.8	74	10	US-09-468-147-190	Sequence 190, App
1270	6	0.8	66	14	US-10-040-862-780	Sequence 780, App	1343	6	0.8	74	10	US-09-468-147-197	Sequence 197, App
1271	6	0.8	66	14	US-10-040-862-1109	Sequence 1109, App	1344	6	0.8	74	10	US-10-319-745-190	Sequence 190, App
1272	6	0.8	66	14	US-10-040-862-1122	Sequence 1122, App	1345	6	0.8	74	15	US-10-319-745-197	Sequence 197, App
1273	6	0.8	66	14	US-10-040-862-1426	Sequence 1426, App	1346	6	0.8	74	15	US-10-424-599-156338	Sequence 156338,
1274	6	0.8	66	14	US-10-040-862-1575	Sequence 1575, App	1347	6	0.8	74	15	US-10-424-599-159151	Sequence 159151,
1275	6	0.8	66	15	US-10-057-4758-780	Sequence 780, App	1348	6	0.8	74	15	US-10-424-599-174651	Sequence 174651,
1276	6	0.8	66	15	US-10-057-4758-1109	Sequence 1109, App	1349	6	0.8	74	15	US-10-424-599-204725	Sequence 204725,
1277	6	0.8	66	15	US-10-057-4758-1122	Sequence 1122, App	1350	6	0.8	74	15	US-10-424-599-270167	Sequence 270167,
1278	6	0.8	66	15	US-10-057-4758-1426	Sequence 1426, App	1351	6	0.8	75	9	US-09-925-299-871	Sequence 871, App
1279	6	0.8	66	15	US-10-057-4758-1575	Sequence 1575, App	1352	6	0.8	75	10	US-09-925-299-871	Sequence 871, App
1280	6	0.8	66	15	US-10-154-8848-780	Sequence 780, App	1353	6	0.8	75	14	US-10-106-698-5859	Sequence 5859, App
1281	6	0.8	66	15	US-10-154-8848-1109	Sequence 1109, App	1354	6	0.8	75	16	US-10-437-963-175393	Sequence 175393,
1282	6	0.8	66	15	US-10-154-8848-1122	Sequence 1122, App	1355	6	0.8	76	9	US-09-764-870-519	Sequence 519, App
1283	6	0.8	66	15	US-10-154-8848-1426	Sequence 1426, App	1356	6	0.8	76	9	US-09-864-761-37192	Sequence 37192, A
1284	6	0.8	66	15	US-10-154-8848-1575	Sequence 1575, App	1357	6	0.8	76	13	US-10-016-157A-204	Sequence 204, App
1285	6	0.8	66	15	US-10-424-599-156756	Sequence 156756, App	1358	6	0.8	76	13	US-10-125-540-519	Sequence 519, App
1286	6	0.8	66	15	US-10-424-599-178963	Sequence 178963, App	1359	6	0.8	76	16	US-10-767-701-52319	Sequence 52319, A
1287	6	0.8	66	15	US-10-424-599-181840	Sequence 181840, App	1360	6	0.8	77	14	US-10-183-360-6	Sequence 6, App1
1288	6	0.8	66	15	US-10-424-599-246562	Sequence 246562, App	1361	6	0.8	77	15	US-10-424-599-279094	Sequence 279094, A
1289	6	0.8	66	15	US-10-424-599-264913	Sequence 264913, App	1362	6	0.8	77	15	US-10-424-599-283478	Sequence 283478, A
1290	6	0.8	66	15	US-10-424-599-284113	Sequence 284113, App	1363	6	0.8	77	16	US-10-437-963-142397	Sequence 142397, A
1291	6	0.8	66	16	US-10-437-963-134507	Sequence 134507, App	1364	6	0.8	77	16	US-10-437-963-150216	Sequence 150216, A
1292	6	0.8	66	16	US-10-764-324-780	Sequence 780, App	1365	6	0.8	77	16	US-10-437-963-181669	Sequence 181669, A
1293	6	0.8	66	16	US-10-764-324-1109	Sequence 1109, App	1366	6	0.8	78	9	US-09-864-761-38666	Sequence 38666, A
1294	6	0.8	66	16	US-10-764-324-1122	Sequence 1122, App	1367	6	0.8	78	9	US-09-764-869-1128	Sequence 1128, App
1295	6	0.8	66	16	US-10-764-324-1426	Sequence 1426, App	1368	6	0.8	78	14	US-10-091-504-1128	Sequence 1128, App
1296	6	0.8	66	16	US-10-764-324-1575	Sequence 1575, App	1369	6	0.8	78	14	US-10-029-386-27708	Sequence 27708, A
1297	6	0.8	67	9	US-09-764-869-1075	Sequence 1075, App	1370	6	0.8	78	15	US-10-029-386-27708	Sequence 1128, App
1298	6	0.8	67	14	US-10-091-504-1075	Sequence 1075, App	1371	6	0.8	78	15	US-10-029-386-27708	Sequence 1128, App
1299	6	0.8	67	14	US-10-029-386-2462	Sequence 2462, App	1372	6	0.8	78	15	US-10-424-599-190752	Sequence 190752, A
1300	6	0.8	67	15	US-10-029-386-1075	Sequence 1075, App	1373	6	0.8	78	15	US-10-424-599-221281	Sequence 221281, A
1301	6	0.8	67	15	US-10-424-599-266448	Sequence 266448, App	1374	6	0.8	78	15	US-10-424-599-259894	Sequence 259894, A
1302	6	0.8	67	15	US-10-424-599-279003	Sequence 279003, App	1375	6	0.8	78	16	US-10-437-963-186912	Sequence 186912, A
1303	6	0.8	67	16	US-10-437-963-113159	Sequence 113159, App	1376	6	0.8	78	16	US-10-767-701-46333	Sequence 46333, A
1304	6	0.8	67	16	US-10-437-963-125914	Sequence 125914, App	1377	6	0.8	79	16	US-10-767-701-34625	Sequence 34625, A
1305	6	0.8	67	16	US-10-767-701-53298	Sequence 53298, A	1378	6	0.8	80	9	US-09-867-550-1672	Sequence 1672, App
1306	6	0.8	67	16	US-10-767-701-54490	Sequence 54490, A	1379	6	0.8	80	15	US-10-424-599-164733	Sequence 164733, App
1307	6	0.8	68	15	US-10-424-599-190762	Sequence 190762, App	1380	6	0.8	80	15	US-10-424-599-168657	Sequence 168657, A
1308	6	0.8	68	15	US-10-424-599-285030	Sequence 285030, App	1381	6	0.8	80	15	US-10-425-114-41516	Sequence 41516, A
1309	6	0.8	68	16	US-10-437-963-154921	Sequence 154921, App	1382	6	0.8	80	16	US-10-437-963-109769	Sequence 109769, A
1310	6	0.8	68	16	US-10-767-701-34585	Sequence 34585, A	1383	6	0.8	80	16	US-10-437-963-114598	Sequence 114598, A
1311	6	0.8	69	13	US-10-002-344A-263	Sequence 263, App	1384	6	0.8	80	17	US-10-472-928-1328	Sequence 1328, App
1312	6	0.8	69	15	US-10-424-599-184634	Sequence 184634, App	1385	6	0.8	81	14	US-10-083-357-1232	Sequence 1232, App
1313	6	0.8	69	15	US-10-424-599-185385	Sequence 185385, App	1386	6	0.8	81	15	US-10-424-599-146659	Sequence 146659, A
1314	6	0.8	69	15	US-10-424-599-266079	Sequence 266079, App	1387	6	0.8	81	15	US-10-424-599-147870	Sequence 147870, A
1315	6	0.8	69	16	US-10-437-963-108280	Sequence 108280, App	1388	6	0.8	81	16	US-10-437-963-126541	Sequence 126541, A
1316	6	0.8	69	16	US-10-437-963-124107	Sequence 124107, App	1389	6	0.8	82	14	US-10-029-386-28424	Sequence 28424, A
1317	6	0.8	69	17	US-10-958-862-263	Sequence 263, App	1390	6	0.8	82	15	US-10-424-599-148973	Sequence 148973, A
1318	6	0.8	70	9	US-09-864-761-35204	Sequence 35204, A	1391	6	0.8	82	15	US-10-424-599-170036	Sequence 170036, A
1319	6	0.8	70	9	US-09-864-761-41767	Sequence 41767, A	1392	6	0.8	82	15	US-10-424-599-256074	Sequence 256074, A
1320	6	0.8	70	9	US-09-734-569-124	Sequence 124, App	1393	6	0.8	82	15	US-10-424-599-256335	Sequence 256335, A
1321	6	0.8	70	15	US-10-424-599-150826	Sequence 150826, App	1394	6	0.8	82	15	US-10-424-599-265435	Sequence 265435, A
1322	6	0.8	70	15	US-10-424-599-172932	Sequence 172932, App	1395	6	0.8	82	16	US-10-437-963-154867	Sequence 154867, A
1323	6	0.8	70	15	US-10-424-599-174450	Sequence 174450, App	1396	6	0.8	83	9	US-09-738-626-6475	Sequence 6475, App
1324	6	0.8	70	15	US-10-424-599-246003	Sequence 246003, App	1397	6	0.8	83	14	US-10-106-698-5912	Sequence 5912, App
1325	6	0.8	70	16	US-10-437-963-103138	Sequence 103138, App	1398	6	0.8	83	15	US-10-424-599-163509	Sequence 163509, A
1326	6	0.8	70	16	US-10-437-963-178820	Sequence 178820, App	1399	6	0.8	83	15	US-10-424-599-207556	Sequence 207556, A
1327	6	0.8	70	16	US-10-437-963-191411	Sequence 191411, App	1400	6	0.8	83	15	US-10-424-599-217575	Sequence 217575, A
1328	6	0.8	70	16	US-10-437-963-203019	Sequence 203019, App	1401	6	0.8	83	15	US-10-450-055-28	Sequence 28, App1
1329	6	0.8	71	9	US-09-864-761-47821	Sequence 47821, A	1402	6	0.8	83	16	US-10-437-963-158225	Sequence 158225, A
1330	6	0.8	71	13	US-10-001-857-179	Sequence 179, App	1403	6	0.8	84	16	US-10-437-963-164590	Sequence 164590, A
1331	6	0.8	71	15	US-10-082-122A-63186	Sequence 63186, A	1404	6	0.8	84	14	US-10-076-747-96	Sequence 96, App1
1332	6	0.8	71	15	US-10-424-599-152953	Sequence 152953, App	1405	6	0.8	84	15	US-10-424-599-160135	Sequence 160135, A
1333	6	0.8	71	15	US-10-424-599-211432	Sequence 211432, App	1406	6	0.8	84	15	US-10-424-599-165866	Sequence 165866, A
1334	6	0.8	71	15	US-10-424-599-229702	Sequence 229702, App	1407	6	0.8	84	15	US-10-424-599-178159	Sequence 178159, A
1335	6	0.8	71	16	US-10-424-599-270147	Sequence 270147, App	1408	6	0.8	84	15	US-10-001-885-144	Sequence 144, App
1336	6	0.8	72	14	US-10-315-515-167	Sequence 167, App	1409	6	0.8	84	16	US-10-767-701-37806	Sequence 37806, A

1410	6	0.8	84	17	US-10-487-078-47	Sequence 47, Appl	1483	6	0.8	98	9	US-09-864-761-43543	Sequence 43543, A
1411	6	0.8	85	14	US-10-029-386-28300	Sequence 28300, A	1484	6	0.8	98	14	US-10-080-170-303	Sequence 303, App
1412	6	0.8	85	15	US-10-282-132A-63478	Sequence 63478, A	1485	6	0.8	98	16	US-10-080-170-303	Sequence 303, App
1413	6	0.8	85	15	US-10-424-599-170793	Sequence 170793, A	1486	6	0.8	98	16	US-10-468-356-303	Sequence 303, App
1414	6	0.8	85	15	US-10-424-599-179221	Sequence 179221, A	1487	6	0.8	99	15	US-10-424-599-160975	Sequence 160975, A
1415	6	0.8	85	15	US-10-424-599-198377	Sequence 198377, A	1488	6	0.8	99	15	US-10-437-963-110403	Sequence 110403, A
1416	6	0.8	85	15	US-10-424-599-205810	Sequence 205810, A	1489	6	0.8	100	15	US-10-424-599-148247	Sequence 148247, A
1417	6	0.8	85	16	US-10-437-963-138562	Sequence 138562, A	1490	6	0.8	100	15	US-10-424-599-172402	Sequence 172402, A
1418	6	0.8	85	16	US-10-466-531-90	Sequence 90, Appl	1491	6	0.8	100	15	US-10-424-599-174842	Sequence 174842, A
1419	6	0.8	85	16	US-10-767-701-47469	Sequence 47469, A	1492	6	0.8	100	15	US-10-424-599-207144	Sequence 207144, A
1420	6	0.8	86	14	US-10-022-609-17	Sequence 17, Appl	1493	6	0.8	100	15	US-10-424-599-236864	Sequence 236864, A
1421	6	0.8	86	15	US-10-424-599-168752	Sequence 168752, A	1494	6	0.8	100	16	US-10-437-963-138763	Sequence 138763, A
1422	6	0.8	86	15	US-10-424-599-210880	Sequence 210880, A	1495	6	0.8	100	16	US-10-437-963-138763	Sequence 138763, A
1423	6	0.8	86	16	US-10-437-963-152565	Sequence 152565, A	1496	6	0.8	100	16	US-10-437-963-138763	Sequence 138763, A
1424	6	0.8	86	16	US-10-437-963-170593	Sequence 170593, A	1497	6	0.8	101	9	US-09-796-692-934	Sequence 934, App
1425	6	0.8	87	15	US-10-424-599-177925	Sequence 177925, A	1498	6	0.8	101	9	US-09-796-692-973	Sequence 973, App
1426	6	0.8	87	15	US-10-425-114-55155	Sequence 55155, A	1499	6	0.8	101	9	US-09-796-692-984	Sequence 984, App
1427	6	0.8	87	16	US-10-437-963-156255	Sequence 156255, A	1500	6	0.8	101	9	US-09-796-692-984	Sequence 984, App
1428	6	0.8	88	15	US-10-424-599-161407	Sequence 161407, A							
1429	6	0.8	88	15	US-10-424-599-234570	Sequence 234570, A							
1430	6	0.8	88	15	US-10-425-114-61398	Sequence 61398, A							
1431	6	0.8	88	16	US-10-437-963-181821	Sequence 181821, A							
1432	6	0.8	88	16	US-10-767-701-34268	Sequence 34268, A							
1433	6	0.8	88	17	US-10-368-133-22	Sequence 22, Appl							
1434	6	0.8	88	17	US-10-368-133-23	Sequence 23, Appl							
1435	6	0.8	88	17	US-10-368-133-24	Sequence 24, Appl							
1436	6	0.8	89	10	US-09-820-649-168	Sequence 168, App							
1437	6	0.8	89	14	US-10-106-698-5940	Sequence 5940, App							
1438	6	0.8	89	14	US-10-160-162-168	Sequence 168, App							
1439	6	0.8	89	15	US-10-424-599-277550	Sequence 277550, A							
1440	6	0.8	89	17	US-10-936-773-168	Sequence 273740, A							
1441	6	0.8	90	15	US-10-424-599-273740	Sequence 273740, A							
1442	6	0.8	90	15	US-10-425-114-36929	Sequence 36929, A							
1443	6	0.8	90	16	US-10-767-701-34774	Sequence 34774, A							
1444	6	0.8	90	16	US-10-767-701-57512	Sequence 57512, A							
1445	6	0.8	91	9	US-09-764-877-1729	Sequence 1729, App							
1446	6	0.8	91	11	US-09-864-408A-1904	Sequence 1904, App							
1447	6	0.8	91	15	US-10-242-515-1729	Sequence 1729, App							
1448	6	0.8	91	15	US-10-424-599-164539	Sequence 164539, A							
1449	6	0.8	91	15	US-10-424-599-217782	Sequence 217782, A							
1450	6	0.8	91	16	US-10-437-963-132749	Sequence 132749, A							
1451	6	0.8	91	16	US-10-437-963-203681	Sequence 203681, A							
1452	6	0.8	92	15	US-10-424-599-184039	Sequence 184039, A							
1453	6	0.8	92	16	US-10-437-963-137121	Sequence 137121, A							
1454	6	0.8	92	16	US-10-767-701-48848	Sequence 48848, A							
1455	6	0.8	93	11	US-09-864-408A-4122	Sequence 4122, App							
1456	6	0.8	93	14	US-10-105-545-26	Sequence 26, Appl							
1457	6	0.8	93	15	US-10-424-599-226309	Sequence 226309, A							
1458	6	0.8	93	15	US-10-424-599-237119	Sequence 237119, A							
1459	6	0.8	93	15	US-10-424-599-280216	Sequence 280216, A							
1460	6	0.8	93	16	US-10-767-701-32997	Sequence 32997, A							
1461	6	0.8	94	11	US-09-891-119A-10	Sequence 10, Appl							
1462	6	0.8	94	15	US-10-460-594-79	Sequence 79, Appl							
1463	6	0.8	94	15	US-10-424-599-147189	Sequence 147189, A							
1464	6	0.8	94	15	US-10-424-599-196499	Sequence 196499, A							
1465	6	0.8	94	15	US-10-424-599-268550	Sequence 268550, A							
1466	6	0.8	94	16	US-10-437-963-118964	Sequence 118964, A							
1467	6	0.8	94	16	US-10-437-963-152974	Sequence 152974, A							
1468	6	0.8	95	10	US-09-764-891-5146	Sequence 5146, App							
1469	6	0.8	95	15	US-10-080-334-217	Sequence 217, App							
1470	6	0.8	95	16	US-10-437-963-190828	Sequence 190828, A							
1471	6	0.8	95	16	US-10-767-701-51523	Sequence 51523, A							
1472	6	0.8	96	14	US-10-012-600B-147	Sequence 147, App							
1473	6	0.8	96	15	US-10-424-599-183424	Sequence 183424, A							
1474	6	0.8	96	16	US-10-437-963-127771	Sequence 127771, A							
1475	6	0.8	97	9	US-09-864-761-43414	Sequence 43414, A							
1476	6	0.8	97	9	US-09-789-561-109	Sequence 109, App							
1477	6	0.8	97	11	US-09-864-408A-3224	Sequence 3224, App							
1478	6	0.8	97	11	US-09-833-245-2145	Sequence 2145, App							
1479	6	0.8	97	15	US-10-424-599-191543	Sequence 191543, A							
1480	6	0.8	97	15	US-10-424-599-217925	Sequence 217925, A							
1481	6	0.8	97	15	US-10-425-114-68846	Sequence 68846, A							
1482	6	0.8	97	17	US-10-883-936-109	Sequence 109, App							

Search completed: May 8, 2005, 16:14:36
Job time : 54 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.
 OM protein - nucleic search, using frame_plus_p2n model
 Run on: May 9, 2005, 22:33:58 ; Search time 981 Seconds
 (without alignments)
 4344.764 Million cell updates/sec

Title: US-10-063-692-38
 Perfect score: 3945
 Sequence: 1 MELGWCWQLGLTFLQLLLS.....LSTAFKVLFFKDWIERNMK 720
 Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0
 Searched: 4390206 seqs, 2959870667 residues
 Total number of hits satisfying chosen parameters: 8780412
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Command line parameters:
 -MODEL=frame+p2n.model -DEV=xlh
 -O=/cgn2_1/USPTO.spool/US10063692/runat_09052005_122312_5068/app_query_faeta_1.903
 -DB-N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
 -LIST=1500 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=1500
 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US10063692@cgn 1.1 668 @runat_09052005_122312_5068 -NCPU=6 -ICPU=3
 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7
 Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description

RESULT 1
 ID ADA00368 standard; cDNA; 2843 BP.
 DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.
 PN US2003027992-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Conservative: 0
 Mismatches: 0
 Indels: 0

RESULT 2
 ID AAZ65034 standard; cDNA; 2846 BP.
 DE Membrane-bound protein PRO1344 encoding cDNA.
 PN WO963088-A2.
 PD 09-DEC-1999.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Conservative: 0
 Mismatches: 0
 Indels: 0

RESULT 3
 ID AAS46009 standard; cDNA; 2846 BP.
 DE Human DNA encoding PRO polypeptide sequence #85.
 PN WO200168848-A2.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.

RESULT 4
 ID AAF92076 standard; cDNA; 2846 BP.
 DE Human PRO1344 cDNA.
 PN WO200116318-A2.
 PD 08-MAR-2001.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Conservative: 0
 Mismatches: 0
 Indels: 0

RESULT 5
 ID AAF44180 standard; cDNA; 2846 BP.
 DE Human PRO1344 (UNQ699) nucleotide sequence SEQ ID NO:230.
 PN WO200073454-A1.
 PD 07-DEC-2000.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Conservative: 0
 Mismatches: 0
 Indels: 0

RESULT 6
 ID ABS74396 standard; cDNA; 2846 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1344.
 PN US2002119130-A1.
 PD 29-AUG-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Conservative: 0
 Mismatches: 0
 Indels: 0

RESULT 7
 ID ACA89459 standard; cDNA; 2846 BP.
 DE cDNA encoding human PRO polypeptide #85.
 PN US2003036141-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Conservative: 0
 Mismatches: 0
 Indels: 0

RESULT 8
 ID ACA73469 standard; cDNA; 2846 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #85.
 PN US2003036146-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Conservative: 0
 Mismatches: 0
 Indels: 0

RESULT 9
 ID ACA05784 standard; cDNA; 2846 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #85.
 PN US2003036162-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Conservative: 0
 Mismatches: 0
 Indels: 0

RESULT 10
 ID ACA66618 standard; cDNA; 2846 BP.
 DE cDNA encoding human PRO protein #85.
 PN US2003036137-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Conservative: 0
 Mismatches: 0
 Indels: 0

RESULT 11
 ID ACA64316 standard; cDNA; 2846 BP.
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.
 PN US2003003531-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 12
ID ACA91182 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 13
ID ACD81559 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 14
ID ACF20193 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040063-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 15
ID ACF19579 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040064-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 16
ID ACD21867 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003027267-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 17
ID ACF13032 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036160-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 18
ID ACD25135 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044925-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 19
ID ACF00184 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 20
ID ACA60381 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.

PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 21
ID ACA72241 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 22
ID ACD04765 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 23
ID ACD18226 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036124-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 24
ID ACD08233 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040054-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 25
ID ACA88667 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 26
ID ACA70109 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036134-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 27
ID ACD13331 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 28
ID ACC74246 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027275-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 29
ID ACD15874 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.

PN US2003027324-A1.
PD 06-FEB-2003. Conservative: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
RESULT 30
ID ACD25442 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 31
ID ACD17919 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036123-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 32
ID ACC88206 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036148-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 33
ID ACD21560 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040060-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 34
ID ACD18627 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044916-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 35
ID ACA58828 standard; cDNA; 2846 BP.
DE cDNA encoding human secreted polypeptide PRO1344.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 36
ID ABX98237 standard; cDNA; 2846 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 169.
PN US2003036156-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 37
ID ACD13988 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032117-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 38
ID ACD09768 standard; cDNA; 2846 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036128-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 39
ID ACC88513 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027266-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 40
ID ACD21253 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 41
ID ABX75625 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1344.
PN US2003022298-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 42
ID ACA64004 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 43
ID ABX97828 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032102-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 44
ID ACA97304 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 45
ID ACA57767 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003036143-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 46
ID ACD14295 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032130-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 47

```
ID ACC91078 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 48
ID ACC88820 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036132-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 49
ID ACD07017 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 50
ID ACA67468 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003017542-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 51
ID ACC81523 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032137-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 52
ID ACA91268 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 53
ID ACC89127 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027269-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 54
ID ACC86483 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027268-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 55
ID ACC89741 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027274-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 56
ID ACC92920 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 57
ID ABX80775 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein cDNA, #94.
PN US2003027162-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 58
ID ACA72548 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003022295-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 59
ID ACA89066 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003022297-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 60
ID ACA69802 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032105-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 61
ID ACA96945 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 62
ID ACA90941 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 63
ID ACA70723 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032111-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 64
ID ACA95233 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
```


Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 65
ID ACD44284 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 66
ID ACC86176 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027263-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 67
ID ACD45167 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane polypeptide PRO1344 cDNA.
PN US200309012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 68
ID ACC90048 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027271-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 69
ID ACD12656 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036125-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 70
ID ACF19886 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040068-A1.
PD 27-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 71
ID ABX76830 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003027280-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 72
ID ACA73162 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 73
ID ACA6705 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 74
ID ACA74549 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003036138-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 75
ID ACA70416 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032109-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 76
ID ACD14602 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003040066-A1.
PD 27-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 77
ID ACA93715 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 78
ID ACA68274 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 79
ID ABX98739 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 80
ID ACC81216 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032120-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 81
ID ACA95540 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 82
ID ACD04458 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.

```
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 83
ID ACC87899 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 84
ID ACF12561 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040058-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 85
ID ACH66262 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 86
ID ABX79455 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein cDNA, #94.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 87
ID ACA96276 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003017540-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 88
ID ACA65050 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032106-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 89
ID ACA73776 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032129-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 90
ID ACA74188 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 91
ID ACA96583 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032107-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 92
ID ACD10689 standard; cDNA; 2846 BP.
DE CDNA encoding human PRO polypeptide #85.
PN US2003032107-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 93
ID ACC91385 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032139-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 94
ID ACA93476 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 95
ID ACD02720 standard; cDNA; 2846 BP.
DE CDNA encoding human PRO polypeptide #85.
PN US2003022301-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 96
ID ACC87285 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 97
ID ACC85869 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027262-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 98
ID ABX81158 standard; cDNA; 2846 BP.
DE Human secreted or transmembrane protein related PCR primer #50.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 99
ID ACA65357 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032110-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 100
ID ACA94174 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032110-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
```

PN US2003036142-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 101
ID ACA97918 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003036145-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 102
ID ACA91420 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 103
ID ACA90634 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 104
ID ACD16181 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044931-A1.
PD 06-MAR-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 105
ID ACD17342 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036150-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 106
ID ACC91999 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040069-A1.
PD 27-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 107
ID ACD02316 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 108
ID ACA74856 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003022293-A1.
PD 30-JAN-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 109
ID ACA91727 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.

PN US2003032128-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 110
ID ACA71371 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032116-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 111
ID ACC90771 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032122-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 112
ID ACA65781 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO protein #85.
PN US2003036139-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 113
ID ACA68944 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 114
ID ACA92974 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 115
ID ACA94926 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003017541-A1.
PD 23-JAN-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 116
ID ACD16488 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003017543-A1.
PD 23-JAN-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 117
ID ACD15567 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036152-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 118
ID ACA98466 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.

PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 119
ID ABX17058 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 120
ID ABX16670 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein #85.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 121
ID ACA67913 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 122
ID ACA63391 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 123
ID ACA97611 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032115-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 124
ID ACA99060 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 125
ID ACC91692 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 126
ID ACD11103 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 127
ID ACD14953 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 128
ID ACA88362 standard; cDNA; 2846 BP.
DE Human secreted and transmembrane polypeptide PRO1344 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 129
ID ACD81869 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 130
ID ACD1117 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 131
ID ACC95846 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 132
ID ACF18409 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 133
ID ACF02527 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003045741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 134
ID ACF02834 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003045743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 135
ID ACP21421 standard; cDNA; 2846 BP.

DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 136
ID ACF10105 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 137
ID ACF77998 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 138
ID ACD46703 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 139
ID ACD49466 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 140
ID ACF28233 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 141
ID ACD8923 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 142
ID ACD84318 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 143
ID ACD99092 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.

PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 144
ID ADA77921 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 145
ID ACF48834 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 146
ID ACD09154 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 147
ID ACF11947 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 148
ID ACF41181 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 149
ID ACF15795 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 150
ID ACF16102 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 151
ID ADB17094 standard; cDNA; 2846 BP.
DE Human cDNA clone (SeqID 37) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 152
ID ACD99092 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.

Query Match: 100.00% Indels: 0
RESULT 152
ID ACD31929 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 153
ID ACF18737 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 154
ID ACF09184 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 155
ID ACF78305 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 156
ID ACF51904 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 157
ID ACF26391 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 158
ID ACF24184 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 159
ID ACF63495 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003071183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 160
ID ACD45475 standard; cDNA; 2846 BP.

ID ACF50369 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 161
ID ACH07840 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 162
ID ACF13646 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 163
ID ACD41572 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 164
ID ADA37741 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 165
ID ACF31985 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 166
ID ACF23263 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 167
ID ACF39953 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 168
ID ACD45475 standard; cDNA; 2846 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 169
ID ACF53132 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 170
ID ACF27312 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 171
ID ACF45150 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 172
ID ACF29768 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 173
ID ACD89844 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 174
ID ACD84625 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 175
ID ACD98785 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 176
ID ACF77077 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 177
ID ACF76770 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 178
ID ACF49755 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 179
ID ACF50062 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 180
ID ADA21427 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1344.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 181
ID ACD09461 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 182
ID ACD08540 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 183
ID ACH03594 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 184
ID ACF12254 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 185
ID ACC94762 standard; cDNA; 2846 BP.

```
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 186
ID ACD22481 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 187
ID ACD22481 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 188
ID ACC97276 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 189
ID ACC97276 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 190
ID ACF13953 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 191
ID ACF14260 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 192
ID ADA10214 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1344.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 193
ID ACF09491 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 194
ID ACD45782 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 195
ID ACD47931 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 196
ID ACD67662 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 197
ID ACF25470 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 198
ID ACF29154 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 199
ID ACD84932 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 200
ID ACD84011 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 201
ID ACD88002 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
```


Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 202
ID ACF30689 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 203
ID ACF32292 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 204
ID ACHI1952 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 205
ID ACHI2259 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 206
ID ADA19899 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003059394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 207
ID ACD40651 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 208
ID ADB17282 standard; cDNA; 2846 BP.
DE Human cDNA clone (SeqID 37) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 209
ID ADA17758 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 210
ID ACF46378 standard; cDNA; 2846 BP.

ID ACF18123 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 211
ID ACF08570 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 212
ID ACF31371 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 213
ID ACF52211 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 214
ID ACD50080 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 215
ID ACF38783 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003088692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 216
ID ACF26698 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 217
ID ACF24798 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 218
ID ACF46378 standard; cDNA; 2846 BP.

```
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 219
ID ACF27926 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 220
ID ACD99230 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 221
ID ACF63802 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 222
ID ACF60442 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 223
ID ACH12566 standard; cDNA; 2846 BP.
DE ACH12566 standard; cDNA; 2846 BP.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 224
ID ACH09989 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 225
ID ACD03844 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 226
ID ACD10382 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 227
ID ACD12024 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 228
ID ACF42409 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 229
ID ADA27866 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 230
ID ACF18430 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 231
ID ACF02220 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 232
ID ACF21728 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 233
ID ACF10412 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 234
ID ACF33864 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 235
```

ID ACF44826 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 236
ID ACD90458 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 237
ID ACD91071 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 238
ID ACF30382 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 239
ID ACD87081 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 240
ID ACF60135 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 241
ID ACF46685 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 242
ID ACF75542 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 243
ID ADA79713 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003073173-A1.

PD 17-APR-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 244
ID ACF17202 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 245
ID ACF22956 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 246
ID ACF07956 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 247
ID ACF08263 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 248
ID ACF40567 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003084448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 249
ID ACF53746 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 250
ID ACD47010 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 251
ID ACF47913 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Query Match: 100.00%
Conservative: 0

```
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 252
ID ACF47299 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068753-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 10-APR-2003. Indels: 0
Query Match: 100.00%
RESULT 253
ID ACF46071 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068742-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 10-APR-2003. Indels: 0
Query Match: 100.00%
RESULT 254
ID ACD86160 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068756-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 10-APR-2003. Indels: 0
Query Match: 100.00%
RESULT 255
ID ACF52518 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003082715-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 01-MAY-2003. Indels: 0
Query Match: 100.00%
RESULT 256
ID ACF52825 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003082716-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 01-MAY-2003. Indels: 0
Query Match: 100.00%
RESULT 257
ID ACF64818 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068737-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 10-APR-2003. Indels: 0
Query Match: 100.00%
RESULT 258
ID ACF76463 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104547-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 05-JUN-2003. Indels: 0
Query Match: 100.00%
RESULT 259
ID ACF61363 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003096359-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 22-MAY-2003. Indels: 0
Query Match: 100.00%
RESULT 260
ID ACF07342 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049753-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 13-MAR-2003. Indels: 0
Query Match: 100.00%
RESULT 261
ID ACD30701 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032125-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 13-FEB-2003. Indels: 0
Query Match: 100.00%
RESULT 262
ID ACD31622 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054454-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 20-MAR-2003. Indels: 0
Query Match: 100.00%
RESULT 263
ID ACD32543 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054477-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 20-MAR-2003. Indels: 0
Query Match: 100.00%
RESULT 264
ID ADA20071 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003055222-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 20-MAR-2003. Indels: 0
Query Match: 100.00%
RESULT 265
ID ACD82108 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.
PN US2003060601-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 27-MAR-2003. Indels: 0
Query Match: 100.00%
RESULT 266
ID ACF17509 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054460-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 20-MAR-2003. Indels: 0
Query Match: 100.00%
RESULT 267
ID ADA94446 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003059832-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 27-MAR-2003. Indels: 0
Query Match: 100.00%
RESULT 268
ID ACF07342 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049753-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 13-MAR-2003. Indels: 0
Query Match: 100.00%
```

PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 269			
ID	ACF20500 standard; cDNA; 2846 BP.		
DE	Human secreted polypeptide PROI344-encoding cDNA, SEQ ID NO:169.		
FN	US2003049763-A1.		
PD	13-MAR-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 270			
ID	ACF20807 standard; cDNA; 2846 BP.		
DE	Human secreted polypeptide PROI344-encoding cDNA, SEQ ID NO:169.		
FN	US2003073172-A1.		
PD	17-APR-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 271			
ID	ACF21114 standard; cDNA; 2846 BP.		
DE	Human secreted polypeptide PROI344-encoding cDNA, SEQ ID NO:169.		
FN	US2003073172-A1.		
PD	17-APR-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 272			
ID	ADC47624 standard; cDNA; 2846 BP.		
DE	Human secreted/transmembrane protein (PRO) cDNA #85.		
FN	US2003068700-A1.		
PD	10-APR-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 273			
ID	ACF47606 standard; cDNA; 2846 BP.		
DE	Human secreted polypeptide PROI344-encoding cDNA, SEQ ID NO:169.		
FN	US2003068736-A1.		
PD	10-APR-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 274			
ID	ACF53439 standard; cDNA; 2846 BP.		
DE	Human secreted polypeptide PROI344-encoding cDNA, SEQ ID NO:169.		
FN	US2003068679-A1.		
PD	10-APR-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 275			
ID	ACD86774 standard; cDNA; 2846 BP.		
DE	Human secreted/transmembrane protein (PRO) cDNA #85.		
FN	US2003068767-A1.		
PD	10-APR-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 276			
ID	AACH05022 standard; cDNA; 2846 BP.		
DE	cDNA encoding human PRO polypeptide #85.		
FN	US2003073182-A1.		
PD	17-APR-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 277			
ID	ACG405022 standard; cDNA; 2846 BP.		
DE	cDNA encoding human PRO polypeptide #85.		
FN	US2003073182-A1.		
PD	17-APR-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

Query Match:	100.00%	Indels:	0
RESULT 277			
ID ACF44519 standard; cDNA; 2846 BP.			
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.			
PN US2003104557-A1.			
PD 05-JUN-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 278			
ID ADA81440 standard; cDNA; 2846 BP.			
DE Human secreted/transmembrane protein (PRO) cDNA #85.			
PN US2003092121-A1.			
PD 15-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 279			
ID ACD22174 standard; cDNA; 2846 BP.			
DE Human secreted/transmembrane protein (PRO) cDNA #85.			
PN US2003027276-A1.			
PD 06-FEB-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 280			
ID ACD24521 standard; cDNA; 2846 BP.			
DE Human secreted/transmembrane protein (PRO) cDNA #85.			
PN US2003044920-A1.			
PD 06-MAR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 281			
ID ACD39724 standard; cDNA; 2846 BP.			
DE cDNA encoding human PRO polypeptide #85.			
PN US2003027265-A1.			
PD 06-FEB-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 282			
ID ACD40031 standard; cDNA; 2846 BP.			
DE cDNA encoding human PRO polypeptide #85.			
PN US2003054461-A1.			
PD 20-MAR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 283			
ID ACF13339 standard; cDNA; 2846 BP.			
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.			
PN US2003064446-A1.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 284			
ID ACF03141 standard; cDNA; 2846 BP.			
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.			
PN US2003049744-A1.			
PD 13-MAR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 285			
ID ACF78612 standard; cDNA; 2846 BP.			
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.			
PN US2003064446-A1.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

```
PN US2003049783-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 286
ID ACD90151 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 295
ID ACD83704 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 296
ID ACF49141 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 297
ID ACH07226 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 298
ID ACH07533 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 299
ID ACH08147 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 300
ID ACH11338 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 301
ID ACH11645 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
PN US2003049783-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 287
ID ACF50676 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 288
ID ACF34171 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 289
ID ACD46396 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 290
ID ACD48238 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 291
ID ACF27619 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 292
ID ACF24491 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 293
ID ACD85546 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
```

Query Match: 100.00% Indels: 0
RESULT 302
ID ACH10296 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 303
ID ACF01299 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 304
ID ACF40874 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 305
ID ACD24214 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 306
ID ACD31315 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 307
ID ACF17816 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054462-A1.
PD 28-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 308
ID ADA38671 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 309
ID ACF32599 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 310
ID ACF40260 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064449-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 311
ID ACF48220 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 312
ID ACF38169 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 313
ID ACF25105 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 314
ID ACF27005 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 315
ID ACF29461 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 316
ID ACD87695 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 317
ID ACF76156 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 318
ID ACF49448 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 319
ID ACF40260 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064449-A1.

Query Match: 100.00% Indels: 0
RESULT 319
ID ACC943905 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 320
ID ACH06250 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 321
ID ACH06557 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 322
ID ADA83238 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 323
ID ACC92613 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 324
ID ACC93227 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 325
ID ACF19272 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 326
ID ACD12963 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 327
ID ACF06421 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040057-A1.

PD 27-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 328
ID ACC94455 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 329
ID ACC97883 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 330
ID ACC94148 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 331
ID ACF42102 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 332
ID ACD31008 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 333
ID ACD43037 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 334
ID ACD43344 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 335
ID ACF14874 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 336
ID ACF06421 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040057-A1.

RESULT 336
ID ACF32792 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 337
ID ACF01606 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 338
ID ACF31678 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 339
ID ACD67355 standard; cDNA; 2846 BP.
DE CDNA encoding human PRO polypeptide #85.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 340
ID ACD48545 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 341
ID ACD48852 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 342
ID ACF51290 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 343
ID ACF54053 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 344
ID ACF25777 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 345
ID ACF39090 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 346
ID ACF28847 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 347
ID ACD90764 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 348
ID ACD86467 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 349
ID ACH05329 standard; cDNA; 2846 BP.
DE CDNA encoding human PRO polypeptide #85.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 350
ID ACF65125 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 351
ID ADB20281 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 352
ID ACF43598 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104552-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 353
ID ACH09068 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 354
ID ACH09375 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 355
ID ADA78533 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 356
ID ACF09798 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 357
ID ACF50983 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 358
ID ACF23877 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 359
ID ACD88309 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 360
ID ACH09682 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 361
ID ACH10603 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 362
ID ACD11410 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 363
ID ACC96460 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 364
ID ACC98490 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 365
ID ACF41795 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 366
ID ACF16716 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 367
ID ACD32236 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 368
ID ACD30394 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 369
ID ACD41265 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064467-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 370
ID ACF07649 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 371
ID ACF31064 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 372
ID ACF77384 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 373
ID ACF11026 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 374
ID ACF32906 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 375
ID ACF26084 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 376
ID ACD83397 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 377
ID ACF23570 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 378
ID ACF42984 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 379
ID ACF43291 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 380
ID ACH05943 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 381
ID ACH08761 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 382
ID ACC90355 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 383
ID ACF10719 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 384
ID ACC93534 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 385
ID ACC96153 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 386

```
ID ACD24828 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PD US2003044921-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 387
ID ACF01913 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003049739-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 388
ID ACF22035 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003059882-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 389
ID ACF22649 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003059884-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 390
ID ACF08877 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003068687-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 391
ID ACF33213 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003073186-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 392
ID ACF54667 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003064443-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 393
ID ACF48527 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003064444-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 394
ID ACD47317 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PD US2003036151-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 395
ID ACD49159 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PD US2003068710-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 396
ID ACF37862 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003068686-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 397
ID ACF30075 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003073178-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 398
ID ACD87388 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PD US2003068774-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 399
ID ACF61977 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PD US2003104538-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 400
ID ACH10910 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PD US2003049781-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 401
ID ACD10075 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PD US2003036158-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 402
ID ACD16800 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PD US2003036151-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
```

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 403
ID ACH65430 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003044806-A1.
PD 06-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 404
ID ACC99097 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040067-A1.
PD 27-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 405
ID ACF00491 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054456-A1.
PD 20-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 406
ID ACD40958 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 407
ID ACF14567 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 408
ID ACF22342 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 409
ID ACF78919 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 410
ID ACF11640 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 411
ID ADA22353 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 412
ID ACF51597 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 413
ID ACF33520 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003084450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 414
ID ACD49773 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 415
ID ACF37555 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003086883-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 416
ID ACF28540 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 417
ID ACD88616 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003086881-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 418
ID ACF75235 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 419
ID ACF61056 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 420
ID ACF44212 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 421
ID ACH08454 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 422
ID ACD39420 standard; DNA; 2846 BP.
DE Human PRO 1344 PCR primer #1.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 423
ID ACC93841 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036122-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 424
ID ACD20946 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 425
ID ACF06728 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040065-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 426
ID ACD20639 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044919-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 427
ID ACD22788 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040077-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 428
ID ACF41488 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

PN US2003044928-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 429
ID ADA06519 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #65.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 430
ID ADA39212 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003059782-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 431
ID ACF07035 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 432
ID ACF77691 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 433
ID ACD46089 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 434
ID ACF46992 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 435
ID ACF54360 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 436
ID ACF45764 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0

PN US2003083461-A1.
 PD 01-MAY-2003.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 471
 ID ADD07529 standard; cDNA; 2846 BP.
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.
 PN US2002193299-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 472
 ID ADC82420 standard; cDNA; 2846 BP.
 DE Human PRO polynucleotide #65.
 PN US2003059833-A1.
 PD 27-MAR-2003.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 473
 ID ADD05642 standard; cDNA; 2846 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #85.
 PN US2003087376-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 474
 ID ADD08600 standard; cDNA; 2846 BP.
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.
 PN US2003073090-A1.
 PD 17-APR-2003.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 475
 ID ADD06849 standard; cDNA; 2846 BP.
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.
 PN US2002193300-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 476
 ID ADC83096 standard; cDNA; 2846 BP.
 DE Human PRO polynucleotide #65.
 PN US2003059783-A1.
 PD 27-MAR-2003.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 477
 ID ADD55203 standard; cDNA; 2846 BP.
 DE Human PRO polynucleotide #65.
 PN US2003077593-A1.
 PD 24-APR-2003.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 478
 ID ADD36041 standard; cDNA; 2846 BP.
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.
 PN US2003105298-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0

PN US2003083461-A1.
 PD 01-MAY-2003.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 479
 ID ADD56161 standard; cDNA; 2846 BP.
 DE Human PRO polynucleotide #65.
 PN US2003077594-A1.
 PD 24-APR-2003.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 480
 ID ADD54599 standard; cDNA; 2846 BP.
 DE Human PRO polynucleotide #65.
 PN US2002132253-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 481
 ID ADE26753 standard; cDNA; 2846 BP.
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.
 PN US2003087304-A1.
 PD 08-MAY-2003.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 482
 ID ADE26220 standard; cDNA; 2846 BP.
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.
 PN US2003087305-A1.
 PD 08-MAY-2003.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 483
 ID ADF67157 standard; cDNA; 2846 BP.
 DE Human PRO1344 nucleotide sequence SEQ ID NO:230.
 PN US2002198148-A1.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 484
 ID ADG01042 standard; cDNA; 2846 BP.
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.
 PN US2003078387-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 485
 ID ADG08595 standard; cDNA; 2846 BP.
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.
 PN US2003180793-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 486
 ID ADG02637 standard; cDNA; 2846 BP.
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.
 PN US2003207397-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 487
 ID ADG01344 standard; cDNA; 2846 BP.
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.
 PN US2003207399-A1.

```
PD 06-NOV-2003
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 488
ID ADF95519 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 489
ID ADF95216 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 490
ID ADG12334 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 491
ID ADH24069 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 492
ID ADH34095 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 493
ID ADH29928 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 494
ID ADH23899 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 495
ID ADH08994 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 496
ID ADG85303 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 497
ID ADH24579 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 498
ID ADH37435 standard; cDNA; 2846 BP.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 499
ID ADH02024 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 500
ID ADH37605 standard; cDNA; 2846 BP.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 501
ID ADG85643 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 502
ID ADH24239 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 503
ID ADH38533 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
```

Query Match:	100.00%	Indels:	0
RESULT 512			
ID ADH52020 standard; cDNA; 2846 BP.			
DE Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN US2003181638-A1.			
PD 25-SEP-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 513			
ID ADH49875 standard; cDNA; 2846 BP.			
DE Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN US2003181639-A1.			
PD 25-SEP-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 514			
ID ADI25385 standard; cDNA; 2846 BP.			
DE Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN US2003181696-A1.			
PD 25-SEP-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 515			
ID ADH90178 standard; cDNA; 2846 BP.			
DE Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN US2003181698-A1.			
PD 25-SEP-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 516			
ID ADI25555 standard; cDNA; 2846 BP.			
DE Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN US2003181699-A1.			
PD 25-SEP-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 517			
ID ADH97729 standard; cDNA; 2846 BP.			
DE Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN US2003181672-A1.			
PD 25-SEP-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 518			
ID ADI35411 standard; cDNA; 2846 BP.			
DE Human PO polynucleotide #65.			
FN US2003050457-A1.			
PD 13-MAR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 519			
ID ADI03577 standard; cDNA; 2846 BP.			
DE Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN US2003181656-A1.			
PD 25-SEP-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 520			
ID ADI03577 standard; cDNA; 2846 BP.			
DE Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN US2003181656-A1.			
PD 25-SEP-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

ID ADI11934 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 521
ID ADH90008 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 522
ID ADH99903 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 523
ID ADH98409 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 524
ID ADI11084 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 525
ID ADI11594 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 526
ID ADH98239 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 527
ID ADH98579 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 528
ID ADH98069 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.

PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 529
ID ABX78612 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003027272-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 530
ID ACA75584 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 531
ID ACA71064 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032112-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 532
ID ACC87592 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027278-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 533
ID ACC86978 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036159-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 534
ID ACD04151 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040070-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 535
ID ABX77859 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003027163-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 536
ID AXH80271 standard; DNA; 2846 BP.
DE Human secreted or transmembrane protein related PCR primer #50.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 537
ID ACA69177 standard; cDNA; 2846 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003032023-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 538
ID ACA69482 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003032113-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 539
ID ACA90327 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 540
ID ACC89434 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027264-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 541
ID ABX90248 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein cDNA, #94.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 542
ID ACA98225 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 543
ID ACA93867 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036149-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 544
ID ACD15260 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044923-A1.
PD 06-MAR-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 545
ID ACD08847 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040062-A1.
PD 27-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 546
ID ACC96767 standard; cDNA; 2846 BP.

DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040056-A1.
PD 27-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 547
ID ACF15488 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044926-A1.
PD 06-MAR-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 548
ID ABX64094 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 549
ID ACA72855 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 550
ID ACD03027 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US200303153-A1.
PD 16-JAN-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 551
ID ACD01842 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003017544-A1.
PD 23-JAN-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 552
ID ACA92034 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003027277-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 553
ID ADI05057 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 554
ID ADI03407 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 555
ID ACC96767 standard; cDNA; 2846 BP.

Query Match: 100.00% Indels: 0

RESULT 555
ID ADI04802 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 556
ID ADH78256 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 557
ID ADI19600 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 558
ID ADH90348 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 559
ID ADI03067 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 560
ID ADH77916 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 561
ID ADH97899 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 562
ID ADI01284 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 563
ID ADI01979 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 564
ID ADI03237 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 565
ID ADI11424 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 566
ID ADI02326 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 567
ID ADI11764 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 568
ID ADI05401 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 569
ID ADH79473 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 570
ID ADI19430 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 571
ID ADI01284 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

ID ADI05231 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 572
ID ADH79643 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 573
ID ADI01469 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 574
ID ADI01639 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 575
ID ADI01809 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 576
ID ADH79813 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 577
ID ADI04631 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 578
ID ADI02767 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 579
ID ADH78086 standard; cDNA; 2846 BP.

DE Human PRO polynucleotide #19.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 580
ID ADI25725 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 581
ID ADI25895 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 582
ID ADH98749 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 583
ID ADH79990 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 584
ID ADL32775 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 585
ID ADM30309 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 586
ID ADL93721 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 587
ID ADC52175 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.

```
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 588
ID ADE74306 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 589
ID ADE74918 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003211574-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 590
ID ADF35356 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 591
ID ADG11606 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 592
ID ADF96131 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003215909-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 593
ID ADG04402 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 594
ID ADG00562 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 595
ID ADH06607 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 596
ID ADH06437 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 597
ID ADG68858 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 598
ID ADH27748 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 599
ID ADH25089 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 600
ID ADH33721 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 601
ID ADG82818 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 602
ID ADH02364 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 603
ID ADH07971 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
```


ID	ADH24409 standard; cDNA; 2846 BP.			
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN	US2003180910-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 613				
ID	ADH33068 standard; cDNA; 2846 BP.			
DE	Human PRO polynucleotide #85.			
FN	US2003068768-A1.			
PD	10-APR-2003.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 614				
ID	ADG69538 standard; cDNA; 2846 BP.			
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN	US2003180844-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 615				
ID	ADH07801 standard; cDNA; 2846 BP.			
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN	US2003180851-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 616				
ID	ADG85913 standard; cDNA; 2846 BP.			
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN	US2003180861-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 617				
ID	ADH39359 standard; cDNA; 2846 BP.			
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN	US2003180916-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 618				
ID	ADH33551 standard; cDNA; 2846 BP.			
DE	Human PRO polynucleotide #19.			
FN	US2003181637-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 619				
ID	ADH33891 standard; cDNA; 2846 BP.			
DE	Human PRO polynucleotide #19.			
FN	US2003181644-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 620				
ID	ADH01101 standard; cDNA; 2846 BP.			
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN	US2003180910-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 621				
ID	ADH01101 standard; cDNA; 2846 BP.			
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN	US2003180910-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 622				
ID	ADH01101 standard; cDNA; 2846 BP.			
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN	US2003180910-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 623				
ID	ADH01101 standard; cDNA; 2846 BP.			
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.			
FN	US2003180910-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:				

```
DE Human PRO polynucleotide #19.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 621
ID ADG69708 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 622
ID ADH20969 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003224359-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 623
ID ADH02194 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 624
ID ADG69198 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 625
ID ADG85983 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 626
ID ADH24919 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 627
ID ADH39536 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 628
ID ADH20009 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003219556-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 629
ID ADH02534 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 630
ID ADG69028 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 631
ID ADH07631 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 632
ID ADG86153 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 633
ID ADH24749 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 634
ID ADH25797 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 635
ID ADH38363 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 0
RESULT 636
ID ADH57202 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181642-A1.
PD 25-SEP-2003.
```

PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 637
ID ADH52190 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 638
ID ADH49556 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 639
ID ADH90518 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 640
ID ADH11254 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 641
ID ADH98919 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 642
ID ADH90688 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 643
ID ADH54807 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 645
ID ADJ98563 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181797-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 646
ID ADJ98733 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 647
ID ADH78892 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 648
ID ADJ99126 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 649
ID ADJ99296 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 650
ID ADJ98914 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 651
ID ADH79062 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 652
ID ADK00922 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 653
ID ADH90688 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 644
ID ADJ54807 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.

```
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 653
ID ADK14443 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 654
ID ADJ64578 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 655
ID ADM31474 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 656
ID ADM38521 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 657
ID ADM40326 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 658
ID ADM80892 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 659
ID ADN37934 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 660
ID ADK65407 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 99.86% Conservative: 0
Best Local Similarity: 99.86% Mismatches: 1
Query Match: 99.86% Indels: 1
```

```
Query Match: 99.87% Indels: 0
RESULT 661
ID AAF74433 standard; cDNA; 2306 BP.
DE Human PRO2 nucleotide sequence SEQ ID NO:3.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 99.72% Mismatches: 0
Query Match: 99.85% Indels: 0
RESULT 662
ID AAS01222 standard; cDNA; 2306 BP.
DE DNA encoding human secreted protein, POLY13.
PN WO200119856-A2.
PD 22-MAR-2001.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 99.72% Mismatches: 0
Query Match: 99.85% Indels: 0
RESULT 663
ID AAA39952 standard; cDNA; 2163 BP.
DE Human TANGO 215 coding sequence cDNA.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHEAPEUTICS INC.
Percent Similarity: 99.86% Conservative: 1
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 99.77% Indels: 0
RESULT 664
ID AAA39951 standard; cDNA; 2747 BP.
DE Human TANGO 215 cDNA.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHEAPEUTICS INC.
Percent Similarity: 99.86% Conservative: 1
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 99.77% Indels: 0
RESULT 665
ID ABZ35333 standard; cDNA; 2845 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 644.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
Percent Similarity: 99.86% Conservative: 0
Best Local Similarity: 99.86% Mismatches: 0
Query Match: 99.67% Indels: 1
RESULT 666
ID ACA67289 standard; cDNA; 2848 BP.
DE cDNA encoding human secreted polypeptide PRO1344.
PN US2003027212-A1.
PD 08-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 99.86% Conservative: 0
Best Local Similarity: 99.86% Mismatches: 0
Query Match: 99.67% Indels: 1
RESULT 667
ID ACA89307 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 99.72% Conservative: 0
Best Local Similarity: 99.72% Mismatches: 2
Query Match: 99.57% Indels: 0
RESULT 668
ID AAH47258 standard; cDNA; 2289 BP.
DE Human serine protease-like protein coding sequence.
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 97.56% Conservative: 0
Best Local Similarity: 97.56% Mismatches: 1
Query Match: 99.40% Indels: 17
```

RESULT 669
ID AAH47256 standard; cDNA; 2784 BP.
DE Human serine protease-like protein encoding cDNA (hC-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 97.56%
Best Local Similarity: 97.56%
Query Match: 99.40%
Conservative: 0
Mismatch: 1
Indels: 17
RESULT 670
ID AAH15142 standard; cDNA; 2784 BP.
DE Human cDNA sequence SEQ ID NO:13201.
PN EP1074637-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 97.56%
Best Local Similarity: 97.56%
Query Match: 99.40%
Conservative: 0
Mismatch: 1
Indels: 17
RESULT 671
ID ADN04639 standard; cDNA; 2784 BP.
DE Antipsoriatic cDNA sequence #529.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 97.56%
Best Local Similarity: 97.56%
Query Match: 99.40%
Conservative: 0
Mismatch: 1
Indels: 17
RESULT 672
ID ADS85021 standard; DNA; 2784 BP.
DE Human atopic dermatitis-related gene sequence SeqID23.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
Percent Similarity: 97.56%
Best Local Similarity: 97.56%
Query Match: 99.40%
Conservative: 0
Mismatch: 1
Indels: 17
RESULT 673
ID ADS85033 standard; DNA; 2784 BP.
DE Human atopic dermatitis-related gene sequence SeqID35.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (UYJU-) UNIV JUNTENDO.
Percent Similarity: 97.56%
Best Local Similarity: 97.56%
Query Match: 99.40%
Conservative: 0
Mismatch: 1
Indels: 17
RESULT 674
ID ADH89027 standard; cDNA; 2305 BP.
DE Human POLYX polynucleotide #13.
PN US2003198959-A1.
PD 23-OCT-2003.
PA (SHIM/) SHIMKETS R A.
PA (PERN/) FERNANDES E.
PA (HERR/) HERRMANN J L.
PA (LIUX/) LIU X.
PA (YANG/) YANG M.
PA (BOLD/) BOLD OG F L.
PA (SMIT/) SMITHSON G.
PA (RASI/) RASTELLI L.
Percent Similarity: 99.86%
Best Local Similarity: 99.58%
Query Match: 99.11%
Conservative: 2
Mismatch: 1
Indels: 1
RESULT 675
ID ADL06663 standard; DNA; 2650 BP.
DE Human 3T3 cell conversion promoter FP938 DNA.
PN CN1403477-A.
PD 19-MAR-2003.
PA (SHAN-) SHANGHAI XINSHIJI GENE TECH DEV CO LTD.
Percent Similarity: 99.86%
Best Local Similarity: 99.86%
Query Match: 96.65%
Conservative: 0
Mismatch: 0
Indels: 1
RESULT 676
ID ADL06661 standard; cDNA; 2650 BP.
DE Human 3T3 cell conversion promoter FP938 cDNA.
PN CN1403477-A.
PD 19-MAR-2003.
PA (SHAN-) SHANGHAI XINSHIJI GENE TECH DEV CO LTD.
Percent Similarity: 99.86%
Best Local Similarity: 99.86%
Query Match: 96.65%
Conservative: 0
Mismatch: 0
Indels: 1
RESULT 677
ID AAA39985 standard; cDNA; 2823 BP.
DE Murine TANGO 215 cDNA.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Percent Similarity: 94.86%
Best Local Similarity: 90.28%
Query Match: 91.69%
Conservative: 33
Mismatch: 37
Indels: 0
RESULT 678
ID AAH47257 standard; cDNA; 2244 BP.
DE Murine serine protease-like protein encoding cDNA (mC-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 94.72%
Best Local Similarity: 90.14%
Query Match: 91.56%
Conservative: 33
Mismatch: 38
Indels: 0
RESULT 679
ID AAD30584 standard; cDNA; 2632 BP.
DE Human protease, PRPS-17 cDNA.
PN WO200208396-A2.
PD 31-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 90.00%
Best Local Similarity: 90.00%
Query Match: 88.73%
Conservative: 0
Mismatch: 1
Indels: 71
RESULT 680
ID ABK30334 standard; cDNA; 2886 BP.
DE Human G-protein-coupled protease #104.
PN US6331427-B1.
PD 18-DEC-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 94.45%
Best Local Similarity: 94.19%
Query Match: 87.47%
Conservative: 2
Mismatch: 5
Indels: 37
RESULT 681
ID AAF74432 standard; cDNA; 1867 BP.
DE Human PRQ1 nucleotide sequence SEQ ID NO:1.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 99.31%
Best Local Similarity: 99.31%
Query Match: 79.40%
Conservative: 0
Mismatch: 3
Indels: 2
RESULT 682
ID AAC90025 standard; cDNA; 2259 BP.
DE Clone HPEY75 coding sequence.
PN WO200061774-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 96.84%
Best Local Similarity: 96.84%
Query Match: 74.69%
Conservative: 0
Mismatch: 1
Indels: 17
RESULT 683
ID ADR41309 standard; cDNA; 2311 BP.
DE Human CD-like molecule HSXDF41 cDNA, SEQ ID NO:108.
PN WO200228930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 99.27%
Best Local Similarity: 99.27%
Query Match: 74.63%
Conservative: 0
Mismatch: 4
Indels: 0
RESULT 684
ID AAI59113 standard; cDNA; 2142 BP.

```
DE Human polynucleotide SEQ ID NO 1316.
PN WO200153312-A1.
PA (HYSE-) HYSQ INC.
Percent Similarity: 96.72%
Best Local Similarity: 96.72%
Query Match: 67.90%
Conservative: 0
Mismatch: 0
Indels: 17
RESULT 685
ID ADQ99336 standard; cDNA; 2142 BP.
DE DNA encoding human GPCR-like protein seqid 1006.
PN US6569662-B1.
PA (HYSE-) HYSQ INC.
Percent Similarity: 96.72%
Best Local Similarity: 96.72%
Query Match: 67.90%
Conservative: 0
Mismatch: 0
Indels: 17
RESULT 686
ID ADB49096 standard; cDNA; 2142 BP.
DE Novel human cDNA SEQ ID NO 1006.
PN US2003104529-A1.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R.
Percent Similarity: 96.72%
Best Local Similarity: 96.72%
Query Match: 67.90%
Conservative: 0
Mismatch: 0
Indels: 17
RESULT 687
ID AAI59076 standard; cDNA; 2144 BP.
DE Human polynucleotide SEQ ID NO 1279.
PN WO200153312-A1.
PA (HYSE-) HYSQ INC.
Percent Similarity: 96.72%
Best Local Similarity: 96.72%
Query Match: 67.90%
Conservative: 0
Mismatch: 0
Indels: 17
RESULT 688
ID ADQ99299 standard; cDNA; 2144 BP.
DE DNA encoding human GPCR-like protein seqid 969.
PN US6569662-B1.
PA (HYSE-) HYSQ INC.
Percent Similarity: 96.72%
Best Local Similarity: 96.72%
Query Match: 67.90%
Conservative: 0
Mismatch: 0
Indels: 17
RESULT 689
ID ADB49059 standard; cDNA; 2144 BP.
DE Novel human cDNA SEQ ID NO 969.
PN US2003104529-A1.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R.
Percent Similarity: 96.72%
Best Local Similarity: 96.72%
Query Match: 67.90%
Conservative: 0
Mismatch: 0
Indels: 17
RESULT 690
ID AAI60862 standard; cDNA; 2040 BP.
DE Human polynucleotide SEQ ID NO 4851.
PN WO200153312-A1.
PA (HYSE-) HYSQ INC.
Percent Similarity: 96.59%
Best Local Similarity: 96.59%
Query Match: 65.34%
Conservative: 0
Mismatch: 0
Indels: 17
RESULT 691
ID AAD33261 standard; cDNA; 2022 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:35.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 99.34%
Best Local Similarity: 99.34%
Query Match: 61.17%
Conservative: 0
Mismatch: 3
Indels: 0
RESULT 692
ID AAD33241 standard; cDNA; 1101 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:15.
PN WO200218435-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 94.12%
Best Local Similarity: 94.12%
Query Match: 43.31%
Conservative: 0
Mismatch: 2
Indels: 17
RESULT 693
ID AAH99144 standard; cDNA; 1058 BP.
DE Human EST-derived coding sequence SEQ ID NO: 1001.
PN WO200154477-A2.
PA (HYSE-) HYSQ INC.
Percent Similarity: 92.00%
Best Local Similarity: 90.80%
Query Match: 31.24%
Conservative: 3
Mismatch: 16
Indels: 4
RESULT 694
ID AAS86826 standard; cDNA; 1058 BP.
DE DNA encoding novel human diagnostic protein #22630.
PN WO200175067-A2.
PA (HYSE-) HYSQ INC.
Percent Similarity: 92.00%
Best Local Similarity: 90.80%
Query Match: 31.24%
Conservative: 3
Mismatch: 16
Indels: 4
RESULT 695
ID AAH08069 standard; cDNA; 705 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:4904.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 97.25%
Best Local Similarity: 97.25%
Query Match: 30.19%
Conservative: 0
Mismatch: 5
Indels: 1
RESULT 696
ID ABK30409 standard; cDNA; 505 BP.
DE Human G-protein-coupled protease #179.
PN US6331427-B1.
PD 18-DEC-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 98.81%
Best Local Similarity: 98.81%
Query Match: 22.64%
Conservative: 0
Mismatch: 1
Indels: 2
RESULT 697
ID AEN74148 standard; cDNA; 997 BP.
DE Bovine embryonic germ (EG) cell cDNA EST #199.
PN WO200194550-A2.
PD 13-DEC-2001.
PA (INFI-) INFING INC.
Percent Similarity: 86.63%
Best Local Similarity: 80.21%
Query Match: 20.82%
Conservative: 12
Mismatch: 24
Indels: 1
RESULT 698
ID AAI60899 standard; cDNA; 438 BP.
DE Human polynucleotide SEQ ID NO 4888.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSQ INC.
Percent Similarity: 97.92%
Best Local Similarity: 97.22%
Query Match: 19.04%
Conservative: 1
Mismatch: 3
Indels: 1
RESULT 699
ID ABZ58473 standard; cDNA; 3467 BP.
DE Horseshoe crab Factor C coding sequence.
PN WO2003002976-A2.
PD 09-JAN-2003.
```


PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Percent Similarity: 94.38%
 Best Local Similarity: 93.26%
 Query Match: 11.99%
 Indels: 0
 Conservative: 1
 Mismatches: 5

RESULT 716
 ID AAF83985 standard; DNA; 3895 BP.
 DE Human serine protease MASP-3 encoding DNA.
 PN WO200140451-A2.
 PD 07-JUN-2001.
 PA (JENS/) JENSENIUS J C.
 PA (THIE/) THIEL S.
 Percent Similarity: 38.53%
 Best Local Similarity: 25.03%
 Query Match: 11.94%
 Indels: 214
 Conservative: 97
 Mismatches: 228

RESULT 717
 ID ACN42374 standard; cDNA; 5269 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1249.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 38.76%
 Best Local Similarity: 24.75%
 Query Match: 11.77%
 Indels: 214
 Conservative: 99
 Mismatches: 219

RESULT 718
 ID AAH43512 standard; cDNA; 3863 BP.
 DE cDNA encoding protease PRPS-1.
 PN WO200171004-A2.
 PD 27-SEP-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 38.39%
 Best Local Similarity: 24.90%
 Query Match: 11.69%
 Indels: 214
 Conservative: 97
 Mismatches: 229

RESULT 719
 ID RAD37042 standard; DNA; 369 BP.
 DE Mouse limulus-clotting factor protease-like EST gene.
 PN WO200203787-A2.
 PD 17-JAN-2002.
 PA (DELT-) DELTAGEN INC.
 PA (DELT-) DELTAGEN INC.
 Percent Similarity: 92.59%
 Best Local Similarity: 84.26%
 Query Match: 11.65%
 Indels: 2
 Conservative: 9
 Mismatches: 8

RESULT 720
 ID ABZ35488 standard; cDNA; 3064 BP.
 DE Human gene expression profile polynucleotide SEQ ID NO 599.
 PN WO200274979-A2.
 PD 26-SEP-2002.
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 Percent Similarity: 35.22%
 Best Local Similarity: 23.01%
 Query Match: 10.35%
 Indels: 245
 Conservative: 95
 Mismatches: 259

RESULT 721
 ID RAD24224 standard; cDNA; 2472 BP.
 DE Human MASP-2 cDNA clone phl-4.
 PN WO200206460-A2.
 PD 24-JAN-2002.
 PA (JENS/) JENSENIUS J C.
 PA (THIE/) THIEL S.
 Percent Similarity: 33.16%
 Best Local Similarity: 22.98%
 Query Match: 10.30%
 Indels: 266
 Conservative: 78
 Mismatches: 246

RESULT 722
 ID ABS52737 standard; cDNA; 2475 BP.
 DE cDNA encoding human MASP-2 protein.
 PN US2002082208-A1.
 PD 27-JUN-2002.
 PA (JENS/) JENSENIUS J C.
 PA (THIE/) THIEL S.
 Percent Similarity: 33.16%
 Best Local Similarity: 22.98%
 Query Match: 10.27%
 Indels: 265
 Conservative: 78
 Mismatches: 247

RESULT 723
 ID ABS52737 standard; cDNA; 2475 BP.
 DE Human cDNA differentially expressed in MYCN activated cells SeqID 23.
 PN US2003119009-A1.
 PD 26-JUN-2003.
 PA (STUA/) STUART S G.
 PA (NUCH/) NUCHTERN J G.
 PA (PLON/) PLON S E.
 PA (SHOH/) SHOHEIT J M.
 Percent Similarity: 35.22%
 Indels: 245
 Conservative: 96
 Mismatches: 259

ID ADP65502 standard; DNA; 2386 BP.
 DE Human mRNA for complement component C1r DNA.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Percent Similarity: 34.64%
 Best Local Similarity: 22.59%
 Query Match: 10.23%
 Indels: 265
 Conservative: 95
 Mismatches: 250

RESULT 724
 ID ADP65013 standard; DNA; 2386 BP.
 DE Human complement component 1, r subcomponent (C1R) DNA sequence.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Percent Similarity: 34.64%
 Best Local Similarity: 22.59%
 Query Match: 10.23%
 Indels: 265
 Conservative: 95
 Mismatches: 250

RESULT 725
 ID ADR24793 standard; DNA; 2386 BP.
 DE Breast cancer prognosis marker #654.
 PN WO2004055545-A2.
 PD 05-AUG-2004.
 PA (ROSE-) ROSETTA INPHARMATICS LLC.
 PA (NECA-) NETHERLANDS CANCER INST.
 Percent Similarity: 34.64%
 Best Local Similarity: 22.59%
 Query Match: 10.23%
 Indels: 265
 Conservative: 95
 Mismatches: 250

RESULT 726
 ID AAX24297 standard; cDNA; 2492 BP.
 DE Human complement component 1, subcomponent r (c1r) cDNA.
 PN WO9907896-A2.
 PD 18-FEB-1999.
 PA (CURA-) CURAGEN CORP.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 35.22%
 Best Local Similarity: 22.88%
 Query Match: 10.23%
 Indels: 245
 Conservative: 96
 Mismatches: 259

RESULT 727
 ID ABA83114 standard; DNA; 2493 BP.
 DE Complement component 1 r ovarian tumour marker gene, SEQ ID NO:65.
 PN WO200175177-A2.
 PD 11-OCT-2001.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Percent Similarity: 35.22%
 Best Local Similarity: 22.88%
 Query Match: 10.23%
 Indels: 245
 Conservative: 96
 Mismatches: 259

RESULT 728
 ID AEN95758 standard; DNA; 2493 BP.
 DE Gene #2256 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 35.22%
 Best Local Similarity: 22.88%
 Query Match: 10.23%
 Indels: 245
 Conservative: 96
 Mismatches: 259

RESULT 729
 ID ABX63613 standard; cDNA; 2555 BP.
 DE Human cDNA #613 differentially expressed in activated vascular tissue.
 PN US2002137081-A1.
 PD 26-SEP-2002.
 PA (BAND/) BANDMAN O.
 PA (BAND/) BANDMAN O.
 Percent Similarity: 35.22%
 Best Local Similarity: 22.88%
 Query Match: 10.23%
 Indels: 245
 Conservative: 96
 Mismatches: 259

RESULT 730
 ID ADJ56217 standard; cDNA; 2555 BP.
 DE Human cDNA differentially expressed in MYCN activated cells SeqID 23.
 PN US2003119009-A1.
 PD 26-JUN-2003.
 PA (STUA/) STUART S G.
 PA (NUCH/) NUCHTERN J G.
 PA (PLON/) PLON S E.
 PA (SHOH/) SHOHEIT J M.
 Percent Similarity: 35.22%
 Indels: 245
 Conservative: 96
 Mismatches: 259

Best Local Similarity: 22.88% Mismatches: 259
 Query Match: 10.23% Indels: 245
 RESULT 731
 ID ADQ27012 standard; cDNA; 2061 BP.
 DE Human MASP-2 polypeptide cDNA sequence.
 PN WO2004050907-A2.
 PD 17-JUN-2004.
 PA (UYAA-) UNIV AARHUS.
 PA (AARH) AARHUS AMT.
 Percent Similarity: 33.03%
 Best Local Similarity: 22.67%
 Query Match: 10.18%
 Indels: 267
 RESULT 732
 ID ABK90781 standard; cDNA; 2476 BP.
 DE cDNA encoding Mannan-binding lectin associated serine protease-2.
 PN US2002082209-A1.
 PD 27-JUN-2002.
 PA (JENS/) JENSENIUS J C.
 PA (THIE/) THIEL S.
 Percent Similarity: 32.63%
 Best Local Similarity: 22.80%
 Query Match: 10.14%
 Indels: 259
 RESULT 733
 ID ADQ21819 standard; DNA; 286 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4638.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 80.61%
 Best Local Similarity: 79.59%
 Query Match: 10.05%
 Indels: 15
 RESULT 734
 ID ABN95607 standard; DNA; 2647 BP.
 DE Gene #2105 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 32.95%
 Best Local Similarity: 21.77%
 Query Match: 8.90%
 Indels: 301
 RESULT 735
 ID ADJ74872 standard; DNA; 2647 BP.
 DE Marker gene SEQ ID NO:124.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Percent Similarity: 32.95%
 Best Local Similarity: 21.77%
 Query Match: 8.90%
 Indels: 301
 RESULT 736
 ID ADR24794 standard; DNA; 2647 BP.
 DE Breast cancer prognosis marker #655.
 PN WO2004065545-A2.
 PD 05-AUG-2004.
 PA (ROSE-) ROSETTA INPHARMATICS LLC.
 PA (NECA-) NETHERLANDS CANCER INST.
 Percent Similarity: 32.95%
 Best Local Similarity: 21.77%
 Query Match: 8.90%
 Indels: 301
 RESULT 737
 ID ACN39359 standard; cDNA; 2647 BP.
 DE Tumour-associated antigenic target (TAT) cDNA DNA88114, SEQ ID NO:3452.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.95%
 Best Local Similarity: 21.77%
 Query Match: 8.90%
 Indels: 301
 RESULT 738
 ID ABX63472 standard; cDNA; 2659 BP.
 DE Human cDNA #472 differentially expressed in activated vascular tissue.
 PN US2002137081-A1.
 PD 26-SEP-2002.

PA (BAND/) BANDMAN O.
 Percent Similarity: 33.14%
 Best Local Similarity: 21.90%
 Query Match: 8.87%
 Indels: 308
 RESULT 739
 ID ADJ56209 standard; cDNA; 2659 BP.
 DE Human cDNA differentially expressed in MYCN activated cells SeqID 15.
 PN US2003119009-A1.
 PD 26-JUN-2003.
 PA (STUA/) STUART S G.
 PA (NUCH/) NUCHTERN J G.
 PA (PLOW/) PLOW S E.
 PA (SHOH/) SHOHET J M.
 Percent Similarity: 33.14%
 Best Local Similarity: 21.90%
 Query Match: 8.87%
 Indels: 308
 RESULT 740
 ID ADQ85290 standard; cDNA; 2648 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2104.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Percent Similarity: 33.03%
 Best Local Similarity: 21.90%
 Query Match: 8.85%
 Indels: 308
 RESULT 741
 ID ADQ84481 standard; cDNA; 2648 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #1295.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Percent Similarity: 33.03%
 Best Local Similarity: 21.90%
 Query Match: 8.85%
 Indels: 308
 RESULT 742
 ID ADE53754 standard; cDNA; 7149 BP.
 DE Human prostate cancer cDNA #101.
 PN US2003190640-A1.
 PD 09-OCT-2003.
 PA (FARI/) FARIS M.
 PA (PEAR-) PEARSON C I.
 Percent Similarity: 32.83%
 Best Local Similarity: 21.89%
 Query Match: 8.83%
 Indels: 305
 RESULT 743
 ID AAH99569 standard; cDNA; 3115 BP.
 DE Human protein encoding cDNA sequence SEQ ID NO:404.
 PN WO200153455-A2.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 36.16%
 Best Local Similarity: 24.21%
 Query Match: 8.80%
 Indels: 169
 RESULT 744
 ID ABA08672 standard; cDNA; 3115 BP.
 DE Human membrane-type Ser kinase homologue cDNA, SEQ ID NO:448.
 PN WO200157188-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 36.16%
 Best Local Similarity: 24.21%
 Query Match: 8.80%
 Indels: 169
 RESULT 745
 ID ADL64960 standard; DNA; 2647 BP.
 DE DNA encoding human complement component 1 protein, CIS.
 PN US2004033582-A1.
 PD 19-FEB-2004.
 PA (EDMO/) EDMONDS M.
 PA (HUIL/) HUI L.

PA (PERE/) PERRONE M.
PA (POWE/) POWELL J R.
PA (RAMA/) RAMANATHAN C S.
PA (SWAN/) SWANSON B.
PA (TSUC/) TSUCHIHASHI Z.
PA (ZEBE/) ZERBA K.
Percent Similarity: 33.22%
Best Local Similarity: 21.76%
Query Match: 8.77%
Conservative: 99
Mismatches: 284
Indels: 293
RESULT 746
ID AAC77788 standard; cDNA; 2725 BP.
DE Human cancer associated gene sequence SEQ ID NO:182.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 32.45%
Best Local Similarity: 21.33%
Query Match: 8.67%
Conservative: 97
Mismatches: 286
Indels: 303
RESULT 747
ID ABK63441 standard; cDNA; 2908 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #1348.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 33.71%
Best Local Similarity: 21.34%
Query Match: 8.63%
Conservative: 98
Mismatches: 248
Indels: 278
RESULT 748
ID ADB58967 standard; DNA; 2908 BP.
DE Toxicity-related gene, SEQ ID 3993.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 33.71%
Best Local Similarity: 21.34%
Query Match: 8.63%
Conservative: 98
Mismatches: 248
Indels: 278
RESULT 749
ID ADB53715 standard; DNA; 2908 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4257.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 33.71%
Best Local Similarity: 21.34%
Query Match: 8.63%
Conservative: 98
Mismatches: 248
Indels: 278
RESULT 750
ID APT41719 standard; DNA; 2908 BP.
DE Toxicity modelling related rat gene SEQ ID No 1421.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 33.71%
Best Local Similarity: 21.34%
Query Match: 8.63%
Conservative: 98
Mismatches: 248
Indels: 278
RESULT 751
ID AAS92433 standard; cDNA; 2358 BP.
DE DNA encoding novel human diagnostic protein #28237.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 33.71%
Best Local Similarity: 21.34%
Query Match: 8.63%
Conservative: 98
Mismatches: 248
Indels: 278
RESULT 752
ID AAA88492 standard; cDNA; 2955 BP.
DE Human matrixase (truncated form) cDNA.
PN WO200053232-A1.
PD 14-SEP-2000.
PA (GEOU) UNIV GEORGETOWN.
Percent Similarity: 36.11%
Best Local Similarity: 24.33%
Query Match: 8.53%
Conservative: 75
Mismatches: 238
Indels: 170
RESULT 753

ID AAF28099 standard; cDNA; 3142 BP.
DE Human membrane-type serine protease MT-SPI coding sequence.
PN WO200123524-A2.
PD 05-APR-2001.
PA (REGC) UNIV CALIFORNIA.
Percent Similarity: 36.11%
Best Local Similarity: 24.33%
Query Match: 8.53%
Conservative: 75
Mismatches: 238
Indels: 170
RESULT 754
ID AAA88493 standard; cDNA; 3149 BP.
DE Human matrixase cDNA.
PN WO200053232-A1.
PD 14-SEP-2000.
PA (GEOU) UNIV GEORGETOWN.
Percent Similarity: 36.11%
Best Local Similarity: 24.33%
Query Match: 8.53%
Conservative: 75
Mismatches: 238
Indels: 170
RESULT 755
ID ADN39650 standard; cDNA; 3149 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C22.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.33%
Query Match: 8.53%
Conservative: 75
Mismatches: 238
Indels: 170
RESULT 756
ID ADR24296 standard; DNA; 3149 BP.
DE Breast cancer prognosis marker #157.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
Percent Similarity: 36.11%
Best Local Similarity: 24.33%
Query Match: 8.53%
Conservative: 75
Mismatches: 238
Indels: 170
RESULT 757
ID AAH57431 standard; cDNA; 3152 BP.
DE Human intestine cell specific cDNA sequence SEQ ID NO:271.
PN WO200132927-A2.
PD 10-MAY-2001.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.33%
Query Match: 8.53%
Conservative: 75
Mismatches: 238
Indels: 170
RESULT 758
ID AAA37657 standard; DNA; 3159 BP.
DE Human peptidase, HPEP-1 coding sequence.
PN WO200042201-A2.
PD 20-JUL-2000.
PA (INCY-) INCYTE PHARM INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.33%
Query Match: 8.53%
Conservative: 75
Mismatches: 238
Indels: 170
RESULT 759
ID ADN04753 standard; cDNA; 3269 BP.
DE Antiposoriatic cDNA sequence #590.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.33%
Query Match: 8.53%
Conservative: 75
Mismatches: 238
Indels: 170
RESULT 760
ID ADP23333 standard; cDNA; 3269 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:427.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.33%
Query Match: 8.53%
Conservative: 75
Mismatches: 238
Indels: 170
RESULT 761

ID ADR66212 standard; DNA; 3269 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 66 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Percent Similarity: 36.11%
Best Local Similarity: 24.33%
Query Match: 8.53%
Conservative: 75
Mismatch: 238
Indels: 170
RESULT 762
ID ADR66554 standard; DNA; 3269 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 66 #3.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Percent Similarity: 36.11%
Best Local Similarity: 24.33%
Query Match: 8.53%
Conservative: 75
Mismatch: 238
Indels: 170
RESULT 763
ID ADI16507 standard; cDNA; 2838 BP.
DE Human NOVX cDNA to treat human pathological conditions SeqID43.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 764
ID ADF90776 standard; DNA; 3128 BP.
DE Human hepatic-fibrosis disease marker SEQ ID 238.
PN JP2003259877-A.
PD 16-SEP-2003.
PA (SUMU-) SUMITOMO SEIYAKU KK.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 765
ID AAX87815 standard; cDNA; 3147 BP.
DE Tumour antigen derived gene-15 (TADG-15) cDNA.
PN WO942120-A1.
PD 26-AUG-1999.
PA (UYAR-) UNIV ARKANSAS.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 766
ID AAH23609 standard; RNA; 3147 BP.
DE Human TADG-15 antisense RNA sequence.
PN WO200129056-A1.
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 767
ID AAH23601 standard; DNA; 3147 BP.
DE Human TADG-15 coding sequence.
PN WO200129056-A1.
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 768
ID AAD13155 standard; DNA; 3147 BP.
DE Human membrane-type serine protease (MTSP) 1 protease domain DNA.

PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 769
ID AAD13113 standard; DNA; 3147 BP.
DE Human membrane-type serine protease (MTSP) 1 DNA.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 770
ID AAL53444 standard; DNA; 3147 BP.
DE Type II transmembrane serine protease 1 coding DNA SEQ ID No 1.
PN WO200272786-A2.
PD 19-SEP-2002.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 771
ID AAL53445 standard; DNA; 3147 BP.
DE Type II transmembrane serine protease 1 domain DNA SEQ ID No 3.
PN WO200272786-A2.
PD 19-SEP-2002.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 772
ID ABZ22450 standard; cDNA; 3147 BP.
DE Human membrane-type serine protease MTSP1 encoding cDNA SEQ ID NO.1.
PN WO200292841-A2.
PD 21-NOV-2002.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 773
ID ABZ22451 standard; cDNA; 3147 BP.
DE Human MTSP1 protease domain encoding cDNA SEQ ID NO:3.
PN WO200292841-A2.
PD 21-NOV-2002.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 774
ID AAL60793 standard; DNA; 3147 BP.
DE Human membrane-type serine protease MTSP1 protease domain DNA.
PN WO2003044179-A2.
PD 30-MAY-2003.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 775
ID AAL60792 standard; DNA; 3147 BP.
DE Human membrane-type serine protease MTSP1 DNA.
PN WO2003044179-A2.
PD 30-MAY-2003.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 776
ID RAD47225 standard; DNA; 3147 BP.
DE Human membrane-type serine protease 1 (MTSP1) DNA.
PN WO200277267-A2.

```

PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
RESULT 777
ID AAD47181 standard; DNA; 3147 BP.
DE Human membrane-type serine protease (MTSP1) protease domain DNA.
PN WO200277263-A2.
PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
RESULT 778
ID AAD47180 standard; DNA; 3147 BP.
DE Human membrane-type serine protease, MTSP1 DNA.
PN WO200277263-A2.
PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 779
ID ABZ58500 standard; cDNA; 3147 BP.
DE Transmembrane serine protease 1 (MTSP1) cDNA.
PN WO2003004681-A2.
PD 16-JAN-2003.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 780
ID ABZ58501 standard; cDNA; 3147 BP.
DE Transmembrane serine protease 1 (MTSP1) protein domain cDNA.
PN WO2003004681-A2.
PD 16-JAN-2003.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 781
ID ADB97550 standard; DNA; 3147 BP.
DE Human MTSP1-encoding DNA, SEQ ID NO:1.
PN WO2003031585-A2.
PD 17-APR-2003.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 782
ID ADB97552 standard; DNA; 3147 BP.
DE Human MTSP1 protease domain-encoding DNA, SEQ ID NO:3.
PN WO2003031585-A2.
PD 17-APR-2003.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 783
ID ADI10370 standard; DNA; 3147 BP.
DE Human cell surface protease coding sequence #1.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 784
ID ADG65325 standard; cDNA; 3147 BP.
DE Human MTSP1 coding sequence.
PN WO2003104394-A2.
PD 18-DEC-2003.
PA (DEND-) DENDREON SAN DIEGO LLC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
RESULT 785
ID ADI28860 standard; cDNA; 3147 BP.
DE Human matrixase (MTSP1) nucleotide sequence.
PN WO2004005471-A2.
PD 15-JAN-2004.
PA (DEND-) DENDREON SAN DIEGO LLC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 786
ID ADJ46894 standard; cDNA; 3147 BP.
DE Human transmembrane serine protease (MTSP) cDNA #1.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 787
ID ADE53755 standard; cDNA; 3145 BP.
DE Human prostate cancer cDNA #102.
PN US2003190640-A1.
PD 09-OCT-2003.
PA (FARI/) FARI M.
PA (PEAR/) PEARSON C I.
Percent Similarity: 34.47%
Best Local Similarity: 22.66%
Query Match: 8.48%
Conservative: 97
Mismatch: 309
Indels: 230
RESULT 788
ID RAD13165 standard; DNA; 3696 BP.
DE Human enterokinase DNA.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 38.05%
Best Local Similarity: 22.90%
Query Match: 8.40%
Conservative: 90
Mismatch: 225
Indels: 143
RESULT 789
ID ADA83984 standard; DNA; 3696 BP.
DE Human PRSS7 gene.
PN WO2002103028-A2.
PD 27-DEC-2002.
PA (BIOM-) BIOMEDICAL CENT.
Percent Similarity: 38.05%
Best Local Similarity: 22.90%
Query Match: 8.40%
Conservative: 90
Mismatch: 225
Indels: 143
RESULT 790
ID ADI10399 standard; DNA; 3696 BP.
DE Human cell surface protease coding sequence #16.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 38.05%
Best Local Similarity: 22.90%
Query Match: 8.40%
Conservative: 90
Mismatch: 225
Indels: 143
RESULT 791
ID ADJ46923 standard; cDNA; 3696 BP.
DE Human transmembrane serine protease (MTSP)-related cDNA #6.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 38.05%
Best Local Similarity: 22.90%
Query Match: 8.40%
Conservative: 90
Mismatch: 225
Indels: 143
RESULT 792
ID ADH72215 standard; DNA; 10989 BP.
DE Human gene of the invention NOV54b SEQ ID NO:1111.
PN WO2003102155-A2.
PD 11-DEC-2003.

```

PA (CURA-) CURAGEN CORP.	Conservative: 93	PA (ROSE/) ROSEN C A.	Conservative: 68
Percent Similarity: 32.74%	Mismatches: 239	Best Local Similarity: 35.13%	Mismatches: 196
Query Match: 8.35%	Indels: 287	Query Match: 8.30%	Indels: 177
RESULT 793		RESULT 801	
ID ABS58378 standard; DNA; 4506 BP.		ID ADH71143 standard; DNA; 10466 BP.	
DE Protein modification and maintenance molecule #11.		DE Human gene of the invention NOV4e	SEQ ID NO:39.
PN WO200260942-A2.		PN WO2003102155-A2.	
PD 08-AUG-2002.		PD 11-DEC-2003.	
PA (INCY-) INCYTE GENOMICS INC.		PA (CURA-) CURAGEN CORP.	
Percent Similarity: 32.74%	Conservative: 93	Percent Similarity: 31.76%	Conservative: 78
Best Local Similarity: 20.84%	Mismatches: 239	Best Local Similarity: 22.30%	Mismatches: 270
Query Match: 8.33%	Indels: 287	Query Match: 8.26%	Indels: 293
RESULT 794		RESULT 802	
ID AAS18801 standard; cDNA; 5598 BP.		ID ADH71135 standard; DNA; 10655 BP.	
DE DNA encoding cancer and neurogenesis associated gene.		DE Human gene of the invention NOV4a	SEQ ID NO:31.
PN WO200190354-A1.		PN WO2003102155-A2.	
PD 29-NOV-2001.		PD 11-DEC-2003.	
PA (UYLE-) UNIV LEEDS.		PA (CURA-) CURAGEN CORP.	
Percent Similarity: 32.74%	Conservative: 93	Percent Similarity: 31.76%	Conservative: 78
Best Local Similarity: 20.84%	Mismatches: 239	Best Local Similarity: 22.30%	Mismatches: 270
Query Match: 8.33%	Indels: 287	Query Match: 8.26%	Indels: 293
RESULT 795		RESULT 803	
ID AAS18804 standard; cDNA; 5667 BP.		ID ADH71145 standard; DNA; 12900 BP.	
DE DNA encoding cancer and neurogenesis associated gene, variant 5G-3V3.		DE Human gene of the invention NOV4f	SEQ ID NO:41.
PN WO200190354-A1.		PN WO2003102155-A2.	
PD 29-NOV-2001.		PD 11-DEC-2003.	
PA (UYLE-) UNIV LEEDS.		PA (CURA-) CURAGEN CORP.	
Percent Similarity: 32.74%	Conservative: 93	Percent Similarity: 31.76%	Conservative: 78
Best Local Similarity: 20.84%	Mismatches: 239	Best Local Similarity: 22.30%	Mismatches: 270
Query Match: 8.33%	Indels: 287	Query Match: 8.26%	Indels: 293
RESULT 796		RESULT 804	
ID AAS18802 standard; cDNA; 6145 BP.		ID AAH23602 standard; DNA; 2900 BP.	
DE DNA encoding cancer and neurogenesis associated gene, variant 5G-3V1.		DE Human cDNA differentially expressed in granulocytic cells #831.	
PN WO200190354-A1.		PN WO200129056-A1.	
PD 29-NOV-2001.		PD 26-APR-2001.	
PA (UYLE-) UNIV LEEDS.		PA (UYAR-) UNIV ARKANSAS.	
Percent Similarity: 32.74%	Conservative: 93	Percent Similarity: 37.93%	Conservative: 79
Best Local Similarity: 20.84%	Mismatches: 239	Best Local Similarity: 25.55%	Mismatches: 225
Query Match: 8.33%	Indels: 287	Query Match: 8.21%	Indels: 174
RESULT 797		RESULT 805	
ID AAS18803 standard; cDNA; 6409 BP.		ID ABK84260 standard; cDNA; 2900 BP.	
DE DNA encoding cancer and neurogenesis associated gene, variant 5G-3V2.		DE Human cDNA differentially expressed in granulocytic cells #831.	
PN WO200190354-A1.		PN WO200228999-A2.	
PD 29-NOV-2001.		PD 11-APR-2002.	
PA (UYLE-) UNIV LEEDS.		PA (GENE-) GENE LOGIC INC.	
Percent Similarity: 32.74%	Conservative: 93	Percent Similarity: 37.93%	Conservative: 79
Best Local Similarity: 20.84%	Mismatches: 239	Best Local Similarity: 25.55%	Mismatches: 225
Query Match: 8.33%	Indels: 287	Query Match: 8.21%	Indels: 174
RESULT 798		RESULT 806	
ID AAS18805 standard; cDNA; 7323 BP.		ID AAD33319 standard; cDNA; 12525 BP.	
DE DNA encoding cancer and neurogenesis associated gene, variant 5R-3V2.		DE Rat C3b/C4b complement receptor like cDNA.	
PN WO200190354-A1.		PN WO200210199-A2.	
PD 29-NOV-2001.		PD 07-FEB-2002.	
PA (UYLE-) UNIV LEEDS.		PA (AMGE-) AMGEN INC.	
Percent Similarity: 32.74%	Conservative: 93	Percent Similarity: 32.94%	Conservative: 94
Best Local Similarity: 20.84%	Mismatches: 239	Best Local Similarity: 20.50%	Mismatches: 222
Query Match: 8.33%	Indels: 287	Query Match: 8.21%	Indels: 286
RESULT 799		RESULT 807	
ID AAS18806 standard; cDNA; 8034 BP.		ID ABS64376 standard; DNA; 8010 BP.	
DE DNA encoding cancer and neurogenesis associated gene, variant 5R23V2.		DE Human cub and sushi domain containing gene #2.	
PN WO200190354-A1.		PN WO200264791-A2.	
PD 29-NOV-2001.		PD 22-AUG-2002.	
PA (UYLE-) UNIV LEEDS.		PA (CURA-) CURAGEN CORP.	
Percent Similarity: 32.74%	Conservative: 93	Percent Similarity: 31.76%	Conservative: 78
Best Local Similarity: 20.84%	Mismatches: 239	Best Local Similarity: 22.30%	Mismatches: 270
Query Match: 8.33%	Indels: 287	Query Match: 8.19%	Indels: 293
RESULT 800		RESULT 808	
ID AAF18150 standard; DNA; 2063 BP.		ID ADH71139 standard; DNA; 8010 BP.	
DE Lung cancer associated polynucleotide sequence SEQ ID 169.		DE Human gene of the invention NOV4c	SEQ ID NO:35.
PN WO200055180-A2.		PN WO2003102155-A2.	
PD 21-SEP-2000.		PD 11-DEC-2003.	
PA (HUMA-) HUMAN GENOME SCI INC.		PA (CURA-) CURAGEN CORP.	

Percent Similarity: 31.76% Conservative: 78
Best Local Similarity: 22.30% Mismatches: 270
Query Match: 8.19% Indels: 293
RESULT 809
ID ADH71141 standard; DNA; 9951 BP.
DE Human gene of the invention NOV4d SEQ ID NO:37.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 31.76% Conservative: 78
Best Local Similarity: 22.30% Mismatches: 270
Query Match: 8.19% Indels: 293
RESULT 810
ID ABS64375 standard; DNA; 10136 BP.
DE Human cub and sushi domain containing gene #1.
PN WO200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 31.76% Conservative: 78
Best Local Similarity: 22.30% Mismatches: 270
Query Match: 8.19% Indels: 293
RESULT 811
ID ADH71165 standard; DNA; 10136 BP.
DE Human gene of the invention NOV4p SEQ ID NO:61.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 31.76% Conservative: 78
Best Local Similarity: 22.30% Mismatches: 270
Query Match: 8.19% Indels: 293
RESULT 812
ID ADH71137 standard; DNA; 10136 BP.
DE Human gene of the invention NOV4b SEQ ID NO:33.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 31.76% Conservative: 78
Best Local Similarity: 22.30% Mismatches: 270
Query Match: 8.19% Indels: 293
RESULT 813
ID ADH71167 standard; DNA; 10136 BP.
DE Human gene of the invention NOV4q SEQ ID NO:63.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 31.76% Conservative: 78
Best Local Similarity: 22.30% Mismatches: 270
Query Match: 8.19% Indels: 293
RESULT 814
ID AAD33320 standard; cDNA; 10433 BP.
DE Human C3b/C4b complement receptor like cDNA #2.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Percent Similarity: 32.48% Conservative: 92
Best Local Similarity: 20.72% Mismatches: 241
Query Match: 8.12% Indels: 287
RESULT 815
ID RAD33318 standard; cDNA; 10673 BP.
DE Human C3b/C4b complement receptor like cDNA #1.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Percent Similarity: 32.48% Conservative: 92
Best Local Similarity: 20.72% Mismatches: 241
Query Match: 8.12% Indels: 287
RESULT 816
ID ADG83835 standard; cDNA; 1401 BP.
DE Rough scale snake venom protease coding sequence.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYQU) UNIV QUEENSLAND.
Percent Similarity: 37.66% Conservative: 79

Best Local Similarity: 23.42% Mismatches: 183
Query Match: 8.10% Indels: 163
RESULT 817
ID AAC77957 standard; cDNA; 2756 BP.
DE Human cancer associated gene sequence SEQ ID NO:351.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 36.89% Conservative: 82
Best Local Similarity: 24.02% Mismatches: 233
Query Match: 8.07% Indels: 171
RESULT 818
ID RAD37039 standard; DNA; 3106 BP.
DE Epithin gene.
PN WO200203787-A2.
PD 17-JAN-2002.
PA (DELT-) DELTAGEN INC.
Percent Similarity: 34.74% Conservative: 81
Best Local Similarity: 22.92% Mismatches: 245
Query Match: 8.07% Indels: 204
RESULT 819
ID AAQ70104 standard; cDNA; 2581 BP.
DE Bovine enterokinase.
PN WO9416083-A1.
PD 21-JUL-1994.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 38.05% Conservative: 80
Best Local Similarity: 24.58% Mismatches: 225
Query Match: 8.05% Indels: 143
RESULT 820
ID ADG83831 standard; cDNA; 1365 BP.
DE Red belly black snake venom protease coding sequence.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYQU) UNIV QUEENSLAND.
Percent Similarity: 36.25% Conservative: 73
Best Local Similarity: 22.95% Mismatches: 189
Query Match: 7.97% Indels: 161
RESULT 821
ID ADG83833 standard; cDNA; 1395 BP.
DE Mainland tiger snake venom protease coding sequence.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYQU) UNIV QUEENSLAND.
Percent Similarity: 37.07% Conservative: 78
Best Local Similarity: 22.97% Mismatches: 187
Query Match: 7.97% Indels: 161
RESULT 822
ID AAQ12680 standard; DNA; 1529 BP.
DE PAP-I-protein C fusion construct.
PN WO9109953-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 35.98% Conservative: 68
Best Local Similarity: 23.99% Mismatches: 182
Query Match: 7.93% Indels: 182
RESULT 823
ID AAA54035 standard; DNA; 1843 BP.
DE Human protein C coding sequence.
PN WO200054787-A1.
PD 21-SEP-2000.
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
Percent Similarity: 34.99% Conservative: 68
Best Local Similarity: 24.42% Mismatches: 220
Query Match: 7.92% Indels: 199
RESULT 824
ID AAF54050 standard; DNA; 1843 BP.
DE Human protein C gene, SEQ ID NO:49.
PN WO200075279-A2.
PD 14-DEC-2000.
PA (UNMI) UNIV MICHIGAN.
Percent Similarity: 34.99% Conservative: 68

```

Best Local Similarity: 24.42% Mismatches: 220
Query Match: 7.92% Indels: 199
RESULT 825
ID ABN97175 standard; DNA; 1843 BP.
DE Gene #3673 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 34.99% Conservative: 68
Best Local Similarity: 24.42% Mismatches: 220
Query Match: 7.92% Indels: 199
RESULT 826
ID ADN42161 standard; cDNA; 2838 BP.
DE Human cDNA encoding NOV 8.
PN US2004033493-A1.
PD 19-FEB-2004.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELDI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENA C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C B.
Percent Similarity: 36.26% Conservative: 72
Best Local Similarity: 24.96% Mismatches: 238
Query Match: 7.92% Indels: 170
RESULT 827
ID AAH26365 standard; cDNA; 1386 BP.
DE DNA encoding human protein C derivative.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL/) LILLY & CO ELI.
Percent Similarity: 36.36% Conservative: 64
Best Local Similarity: 24.96% Mismatches: 176
Query Match: 7.91% Indels: 182
RESULT 828
ID ABO86158 standard; DNA; 3096 BP.
DE Novel human gene. SEQ ID 29.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK/) SMITHKLINE BEECHAM CORP.
PA (SMIK/) SMITHKLINE BEECHAM PLC.
PA (GLAX/) GLAXO GROUP LTD.
Percent Similarity: 34.63% Conservative: 87
Best Local Similarity: 22.58% Mismatches: 278
Query Match: 7.91% Indels: 194
RESULT 829
ID AAN81563 standard; cDNA; 1756 BP.
DE cDNA sequence encoding protein C.
PN EP266190-A.
PD 04-MAY-1988.
PA (ZYMO/) ZYMOGENETICS INC.
Percent Similarity: 36.12% Conservative: 61
Best Local Similarity: 25.05% Mismatches: 172
Query Match: 7.90% Indels: 181
RESULT 830
ID ADB63780 standard; cDNA; 2580 BP.
DE

```

```

DE Human cDNA encoding clone UTERU20087070.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 34.49% Conservative: 110
Best Local Similarity: 21.32% Mismatches: 292
Query Match: 7.90% Indels: 258
RESULT 831
ID AAH26363 standard; cDNA; 1386 BP.
DE DNA encoding human protein C derivative.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL/) LILLY & CO ELI.
Percent Similarity: 36.36% Conservative: 64
Best Local Similarity: 24.96% Mismatches: 176
Query Match: 7.88% Indels: 182
RESULT 832
ID AAH26366 standard; cDNA; 1386 BP.
DE DNA encoding human protein C derivative.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL/) LILLY & CO ELI.
Percent Similarity: 36.36% Conservative: 64
Best Local Similarity: 24.96% Mismatches: 176
Query Match: 7.88% Indels: 182
RESULT 833
ID AAZ46750 standard; DNA; 1245 BP.
DE Truncated human protein C polypeptide encoding DNA.
PN WO9963070-A1.
PD 09-DEC-1999.
PA (ELIL/) LILLY & CO ELI.
Percent Similarity: 36.12% Conservative: 61
Best Local Similarity: 25.05% Mismatches: 172
Query Match: 7.87% Indels: 181
RESULT 834
ID AAK86039 standard; DNA; 1257 BP.
DE Synthetic DNA encoding zymogen protein C.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Percent Similarity: 36.12% Conservative: 61
Best Local Similarity: 25.05% Mismatches: 172
Query Match: 7.87% Indels: 181
RESULT 835
ID ADO18784 standard; DNA; 1257 BP.
DE Mature human zymogen-like protein C coding sequence.
PN WO2004044190-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Percent Similarity: 36.12% Conservative: 61
Best Local Similarity: 25.05% Mismatches: 172
Query Match: 7.87% Indels: 181
RESULT 836
ID AAN60001 standard; DNA; 1260 BP.
DE Sequence encoding polypeptide with human protein C activity.
PN EP191606-A.
PD 20-AUG-1986.
PA (ELIL/) LILLY & CO ELI.
Percent Similarity: 36.12% Conservative: 61
Best Local Similarity: 25.05% Mismatches: 172
Query Match: 7.87% Indels: 181
RESULT 837
ID AAH26361 standard; cDNA; 1260 BP.
DE DNA encoding human protein C.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL/) LILLY & CO ELI.
Percent Similarity: 36.12% Conservative: 61
Best Local Similarity: 25.05% Mismatches: 172
Query Match: 7.87% Indels: 181

```

```
RESULT 838
ID AAC83311 standard; DNA; 1260 BP.
DE DNA encoding human protein C derivative 1.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 36.12%
Best Local Similarity: 25.05%
Conservative: 61
Mismatch: 172
Indels: 181
Query Match:
RESULT 839
ID AAD15223 standard; DNA; 1260 BP.
DE Human mature wild type protein C encoding DNA.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 36.12%
Best Local Similarity: 25.05%
Conservative: 61
Mismatch: 172
Indels: 181
Query Match:
RESULT 840
ID AAK86038 standard; DNA; 1383 BP.
DE Synthetic DNA encoding protein C precursor protein.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Percent Similarity: 36.12%
Best Local Similarity: 25.05%
Conservative: 61
Mismatch: 172
Indels: 181
Query Match:
RESULT 841
ID ADM77501 standard; DNA; 1383 BP.
DE Human protein C wild-type gene sequence.
PN WO200310666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
Percent Similarity: 36.12%
Best Local Similarity: 25.05%
Conservative: 61
Mismatch: 172
Indels: 181
Query Match:
RESULT 842
ID ADO18785 standard; DNA; 1383 BP.
DE Human zymogen-like protein C coding sequence.
PN WO2004044190-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
Percent Similarity: 36.12%
Best Local Similarity: 25.05%
Conservative: 61
Mismatch: 172
Indels: 181
Query Match:
RESULT 843
ID AAN81408 standard; DNA; 1386 BP.
DE DNA encoding human protein C.
PN JP63263083-A.
PD 31-OCT-1988.
PA (FARH ) HOECHST JAPAN LTD.
Percent Similarity: 36.12%
Best Local Similarity: 25.05%
Conservative: 61
Mismatch: 172
Indels: 181
Query Match:
RESULT 844
ID AAN90187 standard; DNA; 1386 BP.
DE DNA encoding zymogen form of human protein C.
PN EP323149-A.
PD 05-JUL-1989.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 36.12%
Best Local Similarity: 25.05%
Conservative: 61
Mismatch: 172
Indels: 181
Query Match:
RESULT 845
ID AAR79724 standard; DNA; 1386 BP.
DE Human protein C cDNA.
PN WO9720043-A1.
PD 05-JUN-1997.
PA (ZYMO ) ZYMOGENETICS INC.
Percent Similarity: 36.12%
Best Local Similarity: 25.05%
Conservative: 61
Mismatch: 172
Indels: 181
Query Match:
RESULT 846
ID AAH26362 standard; cDNA; 1386 BP.
DE DNA encoding human protein C.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 36.12%
Best Local Similarity: 25.05%
Conservative: 61
Mismatch: 172
Indels: 181
Query Match:
RESULT 847
ID RAC83313 standard; DNA; 1386 BP.
DE DNA encoding human protein C derivative 3.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 36.12%
Best Local Similarity: 25.05%
Conservative: 61
Mismatch: 172
Indels: 181
Query Match:
RESULT 848
ID AAC83312 standard; DNA; 1386 BP.
DE DNA encoding human protein C derivative 2.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 36.12%
Best Local Similarity: 25.05%
Conservative: 61
Mismatch: 172
Indels: 181
Query Match:
RESULT 849
ID RAD15224 standard; DNA; 1386 BP.
DE Human wild type protein C encoding DNA.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 36.12%
Best Local Similarity: 25.05%
Conservative: 61
Mismatch: 172
Indels: 181
Query Match:
RESULT 850
ID RAQ13357 standard; cDNA; 1754 BP.
DE Human protein C gene.
PN WO9112320-A.
PD 22-AUG-1991.
PA (ZYMO ) ZYMOGENETICS INC.
Percent Similarity: 36.12%
Best Local Similarity: 25.05%
Conservative: 61
Mismatch: 172
Indels: 181
Query Match:
RESULT 851
ID AAQ12649 standard; cDNA; 1754 BP.
DE Protein C precursor gene.
PN WO9109951-A.
PD 11-JUL-1991.
PA (ZYMO ) ZYMOGENETICS INC.
Percent Similarity: 36.12%
Best Local Similarity: 25.05%
Conservative: 61
Mismatch: 172
Indels: 181
Query Match:
RESULT 852
ID AAQ12678 standard; cDNA; 1755 BP.
DE Human protein C.
PN WO9109953-A.
PD 11-JUL-1991.
PA (ZYMO ) ZYMOGENETICS INC.
Percent Similarity: 36.12%
Best Local Similarity: 25.05%
Conservative: 61
Mismatch: 172
Indels: 181
Query Match:
RESULT 853
ID AAR32795 standard; cDNA; 1755 BP.
DE Human protein C cDNA.
PN US5516650-A.
PD 14-MAY-1996.
```


Best Local Similarity: 22.85% Mismatches: 211
 Query Match: 7.63% Indels: 205
 RESULT 870
 ID AAN60598 standard; DNA; 2459 BP.
 DE Sequence encoding plasmid pDPAP3.
 PN JP61139386-A.
 PD 26-JUN-1986.
 PA (TOYU) TOYO SODA MFG CO LTD.
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 PA (CENG) CENTRAL GLASS CO LTD.
 PA (HODO) HODOGAYA CHEM IND CO LTD.
 Percent Similarity: 35.31% Conservative: 80
 Best Local Similarity: 22.81% Mismatches: 212
 Query Match: 7.62% Indels: 205
 RESULT 871
 ID AAN70389 standard; DNA; 2459 BP.
 DE cDNA encoding human tissue plasminogen activator (TPA) in plasmid pDPAP3.
 PN EP231883-A.
 PD 12-AUG-1987.
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 PA (NIPS) NIPPON SODA CO.
 PA (CENG) CENTRAL GLASS CO LTD.
 PA (TOXJ) TOYO SODA MFG CO LTD.
 PA (NISC) NISSAN CHEM IND LTD.
 PA (NISC) NISSAN CHEMICAL INDS KK.
 Percent Similarity: 35.31% Conservative: 80
 Best Local Similarity: 22.81% Mismatches: 212
 Query Match: 7.62% Indels: 205
 RESULT 872
 ID AAQ03218 standard; DNA; 1389 BP.
 DE DNA sequence encoding human protein C mutant.
 PN EP352651-A.
 PD 31-JAN-1990.
 PA (FARH) HOECHST JAPAN LTD.
 Percent Similarity: 34.78% Conservative: 61
 Best Local Similarity: 23.73% Mismatches: 178
 Query Match: 7.59% Indels: 183
 RESULT 873
 ID AAQ24121 standard; DNA; 2550 BP.
 DE Encodes tPA analogue KK2A.
 PN US5106741-A.
 PD 21-APR-1992.
 PA (UPJO) UPJOHN CO.
 Percent Similarity: 38.66% Conservative: 95
 Best Local Similarity: 23.91% Mismatches: 235
 Query Match: 7.58% Indels: 161
 RESULT 874
 ID AAQ03581 standard; DNA; 1614 BP.
 DE Glycosylated plasminogen activator sequence.
 PN JP02042981-A.
 PD 13-FEB-1990.
 PA (KANF) KANEGAFUCHI CHEM KK.
 Percent Similarity: 35.62% Conservative: 78
 Best Local Similarity: 22.88% Mismatches: 196
 Query Match: 7.57% Indels: 201
 RESULT 875
 ID ADE06939 standard; DNA; 2145 BP.
 DE Novel coding sequence (useful for identifying genetic disorders) #5.
 PN WO2003054152-A2.
 PD 03-JUL-2003.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 36.84% Conservative: 85
 Best Local Similarity: 24.42% Mismatches: 226
 Query Match: 7.54% Indels: 207
 RESULT 876
 ID ADD18497 standard; DNA; 2198 BP.
 DE Human prostate cancer diagnosis related DNA sequence SeqID69.
 PN WO2003012067-A2.
 PD 13-FEB-2003.
 PA (UNMI) UNIV MICHIGAN.
 Percent Similarity: 35.54% Conservative: 93
 Best Local Similarity: 22.43% Mismatches: 236
 Query Match: 7.54% Indels: 222

RESULT 877
 ID ABX77617 standard; cDNA; 2641 BP.
 DE Differentially expressed breast cancer associated cDNA #112.
 PN US2002156263-A1.
 PD 24-OCT-2002.
 PA (CHEN/) CHEN H.
 Percent Similarity: 35.70% Conservative: 93
 Best Local Similarity: 21.93% Mismatches: 208
 Query Match: 7.54% Indels: 227
 RESULT 878
 ID ACN41469 standard; cDNA; 3112 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:344.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Percent Similarity: 34.52% Conservative: 112
 Best Local Similarity: 21.28% Mismatches: 265
 Query Match: 7.52% Indels: 293
 RESULT 879
 ID AAN70779 standard; DNA; 2550 BP.
 DE Sequence encoding tissue plasminogen (TPA) analogue.
 PN WO8703906-A.
 PD 02-JUL-1987.
 PA (UPJO) UPJOHN CO.
 PA (MARO/) MAROTTI K R.
 Percent Similarity: 34.28% Conservative: 83
 Best Local Similarity: 21.86% Mismatches: 229
 Query Match: 7.50% Indels: 211
 RESULT 880
 ID AAQ71243 standard; cDNA; 1554 BP.
 DE Serine protease for fusion protein cleavage.
 PN WO9418227-A2.
 PD 18-AUG-1994.
 PA (DENZ-) DENZYME APS.
 Percent Similarity: 37.30% Conservative: 75
 Best Local Similarity: 23.78% Mismatches: 198
 Query Match: 7.49% Indels: 152
 RESULT 881
 ID AAQ12073 standard; DNA; 2091 BP.
 DE T-PA variant contg. fibronectin for thrombosis lysis (1).
 PN JP03061482-A.
 PD 18-MAR-1991.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 Percent Similarity: 34.06% Conservative: 83
 Best Local Similarity: 21.98% Mismatches: 217
 Query Match: 7.49% Indels: 239
 RESULT 882
 ID ABK63668 standard; cDNA; 1543 BP.
 DE Rat sequence differentially expressed in response to a hepatotoxin #1575.
 PN WO200210453-A2.
 PD 07-FEB-2002.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 37.08% Conservative: 74
 Best Local Similarity: 24.66% Mismatches: 181
 Query Match: 7.47% Indels: 194
 RESULT 883
 ID ADB59220 standard; DNA; 1543 BP.
 DE Toxicity-related gene, SEQ ID 4246.
 PN WO2003064624-A2.
 PD 07-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 37.08% Conservative: 74
 Best Local Similarity: 24.66% Mismatches: 181
 Query Match: 7.47% Indels: 194
 RESULT 884
 ID ADB52603 standard; DNA; 1543 BP.
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3145.
 PN WO2003065993-A2.
 PD 14-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 37.08% Conservative: 74
 Best Local Similarity: 24.66% Mismatches: 181
 Query Match: 7.47% Indels: 194

RESULT 885
ID AAT41842 standard; DNA; 1543 BP.
DE Toxicity modelling related rat gene SEQ ID No 1544.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 37.08%
Best Local Similarity: 24.66%
Query Match: 7.47%
Conservative: 74
Mismatch: 181
Indels: 194

RESULT 886
ID ADP72980 standard; DNA; 1543 BP.
DE Renal toxin progression gene marker #1569.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 37.08%
Best Local Similarity: 24.66%
Query Match: 7.47%
Conservative: 74
Mismatch: 181
Indels: 194

RESULT 887
ID AAQ04903 standard; DNA; 1689 BP.
DE Part of tPA024 gene encoding precursor protein.
PN EP373896-A.
PD 20-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
PA (YAMA) NIPPON STEEL CORP.
Percent Similarity: 35.89%
Best Local Similarity: 23.00%
Query Match: 7.43%
Conservative: 74
Mismatch: 185
Indels: 186

RESULT 888
ID ABX56285 standard; DNA; 3121 BP.
DE Human NOVI2a CG92293-01 DNA SEQ ID 49.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 34.31%
Best Local Similarity: 21.76%
Query Match: 7.43%
Conservative: 90
Mismatch: 271
Indels: 200

RESULT 889
ID AAN70778 standard; DNA; 2543 BP.
DE Sequence encoding tissue plasminogen (TPA) analogue.
PN WO8703906-A.
PD 02-JUL-1987.
PA (UPJO) UPJOHN CO.
PA (MARO) MAROTTI K R.
Percent Similarity: 35.41%
Best Local Similarity: 21.78%
Query Match: 7.41%
Conservative: 92
Mismatch: 210
Indels: 227

RESULT 890
ID ACN41472 standard; cDNA; 2877 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:347.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 32.21%
Best Local Similarity: 21.68%
Query Match: 7.41%
Conservative: 84
Mismatch: 268
Indels: 276

RESULT 891
ID ADG83825 standard; cDNA; 1407 BP.
DE Brown snake venom protease coding sequence.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYQU) UNIV QUEENSLAND.
Percent Similarity: 35.68%
Best Local Similarity: 22.34%
Query Match: 7.40%
Conservative: 74
Mismatch: 197
Indels: 160

RESULT 892
ID AAN81086 standard; DNA; 1738 BP.
DE Pre-pro tissue plasminogen activator coding sequence.
PN EP293934-A.
PD 07-DEC-1988.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 35.68%
Best Local Similarity: 22.34%
Query Match: 7.40%
Conservative: 74
Mismatch: 197
Indels: 160

RESULT 893
ID AAQ12071 standard; DNA; 2097 BP.
DE T-PA with -ve charged finger and/or kringle domain (1).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Percent Similarity: 34.78%
Best Local Similarity: 21.95%
Query Match: 7.40%
Conservative: 83
Mismatch: 199
Indels: 226

RESULT 894
ID ACN41473 standard; cDNA; 2827 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:348.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 32.37%
Best Local Similarity: 21.58%
Query Match: 7.40%
Conservative: 86
Mismatch: 252
Indels: 292

RESULT 895
ID AAN81068 standard; cDNA; 1740 BP.
DE Synthetic pre-pro tissue plasminogen activator homologue.
PN EP292009-A.
PD 23-NOV-1988.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 36.82%
Best Local Similarity: 22.86%
Query Match: 7.38%
Conservative: 80
Mismatch: 181
Indels: 182

RESULT 896
ID AAN91476 standard; DNA; 1557 BP.
DE Sequence of des 1-44E275 t-PA mutant encoded by plasmid p1179.
PN WO8909266-A.
PD 05-OCT-1989.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.62%
Best Local Similarity: 22.71%
Query Match: 7.36%
Conservative: 79
Mismatch: 198
Indels: 199

RESULT 897
ID AAQ12076 standard; DNA; 2100 BP.
DE T-PA variant having Lys416 substituted (3).
PN JP03061484-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Percent Similarity: 34.59%
Best Local Similarity: 21.75%
Query Match: 7.36%
Conservative: 85
Mismatch: 209
Indels: 227

RESULT 898
ID AAL60580 standard; DNA; 2280 BP.
DE Human tissue plasminogen activator (tPA) DNA.
PN WO2003044050-A1.
PD 30-MAY-2003.
PA (PARK/) PARK H.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%
Query Match: 7.36%
Conservative: 86
Mismatch: 215
Indels: 231

RESULT 899
ID AAQ87370 standard; DNA; 2162 BP.
DE Human tPA clone.
PN WO9507351-A1.
PD 16-MAR-1995.
PA (HARD) HARVARD COLLEGE.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%
Query Match: 7.34%
Conservative: 86
Mismatch: 215
Indels: 231

RESULT 900
ID AAV37294 standard; DNA; 2162 BP.
DE Human tissue plasminogen activator gene sequence.
PN US5780272-A.
PD 14-JUL-1998.
PA (HARD) HARVARD COLLEGE.
Percent Similarity: 34.47%
Conservative: 86

Best Local Similarity: 21.75% Mismatches: 215
 Query Match: 7.34% Indels: 231
 RESULT 901
 ID AAN70248 standard; DNA; 2170 BP.
 DE Sequence encoding human tissue plasminogen activator (t-PA) produced by
 DE normal human cells.
 PN EP225177-A.
 PD 10-JUN-1987.
 PA (MITK) MITSUI TOATSU CHEM INC.
 Percent Similarity: 34.47%
 Best Local Similarity: 21.75%
 Mismatches: 215
 Indels: 231
 Query Match: 7.34%
 RESULT 902
 ID AAQ86576 standard; cDNA; 2170 BP.
 DE Human tissue plasminogen activator cDNA.
 PN JP07046983-A.
 PD 21-FEB-1995.
 PA (MITK) MITSUI TOATSU CHEM INC.
 Percent Similarity: 34.47%
 Best Local Similarity: 21.75%
 Mismatches: 215
 Indels: 231
 Query Match: 7.34%
 RESULT 903
 ID AAN90508 standard; cDNA; 2509 BP.
 DE cDNA of human tissue plasminogen activator.
 PN JP01174388-A.
 PD 10-JUL-1989.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 Percent Similarity: 34.47%
 Best Local Similarity: 21.75%
 Mismatches: 215
 Indels: 231
 Query Match: 7.34%
 RESULT 904
 ID AAD56135 standard; DNA; 2509 BP.
 DE Human tissue-type plasminogen activator (t-PA) DNA.
 PN WO2003033009-A2.
 PD 24-APR-2003.
 PA (OMNI-) OMNITO AB.
 Percent Similarity: 34.47%
 Best Local Similarity: 21.75%
 Mismatches: 215
 Indels: 231
 Query Match: 7.34%
 RESULT 905
 ID ABL59544 standard; cDNA; 2519 BP.
 DE Human tissue type plasminogen activator (t-PA) cDNA SEQ ID NO:44.
 PN WO200227028-A1.
 PD 04-APR-2002.
 PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.
 Percent Similarity: 34.47%
 Best Local Similarity: 21.75%
 Mismatches: 215
 Indels: 231
 Query Match: 7.34%
 RESULT 906
 ID ABK52545 standard; DNA; 2519 BP.
 DE Human tissue plasminogen activator (t-PA) DNA sequence.
 PN WO200232446-A2.
 PD 25-APR-2002.
 PA (PFIZ) PFIZER LTD.
 Percent Similarity: 34.47%
 Best Local Similarity: 21.75%
 Mismatches: 215
 Indels: 231
 Query Match: 7.34%
 RESULT 907
 ID ADR24679 standard; DNA; 2519 BP.
 DE Breast cancer prognosis marker #540.
 PN WO2004065545-A2.
 PD 05-AUG-2004.
 PA (ROSE-) ROSETTA INPHARMATICS LLC.
 Percent Similarity: 34.47%
 Best Local Similarity: 21.75%
 Mismatches: 215
 Indels: 231
 Query Match: 7.34%
 RESULT 908
 ID AAN90542 standard; cDNA; 2560 BP.
 DE Plasmid pKG12 contg. DNA encoding human melanoma t-PA.
 PN EP297066-A.
 PD 28-DEC-1988.

PA (KABI) KABIGEN AB.
 Percent Similarity: 34.47%
 Best Local Similarity: 21.75%
 Mismatches: 215
 Indels: 231
 Query Match: 7.34%
 RESULT 909
 ID ADN95625 standard; DNA; 2653 BP.
 DE Human BEC/LEC-related gene sequence SeqID548.
 PN WO2003080640-A1.
 PD 02-OCT-2003.
 PA (LUDW-) LUDWIG INST CANCER RES.
 Percent Similarity: 34.47%
 Best Local Similarity: 21.75%
 Mismatches: 215
 Indels: 231
 Query Match: 7.34%
 RESULT 910
 ID ADO28678 standard; cDNA; 2653 BP.
 DE Human tPA encoding cDNA SEQ ID NO:107.
 PN WO2004044178-A2.
 PD 27-MAY-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.47%
 Best Local Similarity: 21.75%
 Mismatches: 215
 Indels: 231
 Query Match: 7.34%
 RESULT 911
 ID ACN38795 standard; cDNA; 2653 BP.
 DE Tumour-associated antigenic target (TAT) cDNA DNA325090, SEQ ID NO:2534.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.47%
 Best Local Similarity: 21.75%
 Mismatches: 215
 Indels: 231
 Query Match: 7.34%
 RESULT 912
 ID AAD13117 standard; cDNA; 2672 BP.
 DE Human membrane-type serine protease (MTSP) 4-S splice variant cDNA.
 PN WO200157194-A2.
 PD 09-AUG-2001.
 PA (CORV-) CORVAS INT INC.
 Percent Similarity: 35.06%
 Best Local Similarity: 22.70%
 Mismatches: 214
 Indels: 175
 Query Match: 7.34%
 RESULT 913
 ID ADI10378 standard; DNA; 2672 BP.
 DE Human cell surface protease coding sequence #5.
 PN WO200295007-A2.
 PD 28-NOV-2002.
 PA (CORV-) CORVAS INT INC.
 Percent Similarity: 35.06%
 Best Local Similarity: 22.70%
 Mismatches: 214
 Indels: 175
 Query Match: 7.34%
 RESULT 914
 ID ADJ46902 standard; cDNA; 2672 BP.
 DE Human transmembrane serine protease (MTSP) cDNA #5.
 PN US2004001801-A1.
 PD 01-JAN-2004.
 PA (CORV-) CORVAS INT INC.
 Percent Similarity: 35.06%
 Best Local Similarity: 22.70%
 Mismatches: 214
 Indels: 175
 Query Match: 7.34%
 RESULT 915
 ID ADL46102 standard; DNA; 2859 BP.
 DE Human ovarian cancer DNA marker #19992.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Percent Similarity: 34.47%
 Best Local Similarity: 21.75%
 Mismatches: 215
 Indels: 231
 Query Match: 7.34%
 RESULT 916
 ID AAD13116 standard; cDNA; 3104 BP.
 DE Human membrane-type serine protease (MTSP) 4-L splice variant cDNA.
 PN WO200157194-A2.
 PD 09-AUG-2001.

PA (CORV-) CORVAS INT INC.
Percent Similarity: 35.06%
Best Local Similarity: 22.70%
Query Match: 7.34%
Conservative: 74
Mismatch: 214
Indels: 175

RESULT 917
ID ADI10376 standard; DNA; 3104 BP.
DE Human cell surface protease coding sequence #4.
PN WO200295007-A2.
PD 28-NOV-2002.

PA (CORV-) CORVAS INT INC.
Percent Similarity: 35.06%
Best Local Similarity: 22.70%
Query Match: 7.34%
Conservative: 74
Mismatch: 214
Indels: 175

RESULT 918
ID ADJ46900 standard; cDNA; 3104 BP.
DE Human transmembrane serine protease (MTSP) cDNA #4.
PN US2004001801-A1.
PD 01-JAN-2004.

PA (CORV-) CORVAS INT INC.
Percent Similarity: 35.06%
Best Local Similarity: 22.70%
Query Match: 7.34%
Conservative: 74
Mismatch: 214
Indels: 175

RESULT 919
ID AAT15930 standard; DNA; 7360 BP.
DE DHFR/intron (WtraSD)-cpa dicistronic vector.
PN WO9604391-A1.
PD 15-FEB-1996.

PA (GETH) GENENTECH INC.
Percent Similarity: 33.96%
Best Local Similarity: 22.06%
Query Match: 7.31%
Conservative: 88
Mismatch: 248
Indels: 245

RESULT 920
ID ADJ72008 standard; DNA; 1967 BP.
DE Human PMW protein gene sequence SeqID68.
PN WO2004009797-A2.
PD 29-JAN-2004.

PA (INCY-) INCYTE CORP.
Percent Similarity: 36.04%
Best Local Similarity: 24.22%
Query Match: 7.31%
Conservative: 80
Mismatch: 213
Indels: 222

RESULT 921
ID AAN50223 standard; cDNA; 2151 BP.
DE CDNA sequence encoding tissue plasminogen activator.
PN EP143081-A.
PD 29-MAY-1985.

PA (CIBA) CIBA GEIGY AG.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%
Query Match: 7.31%
Conservative: 86
Mismatch: 215
Indels: 231

RESULT 922
ID ABK31797 standard; DNA; 2409 BP.
DE DNA encoding novel human protease #54.
PN WO200200860-A2.
PD 03-JAN-2002.

PA (SUGS-) SUGEN INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175

RESULT 923
ID RAN91192 standard; DNA; 2544 BP.
DE Human tissue plasminogen activator (t-PA) gene.
PN WO8900197-A.
PD 12-JAN-1989.

PA (GETH) GENENTECH INC.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%
Query Match: 7.31%
Conservative: 86
Mismatch: 215
Indels: 231

RESULT 924
ID AAZ34033 standard; cDNA; 3143 BP.
DE Human PRO618 nucleotide sequence.
PN WO9946281-A2.
PD 16-SEP-1999.

PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Conservative: 73
Mismatch: 215
Indels: 175

Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175

RESULT 925
ID AAC78494 standard; cDNA; 3143 BP.
DE Human PRO618 (UNQ354) nucleotide sequence SEQ ID NO:168.
PN WO200053756-A2.
PD 14-SEP-2000.

PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175

RESULT 926
ID AAC58236 standard; cDNA; 3143 BP.
DE Human PRO618 nucleotide sequence SEQ ID NO:23.
PN WO200053754-A1.
PD 14-SEP-2000.

PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175

RESULT 927
ID ACA63601 standard; cDNA; 3143 BP.
DE Novel human secreted and transmembrane protein PRO618 cDNA.
PN US2002192706-A1.
PD 19-DEC-2002.

PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175

RESULT 928
ID ACA71765 standard; cDNA; 3143 BP.
DE Human secreted and transmembrane polypeptide PRO618 cDNA.
PN US2002177553-A1.
PD 28-NOV-2002.

PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175

RESULT 929
ID ABX92405 standard; cDNA; 3143 BP.
DE CDNA encoding human PRO618 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.

PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175

RESULT 930
ID ACA66146 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO618.
PN US2003004102-A1.
PD 02-JAN-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175

RESULT 931
ID ADA24707 standard; cDNA; 3143 BP.
DE Novel human secreted and transmembrane protein PRO618 cDNA.
PN US2003050241-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175

RESULT 932
ID ACD29747 standard; cDNA; 3143 BP.
DE Novel human secreted and transmembrane protein PRO618 cDNA.
PN US2003050240-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175

Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175

Best Local Similarity: 22.70% Mismatches: 215
Query Match: 7.31% Indels: 175
RESULT 933
ID ADA12368 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO618.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 934
ID ACD29162 standard; cDNA; 3143 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #37.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 935
ID ADB73674 standard; cDNA; 3143 BP.
DE Human PRO polynucleotide sequence #37.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 936
ID ADB76390 standard; cDNA; 3143 BP.
DE Human PRO polynucleotide sequence #37.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 937
ID ADC43816 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 938
ID ADC61576 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 939
ID ADC63540 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 940
ID ADC66640 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175

RESULT 941
ID ADC68764 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 942
ID ADC62824 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 943
ID ADC67889 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 944
ID ADC41209 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 945
ID ADC67264 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 946
ID ADC62200 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 947
ID ADC41833 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 948
ID ADE49202 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 949
ID ADB76390 standard; cDNA; 3143 BP.
DE Human PRO polynucleotide sequence #37.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175

ID ADE35256 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US200307700-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Mismatches: 215
 Indels: 175
 Query Match:
 RESULT 950
 ID ADE16370 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US200307700-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Mismatches: 215
 Indels: 175
 Query Match:
 RESULT 951
 ID ADD72985 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US200307700-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Mismatches: 215
 Indels: 175
 Query Match:
 RESULT 952
 ID ADD72343 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US200307700-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Mismatches: 215
 Indels: 175
 Query Match:
 RESULT 953
 ID ADE16994 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US200307700-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Mismatches: 215
 Indels: 175
 Query Match:
 RESULT 954
 ID ADF47008 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US200307700-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Mismatches: 215
 Indels: 175
 Query Match:
 RESULT 955
 ID ADG52765 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US200307700-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Mismatches: 215
 Indels: 175
 Query Match:
 RESULT 956
 ID ADG60085 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US200307700-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Mismatches: 215
 Indels: 175
 Query Match:
 RESULT 957
 ID ADI60845 standard; cDNA; 3143 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US200307700-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Mismatches: 215
 Indels: 175
 Query Match:
 RESULT 958
 ID ACD42566 standard; cDNA; 3143 BP.
 DE Novel human secreted and transmembrane protein PRO618 cDNA.
 PN US2003050239-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Mismatches: 215
 Indels: 175
 Query Match:
 RESULT 959
 ID ADE48502 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US2003104536-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Mismatches: 215
 Indels: 175
 Query Match:
 RESULT 960
 ID ADE89603 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US2003130181-A1.
 PD 10-JUL-2003.
 PA (ASHK/) ASHKENAZI A J.
 PA (BAKE/) BAKER K P.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.
 PA (FERK/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERE/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GIRM/) GIRMALDI J C.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (KUOS/) KUO S S.
 PA (NAPI/) NAPIER M A.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (SHEL/) SHELTON D L.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Mismatches: 215
 Indels: 175
 Query Match:
 RESULT 961
 ID ADF61243 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US2003195345-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Mismatches: 215
 Indels: 175
 Query Match:
 RESULT 962
 ID ADF39935 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US2003198994-A1.

```

PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 963
ID ADF45731 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 964
ID ADF24127 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 965
ID ADF40559 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 966
ID ADF23503 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 967
ID ADF33486 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 968
ID ADF26953 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 969
ID ADF27589 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 970
ID ADF41183 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 971
ID ADF32862 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 972
ID ADF25228 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 973
ID ADF26329 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 974
ID ADF34118 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 975
ID ADF46355 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 976
ID ADG50341 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 977
ID ADG49717 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatches: 215
Indels: 175
RESULT 978
ID ADG51589 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.

```


Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Query Match: 7.31%
 RESULT 979
 ID ADG49093 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US2003216305-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Query Match: 7.31%
 RESULT 980
 ID ADG48469 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US2003216560-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Query Match: 7.31%
 RESULT 981
 ID ADG50965 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US2004005312-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Query Match: 7.31%
 RESULT 982
 ID ADG58909 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US2004005657-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Query Match: 7.31%
 RESULT 983
 ID ADG62365 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US2004006219-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Query Match: 7.31%
 RESULT 984
 ID ADH25390 standard; cDNA; 3143 BP.
 DE Human neurotrophin homologue related nucleotide sequence SEQ ID NO:168.
 PN EP1386931-A1.
 PD 04-FEB-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Query Match: 7.31%
 RESULT 985
 ID ADM17167 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US2004048332-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Query Match: 7.31%
 RESULT 986
 ID ADL07001 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.
 PN US2004063921-A1.
 PD 01-APR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%

Best Local Similarity: 22.70%
 Query Match: 7.31%
 RESULT 987
 ID ADT91614 standard; cDNA; 3143 BP.
 DE Human PRO618 cDNA sequence.
 PN AU2002317529-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.89%
 Best Local Similarity: 22.70%
 Query Match: 7.31%
 RESULT 988
 ID AAZ39663 standard; cDNA; 3547 BP.
 DE Mouse Serine protease, Corin cDNA.
 PN WO9964608-A1.
 PD 16-DEC-1999.
 PA (SCHD) SCHERING AG.
 Percent Similarity: 36.24%
 Best Local Similarity: 21.99%
 Query Match: 7.31%
 RESULT 989
 ID AAN60659 standard; DNA; 2547 BP.
 DE Sequence encoding human pre-tissue plasminogen activator (pre-t-PA).
 PN GB2173804-A.
 PD 22-OCT-1986.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.58%
 Best Local Similarity: 21.76%
 Query Match: 7.30%
 RESULT 990
 ID AAN60736 standard; DNA; 2547 BP.
 DE Sequence encoding modified human tissue plasminogen activator (t-PA).
 PN FR2581652-A.
 PD 14-NOV-1986.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.58%
 Best Local Similarity: 21.76%
 Query Match: 7.30%
 RESULT 991
 ID ABQ61196 standard; cDNA; 2801 BP.
 DE Human PRO618 encoding sequence.
 PN WO200231111-A2.
 PD 18-APR-2002.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 32.13%
 Best Local Similarity: 20.97%
 Query Match: 7.30%
 RESULT 992
 ID AAZ32168 standard; DNA; 1366 BP.
 DE Human low density lipoprotein receptor exon 2 nucleotide sequence.
 PN WO9950454-A2.
 PD 07-OCT-1999.
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 Percent Similarity: 35.22%
 Best Local Similarity: 25.10%
 Query Match: 7.29%
 RESULT 993
 ID ACF05072 standard; cDNA; 1755 BP.
 DE Bovine recombinant prothrombin nucleotide sequence.
 PN WO2003052059-A2.
 PD 26-JUN-2003.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 35.12%
 Best Local Similarity: 24.10%
 Query Match: 7.29%
 RESULT 994
 ID ACF05074 standard; cDNA; 1917 BP.
 DE Bovine recombinant prothrombin nucleotide sequence.
 PN WO2003052059-A2.
 PD 26-JUN-2003.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 35.12%
 Best Local Similarity: 24.10%
 Query Match: 7.29%
 RESULT 995
 ID ACF05072 standard; cDNA; 1755 BP.
 DE Bovine recombinant prothrombin nucleotide sequence.
 PN WO2003052059-A2.
 PD 26-JUN-2003.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 35.12%
 Best Local Similarity: 24.10%
 Query Match: 7.29%
 RESULT 996
 ID ACF05072 standard; cDNA; 1755 BP.
 DE Bovine recombinant prothrombin nucleotide sequence.
 PN WO2003052059-A2.
 PD 26-JUN-2003.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 35.12%
 Best Local Similarity: 24.10%
 Query Match: 7.29%
 RESULT 997
 ID ACF05072 standard; cDNA; 1755 BP.
 DE Bovine recombinant prothrombin nucleotide sequence.
 PN WO2003052059-A2.
 PD 26-JUN-2003.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 35.12%
 Best Local Similarity: 24.10%
 Query Match: 7.29%
 RESULT 998
 ID ACF05072 standard; cDNA; 1755 BP.
 DE Bovine recombinant prothrombin nucleotide sequence.
 PN WO2003052059-A2.
 PD 26-JUN-2003.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 35.12%
 Best Local Similarity: 24.10%
 Query Match: 7.29%
 RESULT 999
 ID ACF05072 standard; cDNA; 1755 BP.
 DE Bovine recombinant prothrombin nucleotide sequence.
 PN WO2003052059-A2.
 PD 26-JUN-2003.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 35.12%
 Best Local Similarity: 24.10%
 Query Match: 7.29%
 RESULT 1000
 ID ACF05072 standard; cDNA; 1755 BP.
 DE Bovine recombinant prothrombin nucleotide sequence.
 PN WO2003052059-A2.
 PD 26-JUN-2003.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 35.12%
 Best Local Similarity: 24.10%
 Query Match: 7.29%

Query Match: 7.29% Indels: 217

RESULT 995

ID ADG83827 standard; cDNA; 1404 BP.

DE Taipan snake venom protease coding sequence.

PN WO2003082914-A1.

PD 09-OCT-2003.

PA (UYQU) UNIV QUEENSLAND.

Percent Similarity: 36.15%

Best Local Similarity: 22.48%

Query Match: 7.28%

Indels: 162

Conservative: 76

Mismatches: 193

Indels: 162

RESULT 996

ID AAN30001 standard; cDNA; 2547 BP.

DE Sequence encoding full length tissue plasminogen activator (t-Pa).

PN EP93619-A.

PD 09-NOV-1983.

PA (GETH) GENENTECH INC.

Percent Similarity: 34.58%

Best Local Similarity: 21.61%

Query Match: 7.28%

Indels: 234

Conservative: 87

Mismatches: 208

Indels: 234

RESULT 997

ID ADQ38420 standard; DNA; 2933 BP.

DE Human SNP containing myocardial infarction-associated gene, SEQ ID 83.

PN WO2004058052-A2.

PD 15-JUL-2004.

PA (APPL-) APPLERA CORP.

Percent Similarity: 34.37%

Best Local Similarity: 21.78%

Query Match: 7.28%

Indels: 231

Conservative: 85

Mismatches: 215

Indels: 231

RESULT 998

ID AAN70741 standard; DNA; 1598 BP.

DE Sequence of synthetic gene for mature human tissue plasminogen activator (tPA).

PN WO8705934-A.

PD 08-OCT-1987.

PA (CREA/) CREA R.

Percent Similarity: 36.31%

Best Local Similarity: 22.90%

Query Match: 7.25%

Indels: 154

Conservative: 75

Mismatches: 202

Indels: 154

RESULT 999

ID AAQ04904 standard; DNA; 1689 BP.

DE Part of tPA023 gene encoding precursor protein.

PN EP373896-A.

PD 20-JUN-1990.

PA (YAMA) YAMANOUCHI PHARM CO LTD.

Percent Similarity: 35.71%

Best Local Similarity: 22.82%

Query Match: 7.25%

Indels: 186

Conservative: 74

Mismatches: 186

Indels: 186

RESULT 1000

ID AAQ13379 standard; DNA; 1689 BP.

DE T-PA67+ mutant with supernumerary N-linked oligosaccharide side chain.

PN US5041376-A.

PD 20-AUG-1991.

PA (TEXA) UNIV TEXAS SYSTEM.

Percent Similarity: 35.71%

Best Local Similarity: 22.82%

Query Match: 7.25%

Indels: 186

Conservative: 74

Mismatches: 186

Indels: 186

RESULT 1001

ID ASK52546 standard; DNA; 1689 BP.

DE Human tissue plasminogen activator (t-PA) coding sequence.

PN WO200232446-A2.

PD 25-APR-2002.

PA (PFIZ) PFIZER LTD.

Percent Similarity: 35.71%

Best Local Similarity: 22.82%

Query Match: 7.25%

Indels: 186

Conservative: 74

Mismatches: 186

Indels: 186

RESULT 1002

ID ACC78881 standard; DNA; 1726 BP.

DE Human tissue-type plasminogen activator (TPA) encoding DNA.

PN WO2003031464-A2.

PD 17-APR-2003.

PA (NEOS-) NEOSE TECHNOLOGIES INC.

Percent Similarity: 35.71%

Best Local Similarity: 22.82%

Query Match: 7.25%

Indels: 186

Conservative: 74

Mismatches: 186

Indels: 186

RESULT 1003

ID ADN49697 standard; DNA; 1726 BP.

DE Human tissue type plasminogen activator TPA DNA SeqID 25.

PN WO2004033651-A2.

PD 22-APR-2004.

PA (NEOS-) NEOSE TECHNOLOGIES INC.

Percent Similarity: 35.71%

Best Local Similarity: 22.82%

Query Match: 7.25%

Indels: 186

Conservative: 74

Mismatches: 186

Indels: 186

RESULT 1004

ID AAT27585 standard; DNA; 1740 BP.

DE Full-length tissue plasminogen activator DNA clone.

PN US504001-A.

PD 02-APR-1996.

PA (ZYMO) ZYMOGENETICS INC.

Percent Similarity: 35.71%

Best Local Similarity: 22.82%

Query Match: 7.25%

Indels: 186

Conservative: 74

Mismatches: 186

Indels: 186

RESULT 1005

ID AAZ31998 standard; cDNA; 1955 BP.

DE Human tissue plasminogen activator coding sequence.

PN US5985607-A.

PD 16-NOV-1999.

PA (CANG-) CANGENE CORP.

Percent Similarity: 35.71%

Best Local Similarity: 22.82%

Query Match: 7.25%

Indels: 186

Conservative: 74

Mismatches: 186

Indels: 186

RESULT 1006

ID AAN91111 standard; DNA; 1974 BP.

DE BgIII fragment of mutant tPA plasmid pTPA102.

PN EP302456-A.

PD 08-FEB-1989.

PA (FUJI) FUJISAWA PHARM CO LTD.

Percent Similarity: 35.71%

Best Local Similarity: 22.82%

Query Match: 7.25%

Indels: 186

Conservative: 74

Mismatches: 186

Indels: 186

RESULT 1007

ID AAN91119 standard; DNA; 2100 BP.

DE Sequence of native tPA in plasmid pST112.

PN EP302456-A.

PD 08-FEB-1989.

PA (FUJI) FUJISAWA PHARM CO LTD.

Percent Similarity: 35.71%

Best Local Similarity: 22.82%

Query Match: 7.25%

Indels: 186

Conservative: 74

Mismatches: 186

Indels: 186

RESULT 1008

ID AAQ05932 standard; DNA; 2100 BP.

DE Plasmid pST112 encoding novel N-terminal for tissue plasminogen activator (tPA).

PN EP373890-A.

PD 01-AUG-1990.

PA (FUJI) FUJISAWA PHARM CO LTD.

Percent Similarity: 35.71%

Best Local Similarity: 22.82%

Query Match: 7.25%

Indels: 186

Conservative: 74

Mismatches: 186

Indels: 186

RESULT 1009

ID AAQ05944 standard; DNA; 2313 BP.

DE Sequence encoding thrombomodulin analogue / t-PA fusion protein.

PN WO9010081-A.

PD 07-SEP-1990.

PA (CODO-) CODON.

Percent Similarity: 37.00%

Best Local Similarity: 22.86%

Query Match: 7.25%

Indels: 182

Conservative: 81

Mismatches: 180

Indels: 182

RESULT 1010

ID AAN60146 standard; cDNA; 2457 BP.

DE cDNA sequence encoding active human uterine tissue plasminogen activator (UTPA).

PN EP178105-A.

PD 16-APR-1986.
PA (INTE-) INTEG GENETICS INC.
Percent Similarity: 35.71%
Best Local Similarity: 22.82%
Query Match: 7.25%
RESULT 1011
ID ADR24680 standard; DNA; 2461 BP.
DE Breast cancer prognosis marker #541.
PD WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Percent Similarity: 35.71%
Best Local Similarity: 22.82%
Query Match: 7.25%
RESULT 1012
ID AAN70491 standard; cDNA; 7533 BP.
DE Entire sequence of high level expression vector pEmpl-tpa for tissue
DE Plasmid pEmpl-tpa.
PD EP237157-A.
PD 16-SEP-1987.
PA (DAMO-) DAMON BIOTECH INC.
PA (ABBO-) ABBOTT BIOTECH INC.
Percent Similarity: 35.71%
Best Local Similarity: 22.82%
Query Match: 7.25%
RESULT 1013
ID AAN81970 standard; DNA; 7533 BP.
DE Plasmid pEmpl-tpa.
PD WO800242-A.
PD 14-JAN-1988.
PA (DAMO-) DAMON BIOTECH INC.
Percent Similarity: 35.71%
Best Local Similarity: 22.82%
Query Match: 7.25%
RESULT 1014
ID ABL52893 standard; DNA; 1686 BP.
DE Tissue type plasminogen activator, tPA, coding sequence.
PD KR141262-B1.
PD 15-JUN-1998.
PA (GLDS-) LG CHEM LTD.
Percent Similarity: 35.71%
Best Local Similarity: 22.65%
Query Match: 7.22%
RESULT 1015
ID AAN91216 standard; DNA; 1689 BP.
DE Mutated cDNA coding sequence of tissue plasminogen activator (t-PA).
PD AU8817430-A.
PD 08-DEC-1988.
PA (NOVO-) NOVO IND AS.
PA (ZYMO-) ZYMOGENETICS INC.
PA (EISA-) EISAI CO LTD.
Percent Similarity: 37.52%
Best Local Similarity: 23.91%
Query Match: 7.22%
RESULT 1016
ID AAO05177 standard; DNA; 1689 BP.
DE Sequence encoding thrombolytic protein with secondary structure of human
DE Tissue plasminogen activator.
PD JP02145184-A.
PD 04-JUN-1990.
PA (YAMA-) YAMANOUCHI PHARM CO LTD.
Percent Similarity: 36.88%
Best Local Similarity: 23.05%
Query Match: 7.22%
RESULT 1017
ID AAO05531 standard; DNA; 1974 BP.
DE Plasmid pTPA102 encoding novel tissue plasminogen activator (t-PA).
PD EP379890-A.
PD 01-AUG-1990.
PA (FUJI-) FUJISAWA PHARM CO LTD.
Percent Similarity: 35.71%
Best Local Similarity: 22.82%

Query Match: 7.22%
RESULT 1018
ID AAO08500 standard; cDNA; 2547 BP.
DE Sequence encoding tissue plasminogen activator (t-PA) mutant Thr 478.
PD WO8912680-A.
PD 28-DEC-1989.
PA (UNIW-) UNIV WASHINGTON.
Percent Similarity: 34.58%
Best Local Similarity: 21.61%
Query Match: 7.22%
RESULT 1019
ID AAO61733 standard; cDNA; 1149 BP.
DE cDNA encoding human serine protease BSSP5 (hBSSP5) SEQ ID NO:1.
PD WO200031243-A1.
PD 02-JUN-2000.
PA (FUSO-) FUSO PHARM IND LTD.
Percent Similarity: 44.00%
Best Local Similarity: 28.00%
Query Match: 7.21%
RESULT 1020
ID AAO53318 standard; cDNA to mRNA; 1800 BP.
DE Human tPA (R129W) coding sequence.
PD JP05304992-A.
PD 19-NOV-1993.
PA (TAKE-) TAKEDA CHEM IND LTD.
Percent Similarity: 34.32%
Best Local Similarity: 21.75%
Query Match: 7.21%
RESULT 1021
ID AAO40654 standard; DNA; 1800 BP.
DE tPA mutein DNA.
PD JP05076361-A.
PD 30-MAR-1993.
PA (TAKE-) TAKEDA CHEM IND LTD.
Percent Similarity: 34.32%
Best Local Similarity: 21.75%
Query Match: 7.21%
RESULT 1022
ID AAO12074 standard; DNA; 2100 BP.
DE T-PA variant having Lys416 substituted (1).
PD JP03061484-A.
PD 18-MAR-1991.
PA (FUJI-) FUJISAWA PHARM CO LTD.
Percent Similarity: 34.57%
Best Local Similarity: 21.76%
Query Match: 7.21%
RESULT 1023
ID AAO12075 standard; DNA; 2105 BP.
DE T-PA variant having Lys416 substituted (2).
PD JP03061484-A.
PD 18-MAR-1991.
PA (FUJI-) FUJISAWA PHARM CO LTD.
Percent Similarity: 34.72%
Best Local Similarity: 21.76%
Query Match: 7.21%
RESULT 1024
ID AAO12867 standard; cDNA; 2512 BP.
DE JM1-229 cell line t-PA.
PD WO9110447-A.
PD 25-JUL-1991.
PA (PORT-) PORTON PROD LTD.
PA (PUBL-) PUBLIC HEALTH LAB SERVIC.
PA (UNLO-) UNIV COLLEGE LONDON.
Percent Similarity: 39.29%
Best Local Similarity: 26.07%
Query Match: 7.21%
RESULT 1025
ID ADR29370 standard; DNA; 4864 BP.
DE Murine Lrp4 dopaminergic neuronal marker DNA SEQ ID NO:1.
PD WO2004065599-A1.
PD 05-AUG-2004.
PA (EISA-) EISAI CO LTD.
Percent Similarity: 36.24%
Conservative: 117
Mismatches: 218
Indels: 110

Best Local Similarity: 21.87% Mismatches: 282
 Query Match: 7.21% Indels: 238
 RESULT 1026
 ID AAN82177 standard; DNA; 1689 BP.
 DE Tissue plasminogen activator with G-183 and S-186 substd for S and T.
 PN JP63230083-A.
 PD 26-SEP-1988.
 PA (EISA) EISAI CO LTD.
 Percent Similarity: 36.82%
 Best Local Similarity: 22.69%
 Mismatches: 181
 Indels: 182
 Query Match: 7.20%
 RESULT 1027
 ID ADB58261 standard; DNA; 1497 BP.
 DE Toxicity-related gene, SEQ ID 3287.
 PN WO2003064624-A2.
 PD 07-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 35.30%
 Best Local Similarity: 22.76%
 Mismatches: 206
 Indels: 155
 Query Match: 7.19%
 RESULT 1028
 ID ADB52793 standard; DNA; 1497 BP.
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3335.
 PN WO2003065993-A2.
 PD 14-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 35.30%
 Best Local Similarity: 22.76%
 Mismatches: 206
 Indels: 155
 Query Match: 7.19%
 RESULT 1029
 ID ABI99227 standard; cDNA; 2519 BP.
 DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:40.
 PN WO2001088188-A2.
 PD 22-NOV-2001.
 PA (YUNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 Percent Similarity: 38.20%
 Best Local Similarity: 25.23%
 Mismatches: 199
 Indels: 146
 Query Match: 7.19%
 RESULT 1030
 ID ADR12597 standard; DNA; 2519 BP.
 DE Gene vaccine nucleic acid #30.
 PN WO2004067040-A1.
 PD 12-AUG-2004.
 PA (KYUS-) KYUSHU TLO CO LTD.
 Percent Similarity: 38.20%
 Best Local Similarity: 25.23%
 Mismatches: 199
 Indels: 146
 Query Match: 7.19%
 RESULT 1031
 ID AAQ01358 standard; DNA; 1780 BP.
 DE Sequence encoding wild type tissue plasminogen activator (t-PA).
 PN EP351246-A.
 PD 17-JAN-1990.
 PA (NOVO) NOVO-NORDISK AS.
 Percent Similarity: 35.61%
 Best Local Similarity: 22.63%
 Mismatches: 192
 Indels: 176
 Query Match: 7.17%
 RESULT 1032
 ID AAQ04354 standard; DNA; 1780 BP.
 DE Sequence encoding tissue plasminogen activator (t-PA) analogue t-PA K419S with altered residue 419.
 PN EP351246-A.
 PD 17-JAN-1990.
 PA (NOVO) NOVO-NORDISK AS.
 Percent Similarity: 35.61%
 Best Local Similarity: 22.63%
 Mismatches: 192
 Indels: 176
 Query Match: 7.17%
 RESULT 1033
 ID AAQ04353 standard; DNA; 1780 BP.
 DE Sequence encoding tissue plasminogen activator (t-PA) analogue t-PA K419S with altered residues 419 and 420.
 PN EP351246-A.

PD 17-JAN-1990.
 PA (NOVO) NOVO-NORDISK AS.
 Percent Similarity: 35.44%
 Best Local Similarity: 22.63%
 Mismatches: 193
 Indels: 176
 Query Match: 7.17%
 RESULT 1034
 ID AAN70088 standard; DNA; 1836 BP.
 DE Hybrid plasminogen activator (PA) contg. urokinase kringle (UKK) 1-131 and tissue plasminogen activator (tPA) 92-527.
 PN EP2131794-A.
 PD 11-MAR-1987.
 PA (AMHP) AMERICAN HOME PROD CORP.
 Percent Similarity: 36.90%
 Best Local Similarity: 22.95%
 Mismatches: 208
 Indels: 200
 Query Match: 7.17%
 RESULT 1035
 ID AAQ42718 standard; DNA; 2544 BP.
 DE Sequence encoding tissue plasminogen activator (t-PA).
 PN WO9312225-A1.
 PD 24-JUN-1993.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.32%
 Best Local Similarity: 21.60%
 Mismatches: 216
 Indels: 231
 Query Match: 7.16%
 RESULT 1036
 ID AAN60813 standard; cDNA; 1630 BP.
 DE Sequence encoding tissue plasminogen activator (TPA) in pUCH.
 PN DE3537176-A.
 PD 10-JUL-1986.
 PA (ZYMO) ZYMOGENETICS INC.
 Percent Similarity: 35.54%
 Best Local Similarity: 22.82%
 Mismatches: 187
 Indels: 186
 Query Match: 7.15%
 RESULT 1037
 ID AAN81090 standard; DNA; 1689 BP.
 DE Mutated t-PA analogue coding sequence in plasmid ZEM99-9100.
 PN EP293934-A.
 PD 07-DEC-1988.
 PA (ZYMO) ZYMOGENETICS INC.
 Percent Similarity: 35.37%
 Best Local Similarity: 22.82%
 Mismatches: 188
 Indels: 186
 Query Match: 7.15%
 RESULT 1038
 ID AAN82179 standard; DNA; 1689 BP.
 DE Tissue plasminogen activator with S-119 substd for M and QGI96-98 substd for NGT.
 PN JP63230083-A.
 PD 26-SEP-1988.
 PA (EISA) EISAI CO LTD.
 Percent Similarity: 36.06%
 Best Local Similarity: 23.17%
 Mismatches: 184
 Indels: 186
 Query Match: 7.15%
 RESULT 1039
 ID AAZ41406 standard; cDNA; 901 BP.
 DE Human normal pancreas tissue derived cDNA 21.
 PN DE19818598-A1.
 PD 21-OCT-1999.
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 Percent Similarity: 42.72%
 Best Local Similarity: 27.18%
 Mismatches: 102
 Indels: 75
 Query Match: 7.14%
 RESULT 1040
 ID AAH19462 standard; DNA; 1221 BP.
 DE Mutant blood coagulant factor VII (FVII-30) coding sequence.
 PN JP2001061479-A.
 PD 13-MAR-2001.
 PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 Percent Similarity: 35.41%
 Best Local Similarity: 22.76%
 Mismatches: 149
 Indels: 183
 Query Match: 7.14%

ID	AAQ06317	standard; DNA; 1605 BP.		
DE	Synthetic gene encoding t-PA, used to prepare pJS023.			
PN	US4963357-A.			
PD	16-OCT-1990.			
PA	(MONS) MONSANTO CO.			
Percent Similarity:	36.77%	Conservative:	77	
Best Local Similarity:	23.09%	Mismatches:	192	
Query Match:	7.12%	Indels:	164	
RESULT 1050				
ID	AAQ46260	standard; DNA; 1605 BP.		
DE	Synthetic tPA gene with optimum yeast codons.			
PN	US5244676-A.			
PD	14-SEP-1993.			
PA	(MONS) MONSANTO CO.			
Percent Similarity:	36.70%	Conservative:	77	
Best Local Similarity:	23.05%	Mismatches:	193	
Query Match:	7.12%	Indels:	164	
RESULT 1051				
ID	ABL70002	standard; DNA; 1184 BP.		
DE	Pancraes cancer related gene sequence SEQ ID NO:8339.			
PN	WO200194629-A2.			
PD	13-DEC-2001.			
PA	(AVAL-) AVALON PHARM.			
Percent Similarity:	43.67%	Conservative:	47	
Best Local Similarity:	28.00%	Mismatches:	112	
Query Match:	7.11%	Indels:	57	
RESULT 1052				
ID	AD884828	standard; DNA; 1184 BP.		
DE	Parnesyl transferase inhibitor modulated leukemia associated gene #47.			
PN	WO2003038129-A2.			
PD	08-MAY-2003.			
PA	(ORTH) ORTHO CLINICAL DIAGNOSTICS INC.			
Percent Similarity:	43.67%	Conservative:	47	
Best Local Similarity:	28.00%	Mismatches:	112	
Query Match:	7.11%	Indels:	57	
RESULT 1053				
ID	ACN40045	standard; cDNA; 1184 BP.		
DE	Tumour-associated antigenic target (TAT) cDNA DNA88261, SEQ ID NO:4579			
PN	WO2004030615-A2.			
PD	15-APR-2004.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	43.67%	Conservative:	47	
Best Local Similarity:	28.00%	Mismatches:	112	
Query Match:	7.11%	Indels:	57	
RESULT 1054				
ID	AA60065	standard; DNA; 2438 BP.		
DE	Factor IX/Factor VII cDNA fusion.			
PN	EP200421-A.			
PD	10-DEC-1986.			
PA	(ZYMO) ZYMOGENETICS INC.			
Percent Similarity:	33.18%	Conservative:	73	
Best Local Similarity:	21.75%	Mismatches:	188	
Query Match:	7.11%	Indels:	239	
RESULT 1055				
ID	AA60597	standard; cDNA; 1446 BP.		
DE	Sequence encoding polypeptide with plasminogen activator activity.			
PN	JP61139386-A.			
PD	26-JUN-1986.			
PA	(TOYJ) TOYO SODA MFG CO LTD.			
PA	(SAGA) SAGAMI CHEM RES CENTRE.			
PA	(CENG) CENTRAL GLASS CO LTD.			
PA	(HODO) HODOGAYA CHEM IND CO LTD.			
Percent Similarity:	35.38%	Conservative:	71	
Best Local Similarity:	22.94%	Mismatches:	186	
Query Match:	7.10%	Indels:	186	
RESULT 1056				
ID	AAQ23498	standard; DNA; 1605 BP.		
DE	Encodes t-PA variant MB1005 with two K2 kringle regions.			
PN	US5100666-A.			
PD	31-MAR-1992.			
PA	(MONS) MONSANTO CO.			
Percent Similarity:	36.70%	Conservative:	77	
Best Local Similarity:	23.05%	Mismatches:	193	

Query Match:	7.10%	Indels:	164
RESULT 1057			
ID AAN90742 standard; DNA; 1609 BP.			
DE Chemically synthesised gene coding for tissue plasminogen activator (t-PA).			
PN EP311589-A.			
PD 12-APR-1989.			
PA (MONS) MONSANTO CO.			
Percent Similarity: 36.70%		Conservative: 77	
Best Local Similarity: 23.05%		Mismatches: 193	
Query Match:	7.10%	Indels:	164
RESULT 1058			
ID AAQ05675 standard; cDNA; 2137 BP.			
DE V-PA beta.			
PN EP383417-A.			
PD 22-AUG-1990.			
PA (SCHD) SCHERING AG.			
Percent Similarity: 37.32%		Conservative: 66	
Best Local Similarity: 25.36%		Mismatches: 183	
Query Match:	7.10%	Indels:	163
RESULT 1059			
ID AAN60700 standard; DNA; 1989 BP.			
DE Sequence encoding tissue plasminogen activator (t-PA) on plasmid pTPA25.			
PN WO8601538-A.			
PD 13-MAR-1986.			
PA (BIOJ) BIOGEN NV.			
Percent Similarity: 35.54%		Conservative: 74	
Best Local Similarity: 22.65%		Mismatches: 187	
Query Match:	7.08%	Indels:	186
RESULT 1060			
ID ADJ57514 standard; cDNA; 2106 BP.			
DE Human FVII-IgG1 Fc domain fusion protein encoding cDNA.			
PN WO2004006962-A2.			
PD 22-JAN-2004.			
PA (NOVO) NOVO NORDISK AS.			
Percent Similarity: 34.23%		Conservative: 77	
Best Local Similarity: 22.03%		Mismatches: 184	
Query Match:	7.08%	Indels:	231
RESULT 1061			
ID AAF29715 standard; DNA; 2138 BP.			
DE HfVIIa immunconjugate coding sequence.			
PN WO200102439-A1.			
PD 11-JAN-2001.			
PA (UYA) UNIV YALE.			
Percent Similarity: 34.23%		Conservative: 77	
Best Local Similarity: 22.03%		Mismatches: 184	
Query Match:	7.08%	Indels:	231
RESULT 1062			
ID ABS76526 standard; cDNA; 3112 BP.			
DE cDNA encoding human ovarian cancer marker OV82.			
PN WO200271928-A2.			
PD 19-SEP-2002.			
PA (MILL) MILLENNIUM PHARM INC.			
Percent Similarity: 31.02%		Conservative: 63	
Best Local Similarity: 20.84%		Mismatches: 220	
Query Match:	7.08%	Indels:	207
RESULT 1063			
ID ADJ57515 standard; cDNA; 7494 BP.			
DE Human FVII-IgG1 Fc domain fusion protein encoding cDNA.			
PN WO2004006962-A2.			
PD 22-JAN-2004.			
PA (NOVO) NOVO NORDISK AS.			
Percent Similarity: 34.23%		Conservative: 77	
Best Local Similarity: 22.03%		Mismatches: 184	
Query Match:	7.06%	Indels:	231
RESULT 1071			
ID AAV40389 standard; cDNA; 1440 BP.			
DE Human Factor VIIa encoding cDNA.			
PN WO9831394-A2.			
PD 23-JUL-1998.			
PA (TEXA) UNIV TEXAS SYSTEM.			
Percent Similarity: 34.23%		Conservative: 77	
Best Local Similarity: 22.03%		Mismatches: 184	
Query Match:	7.06%	Indels:	231
RESULT 1072			
ID AAQ12072 standard; DNA; 2100 BP.			
DE T-PA with -ve charged finger and/or kringle domain (2).			
PN JF03061483-A.			
PD 18-MAR-1991.			
PA (FUJI) FUJISAWA PHARM CO LTD.			
Percent Similarity: 36.12%		Conservative: 88	
Best Local Similarity: 22.24%		Mismatches: 209	
Query Match:	7.06%	Indels:	197
Query Match:	7.07%	Indels:	188
RESULT 1065			
ID AAN82178 standard; DNA; 1689 BP.			
DE Tissue plasminogen activator with S-119 subatd for M.			
PN JP63230083-A.			
PD 26-SEP-1988.			
PA (EISA) EISAI CO LTD.			
Percent Similarity: 36.25%		Conservative: 73	
Best Local Similarity: 23.21%		Mismatches: 201	
Query Match:	7.07%	Indels:	156
RESULT 1066			
ID ABK31785 standard; DNA; 2913 BP.			
DE DNA encoding novel human protease #42.			
PN WO200200860-A2.			
PD 03-JAN-2002.			
PA (SUGE-) SUGEN INC.			
Percent Similarity: 36.67%		Conservative: 78	
Best Local Similarity: 23.43%		Mismatches: 231	
Query Match:	7.07%	Indels:	142
RESULT 1067			
ID ADR43735 standard; cDNA; 3522 BP.			
DE Human protease PRTS-6 coding sequence, SEQ ID 23.			
PN WO200220736-A2.			
PD 14-MAR-2002.			
PA (INCY-) INCYTE GENOMICS INC.			
Percent Similarity: 36.67%		Conservative: 78	
Best Local Similarity: 23.43%		Mismatches: 231	
Query Match:	7.07%	Indels:	142
RESULT 1068			
ID ABZ76262 standard; cDNA; 877 BP.			
DE Human GENSET cDNA clone name VCTRL-1.			
PN WO2003014151-A2.			
PD 20-FEB-2003.			
PA (GEST) GENSET SA.			
Percent Similarity: 41.75%		Conservative: 45	
Best Local Similarity: 27.18%		Mismatches: 105	
Query Match:	7.06%	Indels:	75
RESULT 1069			
ID AAH19460 standard; DNA; 1221 BP.			
DE Mutant blood coagulant factor VII (FVII-5) coding sequence.			
PN JP2001061479-A.			
PD 13-MAR-2001.			
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.			
Percent Similarity: 36.63%		Conservative: 69	
Best Local Similarity: 22.97%		Mismatches: 155	
Query Match:	7.06%	Indels:	165
RESULT 1070			
ID AAO62299 standard; cDNA; 1440 BP.			
DE Factor VIII.			
PN WO9323074-A1.			
PD 25-NOV-1993.			
PA (OKLA-) OKLAHOMA MED RES FOUND.			
Percent Similarity: 34.23%		Conservative: 77	
Best Local Similarity: 22.03%		Mismatches: 184	
Query Match:	7.06%	Indels:	231
RESULT 1071			
ID AAV40389 standard; cDNA; 1440 BP.			
DE Human Factor VIIa encoding cDNA.			
PN WO9831394-A2.			
PD 23-JUL-1998.			
PA (TEXA) UNIV TEXAS SYSTEM.			
Percent Similarity: 34.23%		Conservative: 77	
Best Local Similarity: 22.03%		Mismatches: 184	
Query Match:	7.06%	Indels:	231
RESULT 1072			
ID AAQ12072 standard; DNA; 2100 BP.			
DE T-PA with -ve charged finger and/or kringle domain (2).			
PN JF03061483-A.			
PD 18-MAR-1991.			
PA (FUJI) FUJISAWA PHARM CO LTD.			
Percent Similarity: 36.12%		Conservative: 88	
Best Local Similarity: 22.24%		Mismatches: 209	
Query Match:	7.06%	Indels:	197

RESULT 1073
ID AAX15425 standard; DNA; 2462 BP.
DE DNA encoding coagulation factor VII/VIIa.
PN US5877289-A.
PD 02-MAR-1999.
PA (SCRI) SCRIPPS RES INST.
PA (TEXA) UNIV TEXAS SYSTEM.
Percent Similarity: 34.23%
Best Local Similarity: 22.03%
Query Match: 7.06%
Conservative: 77
Mismatches: 184
Indels: 231
RESULT 1074
ID AAA12968 standard; DNA; 2462 BP.
DE DNA encoding Factor VII/VIIa, SEQ ID NO:25.
PN US6036955-A.
PD 14-MAR-2000.
PA (TEXA) UNIV TEXAS SYSTEM.
PA (SCRI) SCRIPPS RES INST.
Percent Similarity: 34.23%
Best Local Similarity: 22.03%
Query Match: 7.06%
Conservative: 77
Mismatches: 184
Indels: 231
RESULT 1075
ID AAZ56118 standard; DNA; 2462 BP.
DE Vitamin-K-dependent coagulation factor VII/VIIa coding sequence.
PN US6004555-A.
PD 21-DEC-1999.
PA (SCRI) SCRIPPS RES INST.
PA (TEXA) UNIV TEXAS SYSTEM.
Percent Similarity: 34.23%
Best Local Similarity: 22.03%
Query Match: 7.06%
Conservative: 77
Mismatches: 184
Indels: 231
RESULT 1076
ID AAA54032 standard; DNA; 2462 BP.
DE Human factor VII coding sequence.
PN WO200054787-A1.
PD 21-SEP-2000.
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
PA (UYNC-) UNIV NORTH CAROLINA.
Percent Similarity: 34.23%
Best Local Similarity: 22.03%
Query Match: 7.06%
Conservative: 77
Mismatches: 184
Indels: 231
RESULT 1077
ID AAA89784 standard; DNA; 2462 BP.
DE DNA encoding coagulation factor VII/VIIa.
PN US6093399-A.
PD 25-JUL-2000.
PA (SCRI) SCRIPPS RES INST.
PA (TEXA) UNIV TEXAS SYSTEM.
Percent Similarity: 34.23%
Best Local Similarity: 22.03%
Query Match: 7.06%
Conservative: 77
Mismatches: 184
Indels: 231
RESULT 1078
ID ABL67255 standard; DNA; 2462 BP.
DE Thyroid cancer related gene sequence SEQ ID NO:5592.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 34.23%
Best Local Similarity: 22.03%
Query Match: 7.06%
Conservative: 77
Mismatches: 184
Indels: 231
RESULT 1079
ID ABN95753 standard; DNA; 2462 BP.
DE Gene #2251 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 34.23%
Best Local Similarity: 22.03%
Query Match: 7.06%
Conservative: 77
Mismatches: 184
Indels: 231
RESULT 1080
ID ADG71756 standard; DNA; 2462 BP.
DE Vitamin K dependent coagulation factor VII/VIIa.
PN US2003219441-A1.
PD 27-NOV-2003.

PA (TEXA) UNIV TEXAS SYSTEM.
PA (SCRI) SCRIPPS RES INST.
Percent Similarity: 34.23%
Best Local Similarity: 22.03%
Query Match: 7.06%
Conservative: 77
Mismatches: 184
Indels: 231
RESULT 1081
ID AAN60064 standard; DNA; 2483 BP.
DE Factor VII cDNA of lambda VII2463.
PN EP200421-A.
PD 10-DEC-1986.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 34.23%
Best Local Similarity: 22.03%
Query Match: 7.06%
Conservative: 77
Mismatches: 184
Indels: 231
RESULT 1082
ID AAA54031 standard; DNA; 1507 BP.
DE Human factor X coding sequence.
PN WO200054787-A1.
PD 21-SEP-2000.
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
PA (UYNC-) UNIV NORTH CAROLINA.
Percent Similarity: 37.50%
Best Local Similarity: 23.99%
Query Match: 7.05%
Conservative: 67
Mismatches: 191
Indels: 120
RESULT 1083
ID ABZ35322 standard; cDNA; 1507 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 433.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Percent Similarity: 37.50%
Best Local Similarity: 23.99%
Query Match: 7.05%
Conservative: 67
Mismatches: 191
Indels: 120
RESULT 1084
ID ADE84862 standard; DNA; 1507 BP.
DE Farnesyl transferase inhibitor modulated leukemia associated gene #81.
PN WO2003038129-A2.
PD 08-MAY-2003.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Percent Similarity: 37.50%
Best Local Similarity: 23.99%
Query Match: 7.05%
Conservative: 67
Mismatches: 191
Indels: 120
RESULT 1085
ID ABL29871 standard; DNA; 1569 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41086.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Percent Similarity: 38.99%
Best Local Similarity: 25.23%
Query Match: 7.05%
Conservative: 60
Mismatches: 150
Indels: 116
RESULT 1086
ID ADQ22168 standard; DNA; 1570 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4988.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 37.50%
Best Local Similarity: 23.99%
Query Match: 7.05%
Conservative: 67
Mismatches: 191
Indels: 120
RESULT 1087
ID AAH57469 standard; cDNA; 1887 BP.
DE Human liver cell specific cDNA sequence SEQ ID NO:309.
PN WO200132927-A2.
PD 10-MAY-2001.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 37.50%
Best Local Similarity: 23.99%
Query Match: 7.05%
Conservative: 67
Mismatches: 191
Indels: 120
RESULT 1088
ID ADE85980 standard; cDNA; 1996 BP.
DE Human tissue urokinase plasminogen activator coding sequence.
PN WO2003087393-A2.

```
PD 23-OCT-2003.
PA (GLOB-) GLOBAL BIOTECH INC.
Percent Similarity: 34.49%
Best Local Similarity: 22.31%
Query Match: 7.05%
RESULT 1089
ID ACN42307 standard; cDNA; 1783 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1182.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCV-) INCYTE CORP.
Percent Similarity: 33.18%
Best Local Similarity: 22.42%
Query Match: 7.03%
RESULT 1090
ID ACN41281 standard; cDNA; 2227 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:156.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCV-) INCYTE CORP.
Percent Similarity: 31.82%
Best Local Similarity: 21.35%
Query Match: 7.03%
RESULT 1091
ID AAQ05674 standard; cDNA; 2257 BP.
DE v-PA alpha2.
PN EP363417-A.
PD 22-AUG-1990.
PA (SCHD) SCHERING AG.
Percent Similarity: 38.40%
Best Local Similarity: 26.12%
Query Match: 7.03%
RESULT 1092
ID AAC76693 standard; cDNA; 3623 BP.
DE Human ORFX ORF2248 polynucleotide sequence SEQ ID NO:4495.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.00%
Best Local Similarity: 24.78%
Query Match: 7.03%
RESULT 1093
ID AAZ34034 standard; DNA; 1327 BP.
DE Human EST DNA35597.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1094
ID AAC78495 standard; cDNA; 1327 BP.
DE Human EST DNA35597 nucleotide sequence SEQ ID NO:170.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1095
ID AAC58237 standard; cDNA; 1327 BP.
DE Human EST (expressed sequence tag) DNA35597 SEQ ID NO:25.
PN WO200053754-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1096
ID ACA63602 standard; cDNA; 1327 BP.
DE Novel human secreted and transmembrane protein DNA35597.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Conservative: 68
Mismatch: 191
Indel: 156

PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1097
ID ACA71766 standard; cDNA; 1327 BP.
DE Human secreted and transmembrane polypeptide PRO618 EST.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1098
ID ABX92406 standard; cDNA; 1327 BP.
DE Human PRO618 EST polynucleotide sequence.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1099
ID ACA66147 standard; cDNA; 1327 BP.
DE Human secreted/transmembrane protein EST DNA35597.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1100
ID ADA24709 standard; cDNA; 1327 BP.
DE Novel human secreted and transmembrane protein EST DNA35597.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1101
ID ACD29748 standard; cDNA; 1327 BP.
DE Novel human secreted and transmembrane protein EST DNA35597.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1102
ID ADA12370 standard; cDNA; 1327 BP.
DE Human secreted/transmembrane polypeptide PRO618 EST.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1103
ID ACD29163 standard; cDNA; 1327 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #38.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1104
ID ADB73676 standard; cDNA; 1327 BP.
DE Human PRO polynucleotide sequence #38.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Conservative: 68
Mismatch: 191
Indel: 156
```



```

RESULT 1121
ID ADD72345 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1122
ID ADE16996 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1123
ID ADF47010 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1124
ID ADG52767 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1125
ID ADG60087 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1126
ID ADI60847 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US200307700-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1127
ID ACD42567 standard; cDNA; 1327 BP.
DE Novel human secreted and transmembrane protein EST DNA35597.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1128
ID ADE48504 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1129
ID ADF40561 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1130
ID ADF61245 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1131
ID ADF39937 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1132
ID ADF45733 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1133
ID ADF24129 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156

```

PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1135
ID ADF23505 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1136
ID ADF33488 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1137
ID ADF26955 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1138
ID ADF27591 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1139
ID ADF41185 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1140
ID ADF32864 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1141
ID ADF25230 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1142
ID ADF26331 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003199674-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1143
ID ADF34120 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1144
ID ADF46357 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1145
ID ADF50343 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1146
ID ADG49719 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1147
ID ADG51591 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1148
ID ADG49095 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1149
ID ADG48471 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1150
ID ADG50967 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2004005312-A1.
PD 08-JAN-2004.

```
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatches: 191
Indels: 156
RESULT 1151
ID ADG58911 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatches: 191
Indels: 156
RESULT 1152
ID ADG62367 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatches: 191
Indels: 156
RESULT 1153
ID ADH25392 standard; cDNA; 1327 BP.
DE Human neurotrophin homologue related nucleotide sequence SEQ ID NO:170.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatches: 191
Indels: 156
RESULT 1154
ID ADM17169 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatches: 191
Indels: 156
RESULT 1155
ID ADL07003 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatches: 191
Indels: 156
RESULT 1156
ID ADT91616 standard; cDNA; 1327 BP.
DE Human EST nucleotide DNA35597.
PN AU2002317529-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatches: 191
Indels: 156
RESULT 1157
ID RAI99982 standard; cDNA; 1338 BP.
DE Human FVII encoding cDNA SEQ ID NO 2.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Percent Similarity: 33.08%
Best Local Similarity: 21.54%
Query Match: 7.02%
Conservative: 75
Mismatches: 177
Indels: 259
RESULT 1158
ID ADF44970 standard; cDNA; 1338 BP.
DE Human Factor VII coding sequence, SEQ ID 1.
PN WO2003093465-A1.
PD 13-NOV-2003.
PA (MAXY-) MAXYGEN APS.
Percent Similarity: 33.08%
Best Local Similarity: 21.54%
Query Match: 7.02%
Conservative: 75
Mismatches: 177
Indels: 259
RESULT 1159
ID ADO10532 standard; DNA; 1338 BP.
DE Human factor VIIa gene.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Percent Similarity: 33.08%
Best Local Similarity: 21.54%
Query Match: 7.02%
Conservative: 75
Mismatches: 177
Indels: 259
RESULT 1160
ID ADS12865 standard; DNA; 1338 BP.
DE Human FVII expression cassette SEQ ID NO:1.
PN WO2004083361-A2.
PD 30-SEP-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Percent Similarity: 33.08%
Best Local Similarity: 21.54%
Query Match: 7.02%
Conservative: 75
Mismatches: 177
Indels: 259
RESULT 1161
ID RAI99983 standard; cDNA; 1357 BP.
DE Human FVII expression cassette SEQ ID NO 4.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Percent Similarity: 33.08%
Best Local Similarity: 21.54%
Query Match: 7.02%
Conservative: 75
Mismatches: 177
Indels: 259
RESULT 1162
ID ADF44974 standard; DNA; 1357 BP.
DE Human Factor VII-related sequence.
PN WO2003093465-A1.
PD 13-NOV-2003.
PA (MAXY-) MAXYGEN APS.
Percent Similarity: 33.08%
Best Local Similarity: 21.54%
Query Match: 7.02%
Conservative: 75
Mismatches: 177
Indels: 259
RESULT 1163
ID ADS12867 standard; DNA; 1357 BP.
DE Expression optimised human factor VII gene SEQ ID NO:3.
PN WO2004083361-A2.
PD 30-SEP-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Percent Similarity: 33.08%
Best Local Similarity: 21.54%
Query Match: 7.02%
Conservative: 75
Mismatches: 177
Indels: 259
RESULT 1164
ID AAN81091 standard; DNA; 1689 BP.
DE Mutated t-PA analogue coding sequence in plasmid Zm99-9200.
PN EP293934-A.
PD 07-DEC-1988.
PA (ZYMO ) ZYMOGENETICS INC.
Percent Similarity: 33.08%
Best Local Similarity: 23.38%
Query Match: 7.02%
Conservative: 76
Mismatches: 202
Indels: 148
RESULT 1165
ID ACN41282 standard; cDNA; 2177 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:157.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCYTE ) INCYTE CORP.
Percent Similarity: 31.99%
Best Local Similarity: 21.24%
Query Match: 7.02%
Conservative: 83
Mismatches: 242
Indels: 288
```

RESULT 1166
 ID AAO46262 standard; DNA; 1727 BP.
 DE Encodes modified tPA MB1012 with two K2 kringle domains.
 PN US2244676-A.
 PD 14-SEP-1993.
 PA (MONS) MONSANTO CO.
 Percent Similarity: 36.64%
 Best Local Similarity: 22.64%
 Query Match: 7.01%
 Indels: 165
 Conservative: 89
 Mismatches: 238

RESULT 1167
 ID ABL65242 standard; DNA; 2036 BP.
 DE Lung cancer related gene sequence SEQ ID NO:3579.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Percent Similarity: 35.91%
 Best Local Similarity: 24.18%
 Query Match: 7.01%
 Indels: 222
 Conservative: 79
 Mismatches: 212

RESULT 1168
 ID ABL65242 standard; DNA; 2036 BP.
 DE Gene #1612 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 35.91%
 Best Local Similarity: 24.18%
 Query Match: 7.01%
 Indels: 222
 Conservative: 79
 Mismatches: 212

RESULT 1169
 ID ADJ57517 standard; cDNA; 2040 BP.
 DE Human FVII-IgG1 Fc domain fusion protein encoding cDNA.
 PN WO2004006962-A2.
 PD 22-JAN-2004.
 PA (NOVO) NOVO NORDISK AS.
 Percent Similarity: 35.21%
 Best Local Similarity: 22.57%
 Query Match: 7.01%
 Indels: 183
 Conservative: 65
 Mismatches: 150

RESULT 1170
 ID ADJ57518 standard; cDNA; 7427 BP.
 DE Human FVII-IgG1 Fc domain fusion protein encoding cDNA.
 PN WO2004006962-A2.
 PD 22-JAN-2004.
 PA (NOVO) NOVO NORDISK AS.
 Percent Similarity: 35.21%
 Best Local Similarity: 22.57%
 Query Match: 7.01%
 Indels: 183
 Conservative: 65
 Mismatches: 150

RESULT 1171
 ID ABS68099 standard; DNA; 1505 BP.
 DE Clotting Factor IX construct PFIXABCD.
 PN WO200264799-A2.
 PD 22-AUG-2002.
 PA (TRAN-) TRANSKARYOTIC THERAPIES INC.
 Percent Similarity: 34.48%
 Best Local Similarity: 21.94%
 Query Match: 7.00%
 Indels: 217
 Conservative: 80
 Mismatches: 202

RESULT 1172
 ID AAN70249 standard; DNA; 1581 BP.
 DE Sequence encoding wild-type human tissue plasminogen activator (t-PA) from HeLa cells.
 PN EP225286-A.
 PD 10-JUN-1987.
 PA (CIBA) CIBA GEIGY AG.
 Percent Similarity: 35.54%
 Best Local Similarity: 22.47%
 Query Match: 7.00%
 Indels: 186
 Conservative: 75
 Mismatches: 187

RESULT 1173
 ID AAH19459 standard; DNA; 1221 BP.
 DE Wild-type human blood coagulant factor VII (FVII) coding sequence.
 PN JP2001061479-A.
 PD 13-MAR-2001.
 PA (KAGA) ZH KAGAKU & KESSHI RYOHO KENKYUSHO.
 Percent Similarity: 35.21%
 Best Local Similarity: 22.57%
 Query Match: 6.98%
 Indels: 183
 Conservative: 65
 Mismatches: 150

RESULT 1174
 ID ACC78872 standard; DNA; 1332 BP.
 DE Human Factor VIIa encoding DNA.
 PN WO2003031464-A2.
 PD 17-APR-2003.
 PA (NEOS-) NEOSE TECHNOLOGIES INC.
 Percent Similarity: 35.21%
 Best Local Similarity: 22.57%
 Query Match: 6.98%
 Indels: 183
 Conservative: 65
 Mismatches: 150

RESULT 1175
 ID ADN49679 standard; DNA; 1332 BP.
 DE Human Factor VIIa DNA SeqID 7.
 PN WO2004033651-A2.
 PD 22-APR-2004.
 PA (NEOS-) NEOSE TECHNOLOGIES INC.
 Percent Similarity: 35.21%
 Best Local Similarity: 22.57%
 Query Match: 6.98%
 Indels: 183
 Conservative: 65
 Mismatches: 150

RESULT 1176
 ID ACN42308 standard; cDNA; 1667 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1183.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Percent Similarity: 35.05%
 Best Local Similarity: 23.12%
 Query Match: 6.98%
 Indels: 198
 Conservative: 65
 Mismatches: 157

RESULT 1177
 ID ADP12869 standard; DNA; 2412 BP.
 DE Reference mRNA sequence #83.
 PN WO2004042346-A2.
 PD 21-MAY-2004.
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 Percent Similarity: 35.21%
 Best Local Similarity: 22.57%
 Query Match: 6.98%
 Indels: 183
 Conservative: 65
 Mismatches: 150

RESULT 1178
 ID AAQ80296 standard; cDNA; 2422 BP.
 DE cDNA encoding Factor VII.
 PN WO9427631-A1.
 PD 08-DEC-1994.
 PA (ZYMO) ZYMOGENETICS INC.
 Percent Similarity: 35.21%
 Best Local Similarity: 22.57%
 Query Match: 6.98%
 Indels: 183
 Conservative: 65
 Mismatches: 150

RESULT 1179
 ID AAV02230 standard; cDNA; 2422 BP.
 DE Homo sapiens cDNA encoding Ser344Ala modified factor VII.
 PN WO9747651-A1.
 PD 18-DEC-1997.
 PA (NOVO) NOVO-NORDISK AS.
 Percent Similarity: 35.21%
 Best Local Similarity: 22.57%
 Query Match: 6.98%
 Indels: 183
 Conservative: 65
 Mismatches: 150

RESULT 1180
 ID AAZ57385 standard; cDNA; 2422 BP.
 DE Factor VII encoding cDNA SEQ ID NO:1.
 PN US5997864-A.
 PD 07-DEC-1999.
 PA (NOVO) NOVO-NORDISK AS.
 Percent Similarity: 35.21%
 Best Local Similarity: 22.57%
 Query Match: 6.98%
 Indels: 183
 Conservative: 65
 Mismatches: 150

RESULT 1181
 ID AAF57099 standard; cDNA; 2422 BP.
 DE Human Factor VII polypeptide encoding cDNA.
 PN US6183743-B1.
 PD 06-FEB-2001.
 PA (ZYMO) ZYMOGENETICS INC.
 Percent Similarity: 35.21%
 Best Local Similarity: 22.57%
 Query Match: 6.98%
 Indels: 183
 Conservative: 65
 Mismatches: 150

Percent Similarity: 35.21% Conservative: 65
Best Local Similarity: 22.57% Mismatches: 150
Query Match: 6.98% Indels: 183
RESULT 1182
ID ADC24226 standard; cDNA; 2422 BP.
DE Human NOV8a encoding cDNA SEQ ID NO:33.
PN WO2003076584-A2.
PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 35.21% Conservative: 65
Best Local Similarity: 22.57% Mismatches: 150
Query Match: 6.98% Indels: 183
RESULT 1183
ID AAX77712 standard; DNA; 2696 BP.
DE Murine plasminogen DNA.
PN WO9926480-A1.
PD 03-JUN-1999.
PA (GENE-) GENETIX PHARM INC.
Percent Similarity: 33.92% Conservative: 98
Best Local Similarity: 22.38% Mismatches: 272
Query Match: 6.98% Indels: 292
RESULT 1184
ID AAI70086 standard; DNA; 4496 BP.
DE Plasmid pFN0945 encoding human coagulation Factor IX.
PN WO200166149-A2.
PD 13-SEP-2001.
PA (VALE-) VALENTIS INC.
Percent Similarity: 32.69% Conservative: 86
Best Local Similarity: 20.88% Mismatches: 217
Query Match: 6.98% Indels: 273
RESULT 1185
ID ABX14193 standard; DNA; 6098 BP.
DE Plasmid pLN174 for expressing human coagulation Factor VII.
PN WO20027218-A1.
PD 03-OCT-2002.
PA (NOVO) NOVO NORDISK AS.
Percent Similarity: 35.21% Conservative: 65
Best Local Similarity: 22.57% Mismatches: 150
Query Match: 6.98% Indels: 183
RESULT 1186
ID AAL45696 standard; DNA; 1683 BP.
DE Human blood coagulation factor VII activating protease DNA.
PN EP1182258-A1.
PD 27-FEB-2002.
PA (AVET) AVENTIS BEHRING GMBH.
Percent Similarity: 40.00% Conservative: 86
Best Local Similarity: 24.78% Mismatches: 202
Query Match: 6.97% Indels: 138
RESULT 1187
ID AAL45697 standard; DNA; 1683 BP.
DE Human blood coagulation factor VII activating protease mutant DNA.
PN EP1182258-A1.
PD 27-FEB-2002.
PA (AVET) AVENTIS BEHRING GMBH.
Percent Similarity: 40.00% Conservative: 86
Best Local Similarity: 24.78% Mismatches: 202
Query Match: 6.97% Indels: 138
RESULT 1188
ID ABN95170 standard; DNA; 3008 BP.
DE Gene #1668 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 40.00% Conservative: 86
Best Local Similarity: 24.78% Mismatches: 202
Query Match: 6.97% Indels: 138
RESULT 1189
ID ACC51204 standard; cDNA; 3008 BP.
DE Human Plk-1 related cDNA sequence hmft-0306 SEQ ID NO:89.
PN WO2003018807-A1.
PD 06-MAR-2003.
PA (HISM) HISAMITSU PHARM CO LTD.

PA (CHIB-) CHIBA PREFECTURE.
Percent Similarity: 40.00% Conservative: 86
Best Local Similarity: 24.78% Mismatches: 202
Query Match: 6.97% Indels: 138
RESULT 1190
ID AAQ11551 standard; DNA; 1659 BP.
DE Sequence encoding tissue plasminogen activator deriv.
PN JP03065184-A.
PD 20-MAR-1991.
PA (KANF) KANEGAFUCHI CHEM KK.
Percent Similarity: 35.49% Conservative: 73
Best Local Similarity: 22.73% Mismatches: 186
Query Match: 6.95% Indels: 186
RESULT 1191
ID AAN70089 standard; DNA; 2009 BP.
DE Hybrid plasminogen activator (PA) contg. tissue plasminogen activator
DE (tPA) 1-91, urokinase kringle (UKK) 50-131 and tPA 92-527.
PN EP213794-A.
PD 11-MAR-1987.
PA (AMRP) AMERICAN HOME PROD CORP.
Percent Similarity: 35.02% Conservative: 81
Best Local Similarity: 22.24% Mismatches: 197
Query Match: 6.95% Indels: 216
RESULT 1192
ID AAI70087 standard; DNA; 4276 BP.
DE Codon optimised plasmid pFN1645 for human coagulation Factor IX.
PN WO200166149-A2.
PD 13-SEP-2001.
PA (VALE-) VALENTIS INC.
Percent Similarity: 32.82% Conservative: 88
Best Local Similarity: 20.48% Mismatches: 237
Query Match: 6.95% Indels: 242
RESULT 1193
ID AAH19463 standard; DNA; 1206 BP.
DE Mutant blood coagulant factor VII (FVII-31) coding sequence.
PN JP2001061479-A.
PD 13-MAR-2001.
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
Percent Similarity: 35.02% Conservative: 64
Best Local Similarity: 22.57% Mismatches: 146
Query Match: 6.92% Indels: 188
RESULT 1194
ID AAQ12077 standard; DNA; 2100 BP.
DE T-PA variant having Lys416 substituted (4).
PN JP03061484-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Percent Similarity: 34.84% Conservative: 74
Best Local Similarity: 21.95% Mismatches: 191
Query Match: 6.92% Indels: 186
RESULT 1195
ID AAQ13164 standard; DNA; 1721 BP.
DE Gene encoding t-PA variant MB1023.
PN US5037752-A.
PD 06-AUG-1991.
PA (MONS) MONSANTO CO.
Percent Similarity: 35.21% Conservative: 88
Best Local Similarity: 21.80% Mismatches: 220
Query Match: 6.91% Indels: 205
RESULT 1196
ID AAQ63951 standard; cDNA; 2033 BP.
DE Hepatocyte growth factor converting protease coding sequence.
PN EP596524-A2.
PD 11-MAY-1994.
PA (MITU) MITSUBISHI KASEI CORP.
Percent Similarity: 36.57% Conservative: 82
Best Local Similarity: 24.33% Mismatches: 213
Query Match: 6.91% Indels: 214
RESULT 1197
ID AAN60063 standard; cDNA; 2177 BP.
DE Partial Factor VII cDNA.
PN EP200421-A.
PD 10-DEC-1986.

PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 33.33%
Best Local Similarity: 22.29%
Query Match: 6.91%
RESULT 1198
ID ABZ35309 standard; cDNA; 1645 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 420.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Percent Similarity: 38.65%
Best Local Similarity: 26.52%
Query Match: 6.89%
RESULT 1199
ID AAA62807 standard; DNA; 672 BP.
DE Neurosin encoding DNA sequence.
PN WO200031284-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Percent Similarity: 44.57%
Best Local Similarity: 31.40%
Query Match: 6.88%
RESULT 1200
ID AAQ53487 standard; DNA; 732 BP.
DE DNA encoding Zyme APP-cleaving protease.
PN EP576152-A1.
PD 29-DEC-1993.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 44.57%
Best Local Similarity: 31.40%
Query Match: 6.88%
RESULT 1201
ID AAH19461 standard; DNA; 1221 BP.
DE Mutant blood coagulant factor VII (FVII-6) coding sequence.
PN JP2001061479-A.
PD 13-MAR-2001.
PA (KAGA) ZH KAGAKU & KESSHI RYOHO KENKYUSHO.
Percent Similarity: 35.03%
Best Local Similarity: 22.31%
Query Match: 6.88%
RESULT 1202
ID ADE53650 standard; cDNA; 1413 BP.
DE Human kallikrein 6 serine protease encoding cDNA SEQ ID NO:2.
PN WO200309328-A1.
PD 04-DEC-2003.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
PA (UYFL) UNIV FLORIDA STATE.
Percent Similarity: 44.57%
Best Local Similarity: 31.40%
Query Match: 6.88%
RESULT 1203
ID AAT79126 standard; cDNA to mRNA; 1438 BP.
DE Human serine protease 59 (SP59) cDNA.
PN JP09149790-A.
PD 10-JUN-1997.
PA (SUNR) SUNTORY LTD.
Percent Similarity: 44.57%
Best Local Similarity: 31.40%
Query Match: 6.88%
RESULT 1204
ID ADR72625 standard; DNA; 1451 BP.
DE Human renal cell carcinoma-related kallikrein 6 (KLK6) DNA 1.
PN WO2004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Percent Similarity: 44.57%
Best Local Similarity: 31.40%
Query Match: 6.88%
RESULT 1205
ID ADR72877 standard; DNA; 1451 BP.
DE Human ovarian cancer-related tumour marker kallikrein 6 (KLK6) DNA 1.
PN WO2004075713-A2.
PD 10-SEP-2004.

PA (MOUN) MOUNT SINAI HOSPITAL.
Percent Similarity: 44.57%
Best Local Similarity: 31.40%
Query Match: 6.88%
RESULT 1206
ID ADQ83735 standard; cDNA; 1505 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #549.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Percent Similarity: 44.57%
Best Local Similarity: 31.40%
Query Match: 6.88%
RESULT 1207
ID ACN40669 standard; cDNA; 1505 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326750, SEQ ID NO:5592.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.57%
Best Local Similarity: 31.40%
Query Match: 6.88%
RESULT 1208
ID ABS76453 standard; cDNA; 1506 BP.
DE cDNA encoding human ovarian cancer marker OV33.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 44.57%
Best Local Similarity: 31.40%
Query Match: 6.88%
RESULT 1209
ID ABL62164 standard; DNA; 1506 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:501.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 44.57%
Best Local Similarity: 31.40%
Query Match: 6.88%
RESULT 1210
ID ABZ35055 standard; cDNA; 1506 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 167.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Percent Similarity: 44.57%
Best Local Similarity: 31.40%
Query Match: 6.88%
RESULT 1211
ID ADB80566 standard; DNA; 1506 BP.
DE Ovarian cancer-associated transcript #66.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 44.57%
Best Local Similarity: 31.40%
Query Match: 6.88%
RESULT 1212
ID AAD63182 standard; DNA; 1506 BP.
DE Human kallikrein 6 (KLK6) DNA.
PN US2003190656-A1.
PD 09-OCT-2003.
PA (WANG/) WANG Y.
Percent Similarity: 44.57%
Best Local Similarity: 31.40%
Query Match: 6.88%
RESULT 1213
ID AAD62793 standard; DNA; 1506 BP.
DE Human kallikrein 6 (KLK6) DNA.
PN US2003194733-A1.

PD 16-OCT-2003.			
PA (WANG/) WANG Y.	44.57%	Conservative:	34
Percent Similarity:	31.40%	Mismatches:	94
Best Local Similarity:	6.88%	Indels:	49
Query Match:			
RESULT 1214			
ID ACC80976 standard; cDNA; 1506 BP.			
DE Human 2047 protein encoding cDNA.			
PN WO2003037258-A2.			
PD 08-MAY-2003.			
PA (MILL-) MILLENNIUM PHARM INC.			
Percent Similarity:	44.57%	Conservative:	34
Best Local Similarity:	31.40%	Mismatches:	94
Query Match:	6.88%	Indels:	49
RESULT 1215			
ID ADN39211 standard; cDNA; 1506 BP.			
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:529.			
PN WO2003042661-A2.			
PD 22-MAY-2003.			
PA (BOSB-) EOS BIOTECHNOLOGY INC.			
Percent Similarity:	44.57%	Conservative:	34
Best Local Similarity:	31.40%	Mismatches:	94
Query Match:	6.88%	Indels:	49
RESULT 1216			
ID ADP88278 standard; cDNA; 1506 BP.			
DE Ovarian cancer marker gene KLK6, SEQ ID NO:55.			
PN EP1349104-A2.			
PD 01-OCT-2003.			
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.			
Percent Similarity:	44.57%	Conservative:	34
Best Local Similarity:	31.40%	Mismatches:	94
Query Match:	6.88%	Indels:	49
RESULT 1217			
ID ADN29137 standard; DNA; 1506 BP.			
DE Human kallikrein 6 associated DNA seqid 11.			
PN US2004097452-A1.			
PD 20-MAY-2004.			
PA (ISIS-) ISIS PHARM INC.			
Percent Similarity:	44.57%	Conservative:	34
Best Local Similarity:	31.40%	Mismatches:	94
Query Match:	6.88%	Indels:	49
RESULT 1218			
ID ADR24953 standard; DNA; 1506 BP.			
DE Breast cancer prognosis marker #814.			
PN WO2004065545-A2.			
PD 05-AUG-2004.			
PA (ROSE-) ROSETTA INPHARMATICS LLC.			
Percent Similarity:	44.57%	Conservative:	34
Best Local Similarity:	31.40%	Mismatches:	94
Query Match:	6.88%	Indels:	49
RESULT 1219			
ID ADO89075 standard; cDNA; 1506 BP.			
DE Human urological disorder related protein 2047 encoding cDNA SEQ:27.			
PN WO2004065576-A2.			
PD 05-AUG-2004.			
PA (MILL-) MILLENNIUM PHARM INC.			
Percent Similarity:	44.57%	Conservative:	34
Best Local Similarity:	31.40%	Mismatches:	94
Query Match:	6.88%	Indels:	49
RESULT 1220			
ID ADR72627 standard; DNA; 1506 BP.			
DE Human renal cell carcinoma-related kallikrein 6 (KLK6) DNA 3.			
PN WO2004077060-A2.			
PD 10-SEP-2004.			
PA (MOUN) MOUNT SINAI HOSPITAL.			
Percent Similarity:	44.57%	Conservative:	34
Best Local Similarity:	31.40%	Mismatches:	94
Query Match:	6.88%	Indels:	49
RESULT 1221			
ID ADR72879 standard; DNA; 1506 BP.			
DE Human ovarian cancer-related tumour marker kallikrein 6 (KLK6) DNA 3.			
PN WO2004075713-A2.			

PA (OOIC/) OOI C E.
 PA (ROTH/) ROTHENBERG M E.
 PA (SPAD/) SPADERNA S K.
 PA (HJAL/) HJALT T.
 PA (LIUX/) LIU X.
 PA (TAUP/) TAUPIER R J.
 PA (CATI/) CARTERTON E.
 PA (SHEN/) SHENOY S G.
 Percent Similarity: 32.71%
 Best Local Similarity: 21.06%
 Query Match: 6.88%
 Indels: 316
 Conservative: 99
 Mismatches: 257
 Indels: 316

RESULT 1226
 ID AAN91618 standard; cDNA to mRNA; 1500 BP.
 DE Human pro-urokinase coding sequence plus untranslated regions.
 PN EP312942-A.
 PD 26-APR-1989.
 PA (BADI) BASF AG.
 Percent Similarity: 38.59%
 Best Local Similarity: 25.86%
 Query Match: 6.87%
 Indels: 130
 Conservative: 67
 Mismatches: 193
 Indels: 130

RESULT 1227
 ID AAN50457 standard; DNA; 1572 BP.
 DE TPA-(13-527).
 PN JP60041697-A.
 PD 05-MAR-1985.
 PA (ASAH) ASahi CHEM IND CO LTD.
 Percent Similarity: 35.23%
 Best Local Similarity: 22.63%
 Query Match: 6.87%
 Indels: 190
 Conservative: 73
 Mismatches: 188
 Indels: 190

RESULT 1228
 ID AAQ11550 standard; DNA; 1614 BP.
 DE Sequence encoding tissue plasminogen activator deriv.
 PN JP03065184-A.
 PD 20-MAR-1991.
 PA (KANF) KANEGAFUCHI CHEM KK.
 Percent Similarity: 35.63%
 Best Local Similarity: 22.31%
 Query Match: 6.87%
 Indels: 202
 Conservative: 83
 Mismatches: 202
 Indels: 202

RESULT 1229
 ID ADQ08645 standard; DNA; 3016 BP.
 DE Ciona intestinalis nervous system associated gene SeqID47.
 PN JP2004057127-A.
 PD 26-FEB-2004.
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 Percent Similarity: 38.08%
 Best Local Similarity: 24.72%
 Query Match: 6.87%
 Indels: 90
 Conservative: 60
 Mismatches: 188
 Indels: 90

RESULT 1230
 ID AAD37043 standard; DNA; 200 BP.
 DE Targetting arm #1, to disrupt limulus-clotting factor protease-like gene.
 PN WO200203787-A2.
 PD 17-JAN-2002.
 PA (DELT-) DELTAGEN INC.
 Percent Similarity: 90.91%
 Best Local Similarity: 85.45%
 Query Match: 6.84%
 Indels: 0
 Conservative: 3
 Mismatches: 5
 Indels: 0

RESULT 1231
 ID AAQ04728 standard; DNA; 1689 BP.
 DE Sequence encoding a thrombolytic protein.
 PN JP02119776-A.
 PD 07-MAY-1990.
 PA (YAMA) YAMANOUCHI PHARM CO LTD.
 Percent Similarity: 38.24%
 Best Local Similarity: 24.08%
 Query Match: 6.84%
 Indels: 124
 Conservative: 77
 Mismatches: 212
 Indels: 124

RESULT 1232
 ID AAQ05673 standard; cDNA; 2252 BP.
 DE v-PA alpha1.
 PN EP383417-A.
 PD 22-AUG-1990.
 PA (SCHD) SCHERING AG.
 Percent Similarity: 36.85%
 Best Local Similarity: 23.80%
 Indels: 164
 Conservative: 68
 Mismatches: 164

Query Match: 6.84%
 Indels: 166

RESULT 1233
 ID AAN70992 standard; DNA; 1323 BP.
 DE Modified tissue plasminogen activator.
 PN AU8661804-A.
 PD 05-MAR-1987.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 36.86%
 Best Local Similarity: 23.92%
 Query Match: 6.83%
 Indels: 145
 Conservative: 66
 Mismatches: 177
 Indels: 145

RESULT 1234
 ID AAN70991 standard; DNA; 1422 BP.
 DE Modified tissue plasminogen activator.
 PN AU8661804-A.
 PD 05-MAR-1987.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 36.86%
 Best Local Similarity: 23.92%
 Query Match: 6.83%
 Indels: 145
 Conservative: 66
 Mismatches: 177
 Indels: 145

RESULT 1235
 ID AAN91217 standard; DNA; 1689 BP.
 DE Mutated cDNA coding sequence of tissue plasminogen activator (t-PA).
 PN AU8817430-A.
 PD 08-DEC-1988.
 PA (NOVO) NOVO IND AS.
 PA (ZYMO) ZYMOGENETICS INC.
 Percent Similarity: 34.35%
 Best Local Similarity: 21.98%
 Query Match: 6.83%
 Indels: 241
 Conservative: 81
 Mismatches: 192
 Indels: 241

RESULT 1236
 ID AAQ06319 standard; DNA; 1721 BP.
 DE Synthetic gene encoding t-PA variant MB1023.
 PN US4963357-A.
 PD 16-OCT-1990.
 PA (MONS) MONSANTO CO.
 Percent Similarity: 35.21%
 Best Local Similarity: 21.65%
 Query Match: 6.83%
 Indels: 205
 Conservative: 89
 Mismatches: 220
 Indels: 205

RESULT 1237
 ID AAQ13165 standard; DNA; 1721 BP.
 DE Gene encoding t-PA variant MB1083 with longer half-life.
 PN US5037752-A.
 PD 06-AUG-1991.
 PA (MONS) MONSANTO CO.
 Percent Similarity: 35.21%
 Best Local Similarity: 21.65%
 Query Match: 6.83%
 Indels: 205
 Conservative: 89
 Mismatches: 220
 Indels: 205

RESULT 1238
 ID ABL06001 standard; cDNA; 1032 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 12485.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 40.54%
 Best Local Similarity: 25.14%
 Query Match: 6.82%
 Indels: 99
 Conservative: 57
 Mismatches: 121
 Indels: 99

RESULT 1239
 ID ADB58749 standard; DNA; 2737 BP.
 DE Toxicity-related gene, SEQ ID 3775.
 PN WO2003064624-A2.
 PD 07-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 33.81%
 Best Local Similarity: 21.99%
 Query Match: 6.82%
 Indels: 292
 Conservative: 100
 Mismatches: 269
 Indels: 292

RESULT 1240
 ID AAQ00543 standard; cDNA; 1620 BP.
 DE Vampire bat plasminogen activator gene.
 PN EP352119-A.
 PD 24-JAN-1990.
 PA (SCHD) MERCK & CO INC.
 Percent Similarity: 36.85%
 Best Local Similarity: 23.80%
 Indels: 164
 Conservative: 68
 Mismatches: 164

Percent Similarity: 37.62% Conservative: 62
Best Local Similarity: 25.54% Mismatches: 174
Query Match: 6.81% Indels: 146
RESULT 1241
ID AAT27588 standard; DNA; 1680 BP.
DE Novel plasminogen activator DNA.
PN US5504001-A.
PD 02-APR-1996.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 38.38% Conservative: 81
Best Local Similarity: 23.78% Mismatches: 194
Query Match: 6.81% Indels: 149
RESULT 1242
ID AAN70090 standard; DNA; 2009 BP.
DE Hybrid plasminogen activator (PA) contg. tissue plasminogen activator
DE (tPA) 1-261, urokinase kringles (UKK) 50-131 and tPA 262-527.
PN EP213794-A.
PD 11-MAR-1987.
PA (AMHP) AMERICAN HOME PROD CORP.
Percent Similarity: 36.12% Conservative: 78
Best Local Similarity: 23.32% Mismatches: 225
Query Match: 6.81% Indels: 166
RESULT 1243
ID ADH41498 standard; DNA; 3345 BP.
DE Novel human nucleic acid NOV3s.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.76% Conservative: 69
Best Local Similarity: 24.90% Mismatches: 180
Query Match: 6.78% Indels: 126
RESULT 1244
ID AAL38736 standard; DNA; 1389 BP.
DE Contiguous DNA of human factor IX.
PN WO200240544-A2.
PD 23-MAY-2002.
PA (TEXA) UNIV TEXAS SYSTEM.
Percent Similarity: 35.13% Conservative: 72
Best Local Similarity: 22.22% Mismatches: 180
Query Match: 6.77% Indels: 182
RESULT 1245
ID AAX15426 standard; DNA; 1437 BP.
DE DNA encoding coagulation factor IX/IXa.
PN US5877289-A.
PD 02-MAR-1999.
PA (SCRI) SCRIPPS RES INST.
PA (TEXA) UNIV TEXAS SYSTEM.
Percent Similarity: 35.13% Conservative: 72
Best Local Similarity: 22.22% Mismatches: 180
Query Match: 6.77% Indels: 182
RESULT 1246
ID AAA12969 standard; DNA; 1437 BP.
DE DNA encoding Factor IX/IXa, SEQ ID NO:26.
PN US6036955-A.
PD 14-MAR-2000.
PA (TEXA) UNIV TEXAS SYSTEM.
PA (SCRI) SCRIPPS RES INST.
Percent Similarity: 35.13% Conservative: 72
Best Local Similarity: 22.22% Mismatches: 180
Query Match: 6.77% Indels: 182
RESULT 1247
ID AAZ56119 standard; DNA; 1437 BP.
DE Vitamin-K-dependent coagulation factor IX/IXa coding sequence.
PN US6004555-A.
PD 21-DEC-1999.
PA (SCRI) SCRIPPS RES INST.
PA (TEXA) UNIV TEXAS SYSTEM.
Percent Similarity: 35.13% Conservative: 72
Best Local Similarity: 22.22% Mismatches: 180
Query Match: 6.77% Indels: 182
RESULT 1248
ID AAA89785 standard; DNA; 1437 BP.
DE DNA encoding coagulation factor IX/IXa.
PN US6093399-A.
PD 25-JUL-2000.
PA (SCRI) SCRIPPS RES INST.
PA (TEXA) UNIV TEXAS SYSTEM.
Percent Similarity: 35.13% Conservative: 72
Best Local Similarity: 22.22% Mismatches: 180
Query Match: 6.77% Indels: 182
RESULT 1249
ID ADB86697 standard; cDNA; 1437 BP.
DE Factor IX coding sequence.
PN WO2003088899-A2.
PD 30-OCT-2003.
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
Percent Similarity: 35.13% Conservative: 72
Best Local Similarity: 22.22% Mismatches: 180
Query Match: 6.77% Indels: 182
RESULT 1250
ID ACC78873 standard; DNA; 1437 BP.
DE Human Factor IX encoding DNA.
PN WO2003031464-A2.
PD 17-APR-2003.
PA (NEOS-) NEOSE TECHNOLOGIES INC.
Percent Similarity: 35.13% Conservative: 72
Best Local Similarity: 22.22% Mismatches: 180
Query Match: 6.77% Indels: 182
RESULT 1251
ID ADG71757 standard; DNA; 1437 BP.
DE Vitamin K dependent coagulation factor IX/IXa.
PN US2003219441-A1.
PD 27-NOV-2003.
PA (TEXA) UNIV TEXAS SYSTEM.
PA (SCRI) SCRIPPS RES INST.
Percent Similarity: 35.13% Conservative: 72
Best Local Similarity: 22.22% Mismatches: 180
Query Match: 6.77% Indels: 182
RESULT 1252
ID ADN49681 standard; DNA; 1437 BP.
DE Human Factor IX DNA SeqID 9.
PN WO2004033651-A2.
PD 22-APR-2004.
PA (NEOS-) NEOSE TECHNOLOGIES INC.
Percent Similarity: 35.13% Conservative: 72
Best Local Similarity: 22.22% Mismatches: 180
Query Match: 6.77% Indels: 182
RESULT 1253
ID ADH41470 standard; DNA; 1368 BP.
DE Novel human nucleic acid NOV3e.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.79% Conservative: 70
Best Local Similarity: 24.65% Mismatches: 178
Query Match: 6.76% Indels: 126
RESULT 1254
ID ADH41494 standard; DNA; 3345 BP.
DE Novel human nucleic acid NOV3q.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.95% Conservative: 73
Best Local Similarity: 24.14% Mismatches: 180
Query Match: 6.76% Indels: 122
RESULT 1255
ID AAN81088 standard; DNA; 1680 BP.
DE Tissue plasminogen activator analogue coding sequence.
PN EP293934-A.
PD 07-DEC-1988.
PA (ZYMO) ZYMOGENETICS INC.
PA (NOVO) NOVO IND AS.
PA (EISA) EISA CO LTD.
Percent Similarity: 38.86% Conservative: 81
Best Local Similarity: 23.94% Mismatches: 208
Query Match: 6.74% Indels: 125

RESULT 1256
 ID ACN41795 standard; cDNA; 2075 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:670.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Percent Similarity: 34.28%
 Best Local Similarity: 21.48%
 Query Match: 6.74%
 RESULT 1257
 ID ABL18213 standard; DNA; 753 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6112.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 45.17%
 Best Local Similarity: 25.87%
 Query Match: 6.73%
 RESULT 1258
 ID ADH41468 standard; DNA; 1368 BP.
 DE Novel human nucleic acid NOV3d.
 PN WO2003102159-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.79%
 Best Local Similarity: 24.85%
 Query Match: 6.73%
 RESULT 1259
 ID AAA93124 standard; cDNA; 3094 BP.
 DE Human secreted protein coding sequence SEQ ID NO: 47.
 PN WO200049134-A1.
 PD 24-AUG-2000.
 PA (ALPH-) ALPHAGEN INC.
 Percent Similarity: 38.79%
 Best Local Similarity: 24.85%
 Query Match: 6.73%
 RESULT 1260
 ID ADH41462 standard; DNA; 3345 BP.
 DE Novel human nucleic acid NOV3a.
 PN WO2003102159-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.79%
 Best Local Similarity: 24.85%
 Query Match: 6.73%
 RESULT 1261
 ID ADH41496 standard; DNA; 3345 BP.
 DE Novel human nucleic acid NOV3r.
 PN WO2003102159-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.79%
 Best Local Similarity: 24.85%
 Query Match: 6.73%
 RESULT 1262
 ID ADH41492 standard; DNA; 3345 BP.
 DE Novel human nucleic acid NOV3p.
 PN WO2003102159-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.79%
 Best Local Similarity: 24.85%
 Query Match: 6.73%
 RESULT 1263
 ID ADC24228 standard; cDNA; 1361 BP.
 DE Human NOV8b encoding cDNA SEQ ID NO:35.
 PN WO2003076584-A2.
 PD 18-SEP-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 31.00%
 Best Local Similarity: 20.99%
 Query Match: 6.72%
 RESULT 1264

ID AAN91220 standard; DNA; 1680 BP.
 DE Analogue of cDNA coding sequence of tissue plasminogen activator (t-PA).
 PN AU8817430-A.
 PD 08-DEC-1988.
 PA (NOVO) NOVO IND AS.
 PA (ZYMO) ZYMOGENETICS INC.
 PA (EISA) EISAI CO LTD.
 Percent Similarity: 38.28%
 Best Local Similarity: 24.54%
 Query Match: 6.72%
 RESULT 1265
 ID RAT27587 standard; DNA; 1680 BP.
 DE Novel plasminogen activator DNA.
 PN US5504001-A.
 PD 02-APR-1996.
 PA (ZYMO) ZYMOGENETICS INC.
 Percent Similarity: 38.86%
 Best Local Similarity: 23.94%
 Query Match: 6.72%
 RESULT 1266
 ID AAQ41005 standard; DNA; 5472 BP.
 DE Sequence of plasmid pN2gpta-FIX.
 PN AU9221269-A.
 PD 04-MAR-1993.
 PA (IMMO) IMMO AG.
 Percent Similarity: 34.07%
 Best Local Similarity: 21.63%
 Query Match: 6.72%
 RESULT 1267
 ID AAA9883 standard; DNA; 5532 BP.
 DE Plasmid pN2gpta-FIX.
 PN US6103244-A.
 PD 15-AUG-2000.
 PA (IMMO) IMMO AG.
 Percent Similarity: 34.07%
 Best Local Similarity: 21.63%
 Query Match: 6.72%
 RESULT 1268
 ID AAS12901 standard; DNA; 5532 BP.
 DE Plasmid pN2-gpta-FIX DNA sequence.
 PN US6265183-B1.
 PD 24-JUL-2001.
 PA (BAXT) BAXTER AG.
 Percent Similarity: 34.07%
 Best Local Similarity: 21.63%
 Query Match: 6.72%
 RESULT 1269
 ID AAQ10170 standard; DNA; 1236 BP.
 DE Encodes Pro-urokinase derivative UK-S3 with Asn(153) and Thr(155).
 PN EP405285-A.
 PD 02-JAN-1991.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Percent Similarity: 37.11%
 Best Local Similarity: 24.61%
 Query Match: 6.70%
 RESULT 1270
 ID ADH41476 standard; DNA; 1368 BP.
 DE Novel human nucleic acid NOV3h.
 PN WO2003102159-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.79%
 Best Local Similarity: 24.65%
 Query Match: 6.70%
 RESULT 1271
 ID ADH41490 standard; DNA; 1479 BP.
 DE Novel human nucleic acid NOV3o.
 PN WO2003102159-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.79%
 Best Local Similarity: 24.65%
 Query Match: 6.70%
 RESULT 1272
 ID ADH41492 standard; DNA; 3345 BP.
 DE Novel human nucleic acid NOV3a.
 PN WO2003102159-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.79%
 Best Local Similarity: 24.85%
 Query Match: 6.73%

Conservative: 75
 Mismatches: 207
 Indels: 131

Conservative: 81
 Mismatches: 208
 Indels: 125

Conservative: 84
 Mismatches: 198
 Indels: 247

Conservative: 84
 Mismatches: 198
 Indels: 247

Conservative: 84
 Mismatches: 198
 Indels: 247

Conservative: 64
 Mismatches: 175
 Indels: 147

Conservative: 70
 Mismatches: 178
 Indels: 126

Conservative: 70
 Mismatches: 178
 Indels: 126

```

RESULT 1272
ID AAN91740 standard; DNA; 2303 BP.
DE Sequence of prourokinase cDNA.
PN EP316068-A.
PA (COLB ) COLLABORATIVE RES INC.
Percent Similarity: 37.17%
Best Local Similarity: 23.79%
Query Match: 6.69%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1273
ID AAN30030 standard; cDNA; 2304 BP.
DE Sequence encoding full length urokinase.
PN EP92182-A.
PD 26-OCT-1983.
PA (GETH ) GENENTECH INC.
Percent Similarity: 36.99%
Best Local Similarity: 23.98%
Query Match: 6.69%
Conservative: 70
Mismatch: 185
Indels: 154
RESULT 1274
ID ADE25630 standard; cDNA; 2328 BP.
DE Human cDNA differentially expressed in foam cells #34.
PN US2003194721-A1.
PD 16-OCT-2003.
PA (INCV-) INCYTE GENOMICS INC.
Percent Similarity: 38.11%
Best Local Similarity: 25.28%
Query Match: 6.69%
Conservative: 68
Mismatch: 190
Indels: 138
RESULT 1275
ID ACH03958 standard; cDNA; 2341 BP.
DE Human cDNA differentially expressed in lung cancer #163.
PN US2003065157-A1.
PD 03-APR-2003.
PA (LASE/) LASEK A W.
Percent Similarity: 38.11%
Best Local Similarity: 25.28%
Query Match: 6.69%
Conservative: 68
Mismatch: 190
Indels: 138
RESULT 1276
ID ADH41478 standard; DNA; 1368 BP.
DE Novel human nucleic acid NOV31.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.79%
Best Local Similarity: 24.65%
Query Match: 6.68%
Conservative: 70
Mismatch: 178
Indels: 126
RESULT 1277
ID AAV10463 standard; DNA; 1389 BP.
DE Human Factor IX protease genomic DNA.
PN WO9747737-A1.
PD 18-DEC-1997.
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
Percent Similarity: 35.17%
Best Local Similarity: 22.24%
Query Match: 6.68%
Conservative: 68
Mismatch: 146
Indels: 195
RESULT 1278
ID AAN50049 standard; cDNA; 1639 BP.
DE Sequence encoding human factor IX.
PN EP162782-A.
PD 27-NOV-1985.
PA (TRGE ) TRANSGENE SA.
Percent Similarity: 34.73%
Best Local Similarity: 22.14%
Query Match: 6.68%
Conservative: 66
Mismatch: 151
Indels: 191
RESULT 1279
ID AAS14091 standard; DNA; 1667 BP.
DE Human FCTRS5a DNA sequence.
PN WO200166747-A2.
PD 13-SEP-2001.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.79%
Best Local Similarity: 24.65%
Query Match: 6.68%
Conservative: 70
Mismatch: 178
Indels: 126
RESULT 1280
ID ADB32032 standard; cDNA; 1667 BP.
DE Human FCTRS5a cDNA.
PN US2003087816-A1.
PD 08-MAY-2003.
PA (VERM/) VERMET C.
PA (FERN/) FERNANDES E.
PA (SHIM/) SHIMKETS R.
PA (HERR/) HERRMANN J.
PA (MAJU/) MAJUMDER K.
PA (MACD/) MACDOUGALL J.
PA (MISH/) MISHRA V.
PA (MEZE/) MEZES P S.
PA (RAST/) RASTELLI L.
Percent Similarity: 38.79%
Best Local Similarity: 24.65%
Query Match: 6.68%
Conservative: 70
Mismatch: 178
Indels: 126
RESULT 1281
ID AAS14092 standard; DNA; 1691 BP.
DE Human FCTRS5b DNA sequence.
PN WO200166747-A2.
PD 13-SEP-2001.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.79%
Best Local Similarity: 24.65%
Query Match: 6.68%
Conservative: 70
Mismatch: 178
Indels: 126
RESULT 1282
ID ADB32034 standard; cDNA; 1691 BP.
DE Human FCTRS5b cDNA.
PN US2003087816-A1.
PD 08-MAY-2003.
PA (VERM/) VERMET C.
PA (FERN/) FERNANDES E.
PA (SHIM/) SHIMKETS R.
PA (HERR/) HERRMANN J.
PA (MAJU/) MAJUMDER K.
PA (MACD/) MACDOUGALL J.
PA (MISH/) MISHRA V.
PA (MEZE/) MEZES P S.
PA (RAST/) RASTELLI L.
Percent Similarity: 38.79%
Best Local Similarity: 24.65%
Query Match: 6.68%
Conservative: 70
Mismatch: 178
Indels: 126
RESULT 1283
ID AAN40177 standard; cDNA; 2781 BP.
DE Part of the sequence of human factor IX cDNA.
PN GB2125409-A.
PD 07-MAR-1984.
PA (NAVTR ) NAT RES DEV CORP.
Percent Similarity: 34.76%
Best Local Similarity: 21.75%
Query Match: 6.68%
Conservative: 67
Mismatch: 163
Indels: 173
RESULT 1284
ID AAT02460 standard; mRNA; 2802 BP.
DE Human Factor-IX mRNA.
PN WO9530000-A1.
PD 09-NOV-1995.
PA (BIOT-) BIOTECHNOLOGY & BIOLOGICAL SCI RES COUNC.
Percent Similarity: 34.76%
Best Local Similarity: 21.55%
Query Match: 6.68%
Conservative: 68
Mismatch: 163
Indels: 173
RESULT 1285
ID AAQ06049 standard; DNA; 1296 BP.
DE plasmid pUK1 pro-Urokinase sequence.
PN EP390592-A.
PD 03-OCT-1990.
PA (KYOW ) KYOWA HAKKO KOGYO KK.
PA (EXPE-) CENT INST EXPT ANIMALS.
PA (JIKK-) JIKKEN DOBUTSU CHUO KENK.
Percent Similarity: 37.17%
Best Local Similarity: 23.79%
Query Match: 6.67%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1286
ID AAQ55772 standard; cDNA to mRNA; 1296 BP.

```

DE Pro-urokinase derivative.
 PN JF05336985-A.
 PD 21-DEC-1993.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1287
 ID ABK86598 standard; cDNA; 1296 BP.
 DE Human plasminogen activator, urokinase (PLAU) cDNA.
 PN WO200240503-A2.
 PD 23-MAY-2002.
 PA (GENA-) GENAISANCE PHARM INC.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1288
 ID ABA00207 standard; cDNA; 1296 BP.
 DE sc-uPA coding sequence.
 PN EP1232755-A2.
 PD 21-AUG-2002.
 PA (JCRP-) JCR PHARM CO LTD.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1289
 ID ADF28768 standard; cDNA; 1296 BP.
 DE Human urokinase-type plasminogen activator (uPA) encoding cDNA.
 PN WO2003082072-A2.
 PD 09-OCT-2003.
 PA (HARB/) HARBECK N.
 PA (KATE/) KATES R E.
 PA (SCHM/) SCHMITT M.
 PA (FOEK/) FOEKENS J A.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1290
 ID AAN92037 standard; DNA; 1473 BP.
 DE Sequence of variant human prourokinase.
 PN JP01252283-A.
 PD 06-OCT-1989.
 PA (GREC) GREEN CROSS CORP.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1291
 ID AAN50138 standard; DNA; 1474 BP.
 DE Sequence of the signal sequence and noncoding region of the pro-UK
 DE structural gene (Sequence II).
 PN EP154272-A.
 PD 11-SEP-1985.
 PA (GREC) GREEN CROSS CORP.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1292
 ID AAN81558 standard; DNA; 1475 BP.
 DE Pro-UK structural gene, signal sequence and non-coding region.
 PN EP265874-A.
 PD 04-MAY-1988.
 PA (GREC) GREEN CROSS CORP.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1293
 ID AAZ24619 standard; cDNA; 1475 BP.
 DE Human lung tumor associated polynucleotide.
 PN WO9947674-A2.
 PD 23-SEP-1999.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%

Query Match: 6.67%
 RESULT 1294
 ID AAC65858 standard; cDNA; 1475 BP.
 DE Human lung cancer-associated cDNA for contig 10.
 PN WO200061612-A2.
 PD 19-OCT-2000.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1295
 ID ABZ35047 standard; cDNA; 1475 BP.
 DE Human gene expression profile polynucleotide SEQ ID NO 159.
 PN WO200274979-A2.
 PD 26-SEP-2002.
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1296
 ID ABL49077 standard; cDNA; 1475 BP.
 DE Human lung tumour cDNA sequence for contig 10 SEQ ID NO:122.
 PN WO200200174-A2.
 PD 03-JAN-2002.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1297
 ID ABQ92263 standard; cDNA; 1475 BP.
 DE Human lung cancer associated cDNA sequence SEQ ID NO:122.
 PN WO200247534-A2.
 PD 20-JUN-2002.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1298
 ID ADA28212 standard; cDNA; 1475 BP.
 DE Human lung tumour associated cDNA contig 10.
 PN US2003064947-A1.
 PD 03-APR-2003.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1299
 ID ADE53417 standard; cDNA; 1475 BP.
 DE Human lung tumour protein cDNA sequence #119.
 PN US2003119763-A1.
 PD 26-JUN-2003.
 PA (WANG/) WANG T.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1300
 ID ADH36776 standard; cDNA; 1475 BP.
 DE Human lung cancer-related cDNA sequence #119.
 PN WO2003086175-A2.
 PD 23-OCT-2003.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1301
 ID ACC78885 standard; DNA; 1475 BP.
 DE Human urokinase encoding DNA.
 PN WO2003031464-A2.
 PD 17-APR-2003.
 PA (NEOS-) NEOSE TECHNOLOGIES INC.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1302
 ID ABA00207 standard; cDNA; 1296 BP.
 DE sc-uPA coding sequence.
 PN EP1232755-A2.
 PD 21-AUG-2002.
 PA (JCRP-) JCR PHARM CO LTD.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1303
 ID ADF28768 standard; cDNA; 1296 BP.
 DE Human urokinase-type plasminogen activator (uPA) encoding cDNA.
 PN WO2003082072-A2.
 PD 09-OCT-2003.
 PA (HARB/) HARBECK N.
 PA (KATE/) KATES R E.
 PA (SCHM/) SCHMITT M.
 PA (FOEK/) FOEKENS J A.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1304
 ID AAN92037 standard; DNA; 1473 BP.
 DE Sequence of variant human prourokinase.
 PN JP01252283-A.
 PD 06-OCT-1989.
 PA (GREC) GREEN CROSS CORP.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1305
 ID AAN50138 standard; DNA; 1474 BP.
 DE Sequence of the signal sequence and noncoding region of the pro-UK
 DE structural gene (Sequence II).
 PN EP154272-A.
 PD 11-SEP-1985.
 PA (GREC) GREEN CROSS CORP.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1306
 ID AAN81558 standard; DNA; 1475 BP.
 DE Pro-UK structural gene, signal sequence and non-coding region.
 PN EP265874-A.
 PD 04-MAY-1988.
 PA (GREC) GREEN CROSS CORP.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%
 RESULT 1307
 ID AAZ24619 standard; cDNA; 1475 BP.
 DE Human lung tumor associated polynucleotide.
 PN WO9947674-A2.
 PD 23-SEP-1999.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.67%

```
RESULT 1302
ID ADM56579 standard; cDNA; 1475 BP.
DE Human lung tumour cDNA #119.
PN US2003138438-A1.
PD 24-JUL-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 37.17%
Best Local Similarity: 37.17%
Query Match: 37.17%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1303
ID ADM99623 standard; cDNA; 1475 BP.
DE Human lung squamous cell carcinoma cDNA seqid 122.
PN US6660838-B1.
PD 09-DEC-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 37.17%
Best Local Similarity: 37.17%
Query Match: 37.17%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1304
ID ADM49705 standard; DNA; 1475 BP.
DE Human urokinase DNA SeqID 33.
PN WO2004033651-A2.
PD 22-APR-2004.
PA (NEOS-) NEOSE TECHNOLOGIES INC.
Percent Similarity: 37.17%
Best Local Similarity: 37.17%
Query Match: 37.17%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1305
ID AAN91617 standard; DNA; 1500 BP.
DE Sequence of entire prourokinase (PKU) gene from PKU-producing tumour cell
DE line A1CC CCL138 clone pUC20.
PN EP312941-A.
PD 26-APR-1989.
PA (BADI) BASF AG.
Percent Similarity: 37.17%
Best Local Similarity: 37.17%
Query Match: 37.17%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1306
ID AAN91215 standard; cDNA; 1738 BP.
DE cDNA coding sequence of tissue plasminogen activator (t-PA).
PN AU8817430-A.
PD 08-DEC-1988.
PA (NOVO) NOVO IND AS.
PA (ZYMO) ZYMOGENETICS INC.
PA (EISA) EISAI CO LTD.
Percent Similarity: 35.65%
Best Local Similarity: 35.65%
Query Match: 35.65%
Conservative: 74
Mismatch: 185
Indels: 186
RESULT 1307
ID AAH28220 standard; DNA; 1964 BP.
DE Nucleotide sequence of urokinase plasminogen activator.
PN WO200149309-A2.
PD 12-JUL-2001.
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
Percent Similarity: 37.17%
Best Local Similarity: 37.17%
Query Match: 37.17%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1308
ID RAD27855 standard; cDNA; 1964 BP.
DE Human uPA cDNA.
PN WO200196606-A2.
PD 20-DEC-2001.
PA (NYXT-) NYXTIS NEURO THERAPIES INC.
Percent Similarity: 37.17%
Best Local Similarity: 37.17%
Query Match: 37.17%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1309
ID ACN39065 standard; cDNA; 2254 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325332, SEQ ID NO:2968.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 37.17%
Best Local Similarity: 37.17%
Query Match: 37.17%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1310
ID AAZ24620 standard; cDNA; 2281 BP.
DE Human lung tumour associated polynucleotide.
PN WO9947674-A2.
PD 23-SEP-1999.
PA (CORI-) CORIXA CORP.
Percent Similarity: 37.17%
Best Local Similarity: 37.17%
Query Match: 37.17%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1311
ID AAC5859 standard; cDNA; 2294 BP.
DE Human lung cancer-associated cDNA for contig 12.
PN WO200061612-A2.
PD 19-OCT-2000.
PA (CORI-) CORIXA CORP.
Percent Similarity: 37.17%
Best Local Similarity: 37.17%
Query Match: 37.17%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1312
ID ABL49078 standard; cDNA; 2294 BP.
DE Human lung tumour cDNA sequence for contig 12 SEQ ID NO:123.
PN WO200200174-A2.
PD 03-JAN-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 37.17%
Best Local Similarity: 37.17%
Query Match: 37.17%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1313
ID ABQ22264 standard; cDNA; 2294 BP.
DE Human lung cancer associated cDNA sequence SEQ ID NO:123.
PN WO200247534-A2.
PD 20-JUN-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 37.17%
Best Local Similarity: 37.17%
Query Match: 37.17%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1314
ID ADA28213 standard; cDNA; 2294 BP.
DE Human lung tumour associated cDNA contig 12.
PN US2003064947-A1.
PD 03-APR-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 37.17%
Best Local Similarity: 37.17%
Query Match: 37.17%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1315
ID ADE53418 standard; cDNA; 2294 BP.
DE Human lung tumour protein cDNA sequence #120.
PN US2003119763-A1.
PD 26-JUN-2003.
PA (WANG/) WANG T.
Percent Similarity: 37.17%
Best Local Similarity: 37.17%
Query Match: 37.17%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1316
ID ADH36777 standard; cDNA; 2294 BP.
DE Human lung cancer-related cDNA sequence #120.
PN WO2003086175-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 37.17%
Best Local Similarity: 37.17%
Query Match: 37.17%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1317
ID ADK61310 standard; DNA; 2294 BP.
DE Ovarian cancer-related DNA #465 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
```

Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.67% Indels: 154
 RESULT 1318
 ID ADI131891 standard; cDNA; 2294 BP.
 DE Human cDNA #1217.
 PN US6607879-B1.
 PD 19-AUG-2003.
 PA (INCYTE) INCYTE CORP.
 Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.67% Indels: 154
 RESULT 1319
 ID ADM56580 standard; cDNA; 2294 BP.
 DE Human lung tumour cDNA #120.
 PN US2003138438-A1.
 PD 24-JUL-2003.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.67% Indels: 154
 RESULT 1320
 ID ADN89624 standard; cDNA; 2294 BP.
 DE Human lung squamous cell carcinoma cDNA seqid 123.
 PN US660838-B1.
 PD 09-DEC-2003.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.67% Indels: 154
 RESULT 1321
 ID ACN44243 standard; cDNA; 2297 BP.
 DE Human mRNA sequence hCT11616.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.67% Indels: 154
 RESULT 1322
 ID AAN80981 standard; DNA; 2298 BP.
 DE Sequence of the single chain urokinase plasminogen activator (SCU-PA)
 DE cDNA insert prepared from human Hep3 cells.
 PN EP288435-A.
 PD 26-OCT-1988.
 PA (CIBA) CIBA GEIGY AG.
 Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.67% Indels: 154
 RESULT 1323
 ID AAN60703 standard; DNA; 2299 BP.
 DE Sequence encoding human urokinase.
 PN JP61181377-A.
 PD 14-AUG-1986.
 PA (NISC) NISSAN CHEM IND LTD.
 PA (HODO) HODOGAYA CHEM IND CO LTD.
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 PA (CENG) CENTRAL GLASS CO LTD.
 PA (NIPS) NIPPON SODA CO.
 PA (TOYJ) TOYO SODA MFG CO LTD.
 Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.67% Indels: 154
 RESULT 1324
 ID AAN70390 standard; DNA; 2301 BP.
 DE cDNA encoding human prourokinase in plasmid pKU22.
 PN EP231883-A.
 PD 12-AUG-1987.
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 PA (NIPS) NIPPON SODA CO.
 PA (CENG) CENTRAL GLASS CO LTD.
 PA (TOYJ) TOYO SODA MFG CO LTD.
 PA (NISC) NISSAN CHEM IND LTD.

PA (NISC) NISSAN CHEMICAL INDS KK.
 Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.67% Indels: 154
 RESULT 1325
 ID AAN91075 standard; DNA; 2301 BP.
 DE DNA encoding natural human prourokinase and 5' UTR and 3' UTR.
 PN WO8901513-A.
 PD 23-FEB-1989.
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 PA (CENG) CENTRAL GLASS CO LTD.
 PA (HODO) HODOGAYA CHEM KK.
 PA (NIPS) NIPPON SODA CO.
 PA (NISC) NISSAN CHEM IND LTD.
 Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.67% Indels: 154
 RESULT 1326
 ID AAQ73483 standard; cDNA; 2303 BP.
 DE Full length human urokinase protein cDNA.
 PN EP620279-A1.
 PD 19-OCT-1994.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.67% Indels: 154
 RESULT 1327
 ID ABL59543 standard; cDNA; 2304 BP.
 DE Human pro-urokinase (uPA) cDNA SEQ ID NO:43.
 PN WO200227028-A1.
 PD 04-APR-2002.
 PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.
 Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.67% Indels: 154
 RESULT 1328
 ID ABX76437 standard; DNA; 2304 BP.
 DE Lung cancer-associated polynucleotide #301.
 PN WO200286443-A2.
 PD 31-OCT-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.67% Indels: 154
 RESULT 1329
 ID ABX76275 standard; DNA; 2304 BP.
 DE Lung cancer-associated polynucleotide #140.
 PN WO200286443-A2.
 PD 31-OCT-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.67% Indels: 154
 RESULT 1330
 ID ABX17681 standard; DNA; 2304 BP.
 DE DNA encoding Human urokinase plasminogen activator #1.
 PN WO200279515-A1.
 PD 10-OCT-2002.
 PA (ISIS-) ISIS PHARM INC.
 Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.67% Indels: 154
 RESULT 1331
 ID ACF12920 standard; cDNA; 2304 BP.
 DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:183.
 PN WO2002101075-A2.
 PD 19-DEC-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.67% Indels: 154
 RESULT 1332
 ID ADG89387 standard; DNA; 2304 BP.

DE Cancer detection method related gene #50.
PN WO2003078662-A1.
PD 25-SEP-2003.
PA (GENO-) GENOMIC HEALTH INC.
Percent Similarity: 37.17% Conservative: 72
Best Local Similarity: 23.79% Mismatches: 184
Query Match: 6.67% Indels: 154
RESULT 1333
ID ADN39095 standard; cDNA; 2304 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:413.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 37.17% Conservative: 72
Best Local Similarity: 23.79% Mismatches: 184
Query Match: 6.67% Indels: 154
RESULT 1334
ID ADN39740 standard; cDNA; 2304 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C112.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 37.17% Conservative: 72
Best Local Similarity: 23.79% Mismatches: 184
Query Match: 6.67% Indels: 154
RESULT 1335
ID ADN95543 standard; DNA; 2304 BP.
DE Human BRC/LEC-related gene sequence SeqID466.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
Percent Similarity: 37.17% Conservative: 72
Best Local Similarity: 23.79% Mismatches: 184
Query Match: 6.67% Indels: 154
RESULT 1336
ID ADL70594 standard; cDNA; 2304 BP.
DE Cervical cancer marker M58, urokinase, cDNA.
PN WO2004018999-A2.
PD 04-MAR-2004.
PA (MILL-) MILLENIUM PHARM INC.
Percent Similarity: 37.17% Conservative: 72
Best Local Similarity: 23.79% Mismatches: 184
Query Match: 6.67% Indels: 154
RESULT 1337
ID ADP07333 standard; DNA; 2304 BP.
DE Human UPA DNA.
PN DE10255104-A1.
PD 11-MAR-2004.
PA (EPIG-) EPIGENOMICS AG.
Percent Similarity: 37.17% Conservative: 72
Best Local Similarity: 23.79% Mismatches: 184
Query Match: 6.67% Indels: 154
RESULT 1338
ID ADP23870 standard; cDNA; 2304 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:1048.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Percent Similarity: 37.17% Conservative: 72
Best Local Similarity: 23.79% Mismatches: 184
Query Match: 6.67% Indels: 154
RESULT 1339
ID ABZ35347 standard; cDNA; 2336 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 458.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH-) ORTHO CLINICAL DIAGNOSTICS INC.
Percent Similarity: 37.17% Conservative: 72
Best Local Similarity: 23.79% Mismatches: 184
Query Match: 6.67% Indels: 154
RESULT 1340
ID ADB47346 standard; cDNA; 2336 BP.
DE Human cDNA upregulated in dendritic cells SEQ ID NO 46.
PN US2003134283-A1.
PD 17-JUL-2003.
PA (PETE-) PETERSON D P.
PA (PEAR-) PEARSON C I.
PA (COCK-) COCKS B G.
Percent Similarity: 37.17% Conservative: 72
Best Local Similarity: 23.79% Mismatches: 184
Query Match: 6.67% Indels: 154
RESULT 1341
ID ADE54011 standard; cDNA; 2336 BP.
DE Human prostate cancer cDNA #358.
PN US2003190640-A1.
PD 09-OCT-2003.
PA (FARI-) FARIS M.
PA (PEAR-) PEARSON C I.
Percent Similarity: 37.17% Conservative: 72
Best Local Similarity: 23.79% Mismatches: 184
Query Match: 6.67% Indels: 154
RESULT 1342
ID AAQ20360 standard; cDNA; 2377 BP.
DE Human pro-urokinase cDNA.
PN DE4122688-A.
PD 16-JAN-1992.
PA (FARM-) FARMITALIA ERBA SRL CARLO.
Percent Similarity: 37.17% Conservative: 72
Best Local Similarity: 23.79% Mismatches: 184
Query Match: 6.67% Indels: 154
RESULT 1343
ID AAQ04107 standard; cDNA; 2427 BP.
DE Human pro-urokinase cDNA of clone pcUK176.
PN EP365894-A.
PD 02-MAY-1990.
PA (FARM-) FARMITALIA ERBA SPA CARLO.
Percent Similarity: 37.17% Conservative: 72
Best Local Similarity: 23.79% Mismatches: 184
Query Match: 6.67% Indels: 154
RESULT 1344
ID ADQ22641 standard; DNA; 2655 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5461.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 37.17% Conservative: 72
Best Local Similarity: 23.79% Mismatches: 184
Query Match: 6.67% Indels: 154
RESULT 1345
ID ADH41464 standard; DNA; 1368 BP.
DE Novel human nucleic acid NOV3b.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.79% Conservative: 70
Best Local Similarity: 24.65% Mismatches: 178
Query Match: 6.65% Indels: 126
RESULT 1346
ID ADH41488 standard; DNA; 1368 BP.
DE Novel human nucleic acid NOV3n.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.79% Conservative: 70
Best Local Similarity: 24.65% Mismatches: 178
Query Match: 6.65% Indels: 126
RESULT 1347
ID ABQ78854 standard; DNA; 1386 BP.
DE Nucleic acid relating to the invention #1.
PN RU2181147-C2.
PD 10-APR-2002.
PA (CHAR-) CHARIKOVA E V.
Percent Similarity: 34.73% Conservative: 66
Best Local Similarity: 22.14% Mismatches: 151
Query Match: 6.65% Indels: 191

Best Local Similarity:	22.14%	Mismatches:	151
Query Match:	6.65%	Indels:	191
RESULT 1356			
ID AAN50351 standard; cDNA; 1638 BP.			
DE Sequence encoding human factor IX.			
PN W08050376-A.			
PD 05-DEC-1985.			
PA (TRGE) TRANSGENE SA.			
PA (DSAL/) DE LA SALLE H.			
Percent Similarity:	34.73%	Conservative:	66
Best Local Similarity:	22.14%	Mismatches:	151
Query Match:	6.65%	Indels:	191
RESULT 1357			
ID AAN50362 standard; cDNA; 1639 BP.			
DE Sequence encoding human factor IX, called DNA FIX.			
PN W08050125-A.			
PD 21-NOV-1985.			
PA (TRGE) TRANSGENE SA.			
PA (JAYE/) JAYE M.			
Percent Similarity:	34.73%	Conservative:	66
Best Local Similarity:	22.14%	Mismatches:	151
Query Match:	6.65%	Indels:	191
RESULT 1358			
ID AAA54034 standard; DNA; 2775 BP.			
DE Human factor IX coding sequence.			
PN W0200054787-A1.			
PD 21-SEP-2000.			
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.			
PA (UYNC-) UNIV NORTH CAROLINA.			
Percent Similarity:	34.73%	Conservative:	66
Best Local Similarity:	22.14%	Mismatches:	151
Query Match:	6.65%	Indels:	191
RESULT 1359			
ID RAN40142 standard; cDNA; 2781 BP.			
DE Part of the sequence of human factor IX cDNA.			
PN W084000560-A.			
PD 16-FEB-1984.			
PA (NATR) NAT RES DEV CORP.			
PA (BROW/) BROWNLEE G G.			
Percent Similarity:	34.76%	Conservative:	68
Best Local Similarity:	21.55%	Mismatches:	163
Query Match:	6.65%	Indels:	173
RESULT 1360			
ID ABV77053 standard; DNA; 2804 BP.			
DE Nucleotide sequence of human Factor IX.			
PN W0200286091-A2.			
PD 31-OCT-2002.			
PA (REGC) UNIV CALIFORNIA.			
Percent Similarity:	34.73%	Conservative:	66
Best Local Similarity:	22.14%	Mismatches:	151
Query Match:	6.65%	Indels:	191
RESULT 1361			
ID AAN60543 standard; cDNA; 2807 BP.			
DE Factor-IX cDNA.			
PN W08606408-A.			
PD 06-NOV-1986.			
PA (GEMY) GENETICS INST INC.			
PA (KAUF/) KAUFMAN R J.			
Percent Similarity:	34.73%	Conservative:	66
Best Local Similarity:	22.14%	Mismatches:	151
Query Match:	6.65%	Indels:	191
RESULT 1362			
ID ADH42198 standard; DNA; 2807 BP.			
DE Novel human nucleic acid NOV47C.			
PN W02003102159-A2.			
PD 11-DEC-2003.			
PA (CURA-) CURAGEN CORP.			
Percent Similarity:	34.73%	Conservative:	66
Best Local Similarity:	22.14%	Mismatches:	151
Query Match:	6.65%	Indels:	191
RESULT 1363			
ID ABA09219 standard; cDNA; 3421 BP.			
DE Human corin homologue-encoding cDNA, SEQ ID NO:995.			

PN WO200157188-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC. 33.13% Conservative: 103
 Best Local Similarity: 20.68% Mismatches: 266
 Query Match: 6.65% Indels: 287
 RESULT 1364
 ID AAZ29662 standard; cDNA; 4933 BP.
 DE Human serine protease, Corin cDNA.
 PN WO9964608-A1.
 PD 16-DEC-1999.
 PA (SCHD) SCHERING AG. 33.13% Conservative: 103
 Best Local Similarity: 20.68% Mismatches: 266
 Query Match: 6.65% Indels: 287
 RESULT 1365
 ID AAD13164 standard; DNA; 4933 BP.
 DE Human corin DNA.
 PN WO200157194-A2.
 PD 09-AUG-2001.
 PA (CORV-) CORVAS INT INC. 33.13% Conservative: 103
 Best Local Similarity: 20.68% Mismatches: 266
 Query Match: 6.65% Indels: 287
 RESULT 1366
 ID ADI10397 standard; DNA; 4933 BP.
 DE Human cell surface protease coding sequence #15.
 PN WO200295007-A2.
 PD 28-NOV-2002.
 PA (CORV-) CORVAS INT INC. 33.13% Conservative: 103
 Best Local Similarity: 20.68% Mismatches: 266
 Query Match: 6.65% Indels: 287
 RESULT 1367
 ID ADJ46921 standard; cDNA; 4933 BP.
 DE Human transmembrane serine protease (WTSP)-related cDNA #5.
 PN US2004001801-A1.
 PD 01-JAN-2004.
 PA (CORV-) CORVAS INT INC. 33.13% Conservative: 103
 Best Local Similarity: 20.68% Mismatches: 266
 Query Match: 6.65% Indels: 287
 RESULT 1368
 ID ADR29371 standard; DNA; 4933 BP.
 DE Human corin dopaminergic neuronal marker DNA SEQ ID NO:1.
 PN WO2004065599-A1.
 PD 05-AUG-2004.
 PA (EISA) EISAI CO LTD. 33.13% Conservative: 103
 Best Local Similarity: 20.68% Mismatches: 266
 Query Match: 6.65% Indels: 287
 RESULT 1369
 ID ADP21389 standard; DNA; 4942 BP.
 DE Gene PRSC for screening for cardiac therapeutic preparation.
 PN WO2004050894-A2.
 PD 17-JUN-2004.
 PA (ARTE-) ARTESIAN THERAPEUTICS INC. 33.13% Conservative: 103
 Best Local Similarity: 20.68% Mismatches: 266
 Query Match: 6.65% Indels: 287
 RESULT 1370
 ID AAA33835 standard; DNA; 5753 BP.
 DE Vector pTGF36 comprising human clotting factor IX.
 PN WO200049147-A1.
 PD 24-AUG-2000.
 PA (THER-) THERAGENE BIOMEDICAL LAB GMBH. 34.73% Conservative: 66
 Best Local Similarity: 22.14% Mismatches: 151
 Query Match: 6.65% Indels: 191
 RESULT 1371
 ID AAD18173 standard; DNA; 5753 BP.
 DE Human wild-type factor IX protein encoding vector pTGF36hyg.
 PN WO200170968-A2.

PD 27-SEP-2001.
 PA (OCTA-) OCTAGENE GMBH. 34.73% Conservative: 66
 Best Local Similarity: 22.14% Mismatches: 151
 Query Match: 6.65% Indels: 191
 RESULT 1372
 ID AA53846 standard; DNA; 5905 BP.
 DE Vector pTGF53 comprising human clotting factor IX.
 PN WO200049147-A1.
 PD 24-AUG-2000.
 PA (THER-) THERAGENE BIOMEDICAL LAB GMBH. 34.73% Conservative: 66
 Best Local Similarity: 22.14% Mismatches: 151
 Query Match: 6.65% Indels: 191
 RESULT 1373
 ID AAA53847 standard; DNA; 6052 BP.
 DE Vector pTGF64 comprising human clotting factor IX.
 PN WO200049147-A1.
 PD 24-AUG-2000.
 PA (THER-) THERAGENE BIOMEDICAL LAB GMBH. 34.73% Conservative: 66
 Best Local Similarity: 22.14% Mismatches: 151
 Query Match: 6.65% Indels: 191
 RESULT 1374
 ID AAH77500 standard; DNA; 13928 BP.
 DE Haemophilia B genetic therapy related oligonucleotide #3.
 PN CN1302864-A.
 PD 11-JUL-2001.
 PA (XIAJ/) XIA J. 34.76% Conservative: 68
 Best Local Similarity: 21.55% Mismatches: 163
 Query Match: 6.65% Indels: 173
 RESULT 1375
 ID AAN93079 standard; DNA; 2266 BP.
 DE Sequence encoding prourokinase.
 PN EP299706-A.
 PD 18-JAN-1989.
 PA (COLB) COLLABORATIVE RES INC. 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.64% Indels: 154
 RESULT 1376
 ID AAQ06133 standard; DNA; 1236 BP.
 DE Sequence encoding human pro-urokinase variant.
 PN EP398382-A.
 PD 22-NOV-1990.
 PA (GREC) GREEN CROSS CORP. 37.30% Conservative: 70
 Best Local Similarity: 23.63% Mismatches: 174
 Query Match: 6.63% Indels: 147
 RESULT 1377
 ID AAT61671 standard; cDNA; 1236 BP.
 DE Human native prourokinase cDNA.
 PN EP398361-A.
 PD 22-NOV-1990.
 PA (GREC) GREEN CROSS CORP. 37.11% Conservative: 69
 Best Local Similarity: 23.63% Mismatches: 175
 Query Match: 6.63% Indels: 147
 RESULT 1378
 ID AAQ40317 standard; cDNA; 1736 BP.
 DE Sequence encoding human pre-pro tissue plasminogen activator (t-PA).
 PN US5200340-A.
 PD 06-APR-1993.
 PA (ZYNO) ZYMOGENETICS INC. 35.01% Conservative: 76
 Best Local Similarity: 21.84% Mismatches: 185
 Query Match: 6.63% Indels: 192
 RESULT 1379
 ID AAX28626 standard; DNA; 2792 BP.
 DE Nucleotide sequence of human factor IX-R338A.
 PN WO9903496-A1.
 PD 28-JAN-1999.

PA (UVNC-) UNIV NORTH CAROLINA.
 PA (STAF/) STAFFORD D W.
 PA (CHAF/) CHANG J L.
 Percent Similarity: 34.73% Conservative: 66
 Best Local Similarity: 22.14% Mismatches: 151
 Query Match: 6.63% Indels: 191
 RESULT 1380
 ID AAN70356 standard; cDNA to mRNA; 1475 BP.
 DE Human urine-derived high molecular weight type urokinase A and B-chain
 DE pre-structural gene.
 PN EP232544-A.
 PD 19-AUG-1987.
 PA (GREG) GREEN CROSS CORP.
 Percent Similarity: 39.08% Conservative: 77
 Best Local Similarity: 24.43% Mismatches: 189
 Query Match: 6.62% Indels: 132
 RESULT 1381
 ID AB235272 standard; cDNA; 2344 BP.
 DE Human gene expression profile polynucleotide SEQ ID NO 383.
 PN WO200274979-A2.
 PD 26-SEP-2002.
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 Percent Similarity: 37.17% Conservative: 72
 Best Local Similarity: 23.79% Mismatches: 184
 Query Match: 6.62% Indels: 154
 RESULT 1382
 ID AAQ06134 standard; DNA; 1236 BP.
 DE Sequence encoding human pro-urokinase variant.
 PN EP398362-A.
 PD 22-NOV-1990.
 PA (GREG) GREEN CROSS CORP.
 Percent Similarity: 37.11% Conservative: 69
 Best Local Similarity: 23.63% Mismatches: 175
 Query Match: 6.60% Indels: 147
 RESULT 1383
 ID ABN99361 standard; DNA; 2387 BP.
 DE Human secreted protein (SCBP) coding sequence 2.
 PN WO200226982-A2.
 PD 04-APR-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 34.38% Conservative: 47
 Best Local Similarity: 23.82% Mismatches: 133
 Query Match: 6.60% Indels: 159
 RESULT 1384
 ID AAQ10577 standard; DNA; 1465 BP.
 DE Coding sequence for human factor IX, contained in plasmid pHEX1.
 PN US4994371-A.
 PD 19-FEB-1991.
 PA (DAVI/) DAVIE E W.
 Percent Similarity: 34.73% Conservative: 64
 Best Local Similarity: 22.52% Mismatches: 152
 Query Match: 6.59% Indels: 190
 RESULT 1385
 ID AAN50141 standard; cDNA; 1475 BP.
 DE Sequence encoding pro-urokinase (sequence IV).
 PN EP154272-A.
 PD 11-SEP-1985.
 PA (GREG) GREEN CROSS CORP.
 Percent Similarity: 36.99% Conservative: 71
 Best Local Similarity: 23.79% Mismatches: 185
 Query Match: 6.59% Indels: 154
 RESULT 1386
 ID AD843392 standard; cDNA; 2304 BP.
 DE Human uPA cDNA, SEQ ID 561.
 PN WO2003054143-A2.
 PD 03-JUL-2003.
 PA (NEUR-) NEUROGENETICS INC.
 Percent Similarity: 37.74% Conservative: 67
 Best Local Similarity: 25.09% Mismatches: 192
 Query Match: 6.59% Indels: 138
 RESULT 1387
 ID ADH54434 standard; cDNA; 2304 BP.

DE Human uPA gene cDNA sequence SeqID561.
 PN US2003224380-A1.
 PD 04-DEC-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 Percent Similarity: 37.74% Conservative: 67
 Best Local Similarity: 25.09% Mismatches: 192
 Query Match: 6.59% Indels: 138
 RESULT 1388
 ID ACN43224 standard; cDNA; 4633 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2099.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Percent Similarity: 35.02% Conservative: 87
 Best Local Similarity: 23.44% Mismatches: 266
 Query Match: 6.59% Indels: 224
 RESULT 1389
 ID AAQ10169 standard; DNA; 1236 BP.
 DE Encodes Pro-urokinase derivative UK-T4 with Ser(153) and Thr(155).
 PN EP405285-A.
 PD 02-JAN-1991.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Percent Similarity: 37.11% Conservative: 65
 Best Local Similarity: 24.41% Mismatches: 175
 Query Match: 6.58% Indels: 147
 RESULT 1390
 ID ADH41472 standard; DNA; 1479 BP.
 DE Novel human nucleic acid NOV3f.
 PN WO2003102159-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.79% Conservative: 71
 Best Local Similarity: 24.44% Mismatches: 178
 Query Match: 6.58% Indels: 126
 RESULT 1391
 ID AAN71330 standard; DNA; 2304 BP.
 DE Sequence encoding modified prourokinase.
 PN EP236040-A.
 PD 09-SEP-1987.
 PA (COLB) COLLABORATIVE RES INC.
 Percent Similarity: 37.15% Conservative: 71
 Best Local Similarity: 23.83% Mismatches: 181
 Query Match: 6.57% Indels: 154
 RESULT 1392
 ID ADQ38774 standard; DNA; 2359 BP.
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 437.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Percent Similarity: 37.43% Conservative: 66
 Best Local Similarity: 24.95% Mismatches: 195
 Query Match: 6.57% Indels: 136
 RESULT 1393
 ID ADQ38775 standard; DNA; 2375 BP.
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 438.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Percent Similarity: 37.43% Conservative: 66
 Best Local Similarity: 24.95% Mismatches: 195
 Query Match: 6.57% Indels: 136
 RESULT 1394
 ID AB211297 standard; cDNA; 2505 BP.
 DE Human polynucleotide SEQ ID NO 179.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 33.25% Conservative: 102
 Best Local Similarity: 20.87% Mismatches: 252
 Query Match: 6.57% Indels: 301
 RESULT 1395
 ID ADH43615 standard; cDNA; 2505 BP.
 DE Novel human arginine-rich protein cDNA #179.

PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG//) TANG Y T.
PA (XUEA//) XUE A.
PA (DRMA//) DRMANAC R T.
Percent Similarity: 33.25%
Best Local Similarity: 20.87%
Query Match: 6.57%
Conservative: 102
Mismatch: 252
Indels: 301
RESULT 1396
ID AAD27077 standard; DNA; 1236 BP.
DE Human urokinase-type plasminogen activator tcuPA and scuPA DNA.
PN WO200197752-A2.
PD 27-DEC-2001.
PA (UYPE-) UNIV PENNSYLVANIA.
Percent Similarity: 37.11%
Best Local Similarity: 23.44%
Query Match: 6.55%
Conservative: 70
Mismatch: 175
Indels: 147
RESULT 1397
ID ADE85976 standard; cDNA; 1236 BP.
DE Human single chain urokinase plasminogen activator coding sequence.
PN WO2003086278-A2.
PD 23-OCT-2003.
PA (TEXA) UNIV TEXAS SYSTEM.
Percent Similarity: 38.10%
Best Local Similarity: 25.00%
Query Match: 6.55%
Conservative: 66
Mismatch: 181
Indels: 131
RESULT 1398
ID ADI31601 standard; cDNA; 1236 BP.
DE Human cDNA #927.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Percent Similarity: 38.10%
Best Local Similarity: 25.00%
Query Match: 6.55%
Conservative: 66
Mismatch: 181
Indels: 131
RESULT 1399
ID AAQ10224 standard; DNA; 1455 BP.
DE Encodes human prourokinase derivative APUK (k,k).
PN WO9015867-A.
PD 27-DEC-1990.
PA (NIPS) NIPPON SODA CO.
Percent Similarity: 38.10%
Best Local Similarity: 25.00%
Query Match: 6.53%
Conservative: 66
Mismatch: 181
Indels: 131
RESULT 1400
ID AAQ81549 standard; cDNA; 1548 BP.
DE Factor-IX cDNA.
PN WO9505201-A1.
PD 23-FEB-1995.
PA (GENE-) GENETIC THERAPY INC.
Percent Similarity: 34.54%
Best Local Similarity: 22.14%
Query Match: 6.55%
Conservative: 65
Mismatch: 152
Indels: 191
RESULT 1401
ID ABL28971 standard; DNA; 3736 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38386.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 44.91%
Best Local Similarity: 26.32%
Query Match: 6.55%
Conservative: 53
Mismatch: 118
Indels: 39
RESULT 1402
ID AAQ10282 standard; DNA; 1316 BP.
DE Structural gene encoding single-chain urine plasminogen activator.
PN EP408945-A.
PD 23-JAN-1991.
PA (CHEF) GRUENENTHAL GMBH.
Percent Similarity: 38.46%
Best Local Similarity: 25.19%
Query Match: 6.54%
Conservative: 69
Mismatch: 183
Indels: 137
RESULT 1403
ID AAQ10168 standard; DNA; 1236 BP.
DE Encodes Pro-urokinase derivative UK-T6 with Thr at position 155.
PN EP405285-A.
PD 02-JAN-1991.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Percent Similarity: 36.91%
Best Local Similarity: 24.41%
Query Match: 6.53%
Conservative: 64
Mismatch: 176
Indels: 147
RESULT 1404
ID AAQ41450 standard; DNA; 1236 BP.
DE Mutant human prourokinase gene.
PN EP541952-A1.
PD 19-MAY-1993.
PA (GREC) GREEN CROSS CORP.
Percent Similarity: 37.70%
Best Local Similarity: 24.80%
Query Match: 6.53%
Conservative: 65
Mismatch: 183
Indels: 131
RESULT 1405
ID AAQ48228 standard; DNA; 1236 BP.
DE PUK gene.
PN JP05192142-A.
PD 03-AUG-1993.
PA (GREC) GREEN CROSS CORP.
Percent Similarity: 37.70%
Best Local Similarity: 24.80%
Query Match: 6.53%
Conservative: 65
Mismatch: 183
Indels: 131
RESULT 1406
ID AAQ10225 standard; DNA; 1455 BP.
DE Encodes human prourokinase derivative APUK (k,q).
PN WO9015867-A.
PD 27-DEC-1990.
PA (NIPS) NIPPON SODA CO.
Percent Similarity: 38.10%
Best Local Similarity: 25.00%
Query Match: 6.53%
Conservative: 66
Mismatch: 181
Indels: 131
RESULT 1407
ID AAN60591 standard; DNA; 2301 BP.
DE Sequence encoding modified human pro-urokinase clone.
PN WO8604351-A.
PD 31-JUL-1986.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (MIYA) MIYAKE T.
PA (HODO) HODOGAYA-CHEM CO LTD.
PA (NIPS) NIPPON SODA CO.
PA (TOXJ) TOYO SODA MFG CO LTD.
PA (NISC) NISSAN CHEM IND LTD.
PA (NIPC) NIPPON CHEM IND CO LTD.
PA (NISC) NISSAN CHEM IND LTD.
PA (TOXJ) TOYO SODA MFG CO LTD.
PA (NIPS) NIPPON SODA CO.
Percent Similarity: 37.31%
Best Local Similarity: 24.81%
Query Match: 6.51%
Conservative: 66
Mismatch: 197
Indels: 134
RESULT 1408
ID AAA61734 standard; cDNA; 834 BP.
DE cDNA encoding mouse serine protease BSSPS (mBSSPS) SEQ ID NO:3.
PN WO200031243-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Percent Similarity: 40.85%
Best Local Similarity: 27.45%
Query Match: 6.50%
Conservative: 41
Mismatch: 116
Indels: 65
RESULT 1409
ID AAT80075 standard; cDNA; 1335 BP.
DE Inhibitor resistant urokinase gene.
PN US5648253-A.
PD 15-JUL-1997.
PA (TSIT-) TSI CORP.
Percent Similarity: 37.11%
Best Local Similarity: 23.44%
Query Match: 6.50%
Conservative: 70
Mismatch: 175
Indels: 147
RESULT 1410
ID AAN50477 standard; cDNA; 1386 BP.
DE Sequence encoding human pre-pro-urokinase in pULB 1000.

PN BE900826-A.
 PA (UNIO) UCB SA.
 Percent Similarity: 36.93%
 Best Local Similarity: 24.81%
 Query Match: 6.49%
 RESULT 1411
 ID ACN411794 standard; cDNA; 2113 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:669.
 PN WO2004023973-A2.
 PA (INCY-) INCYTE CORP.
 Percent Similarity: 37.75%
 Best Local Similarity: 24.11%
 Query Match: 6.49%
 RESULT 1412
 ID AAT61457 standard; DNA; 3546 BP.
 DE C-proteinase clone PCP-2.
 PN WO9706242-A1.
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 Percent Similarity: 30.25%
 Best Local Similarity: 21.85%
 Query Match: 6.49%
 RESULT 1413
 ID AA288362 standard; cDNA; 1296 BP.
 DE Human pro-uroporokinas CT92 nucleotide sequence.
 PN WO200000624-A1.
 PA (CROP-) CROPTTECH DEV CORP.
 Percent Similarity: 37.17%
 Best Local Similarity: 23.79%
 Query Match: 6.46%
 RESULT 1414
 ID AAN70447 standard; cDNA; 2310 BP.
 DE Sequence of human tissue plasminogen activator (t-PA) cDNA clone.
 PN EP236209-A.
 PA (GENE-) GENETICA.
 Percent Similarity: 35.46%
 Best Local Similarity: 22.70%
 Query Match: 6.46%
 RESULT 1415
 ID ADQ18557 standard; DNA; 3546 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1376.
 PN WO2004048938-A2.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 35.98%
 Best Local Similarity: 26.27%
 Query Match: 6.46%
 RESULT 1416
 ID ABZ34743 standard; cDNA; 3552 BP.
 DE Coding sequence SEQ ID 101, downregulated in osteogenesis.
 PN WO200281745-A2.
 PA (AVET) AVENTIS PHARMA SA.
 Percent Similarity: 35.98%
 Best Local Similarity: 26.27%
 Query Match: 6.46%
 RESULT 1417
 ID ABL92109 standard; cDNA; 3557 BP.
 DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 241.
 PN WO200210217-A2.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Percent Similarity: 35.98%
 Best Local Similarity: 26.27%
 Query Match: 6.46%
 RESULT 1418
 ID ABX72034 standard; DNA; 3557 BP.
 DE DNA encoding human tumour endothelial marker TEM 25.
 PN WO200283874-A2.

PD 24-OCT-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Percent Similarity: 35.98%
 Best Local Similarity: 26.27%
 Query Match: 6.46%
 RESULT 1419
 ID ADQ23028 standard; DNA; 3889 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5848.
 PN WO2004048938-A2.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 35.98%
 Best Local Similarity: 26.27%
 Query Match: 6.46%
 RESULT 1420
 ID AAQ06135 standard; DNA; 1236 BP.
 DE Sequence encoding human pro-uroporokinas variant.
 PN EP398362-A.
 PA (GREG) GREEN CROSS CORP.
 Percent Similarity: 36.91%
 Best Local Similarity: 23.44%
 Query Match: 6.45%
 RESULT 1421
 ID AAQ04485 standard; DNA; 1236 BP.
 DE Plasmid pSRIUKS11d encoding UK-S1.
 PN EP370205-A.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Percent Similarity: 37.60%
 Best Local Similarity: 23.80%
 Query Match: 6.45%
 RESULT 1422
 ID AAQ10223 standard; DNA; 1467 BP.
 DE Encodes human prouroporokinas derivative AHUK (q,q).
 PN WO9015867-A.
 PA (NIPS) NIPPON SODA CO.
 Percent Similarity: 38.10%
 Best Local Similarity: 24.80%
 Query Match: 6.45%
 RESULT 1423
 ID ADA50521 standard; DNA; 714 BP.
 DE Human protease gene SEQ ID NO:25.
 PN WO2003040393-A2.
 PA (DECO-) DECODE GENETICS EHF.
 Percent Similarity: 44.98%
 Best Local Similarity: 29.00%
 Query Match: 6.44%
 RESULT 1424
 ID ADB58493 standard; DNA; 2045 BP.
 DE Toxicity-related gene, SEQ ID 3519.
 PN WO2003064624-A2.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 33.83%
 Best Local Similarity: 21.28%
 Query Match: 6.44%
 RESULT 1425
 ID ADB53088 standard; DNA; 2045 BP.
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3630.
 PN WO2003065993-A2.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 33.83%
 Best Local Similarity: 21.28%
 Query Match: 6.44%
 RESULT 1426
 ID AAQ05535 standard; DNA; 2249 BP.
 DE Plasmid plgn delta GFTPA encoding novel mutant tissue plasminogen activator (tPA).
 PN EP379890-A.

PD 01-AUG-1990.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 Percent Similarity: 37.31%
 Best Local Similarity: 24.23%
 Query Match: 6.44%
 RESULT 1427
 ID ADR44281 standard; DNA; 3405 BP.
 DE Mosquito C-type lectin (CTL) gene sequence SEQ ID NO:27.
 PD 01-SEP-2004.
 PA (EMBL-) EMBL.
 Percent Similarity: 32.17%
 Best Local Similarity: 20.87%
 Query Match: 6.44%
 RESULT 1428
 ID AAQ04486 standard; DNA; 1236 BP.
 DE Plasmid pUKS3 encoding UK-S3.
 PD EP370205-A.
 PD 30-MAY-1990.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Percent Similarity: 36.91%
 Best Local Similarity: 24.22%
 Query Match: 6.43%
 RESULT 1429
 ID AAQ32850 standard; cDNA; 2487 BP.
 DE BMP1.
 PD WO9221365-A1.
 PD 10-DEC-1992.
 PA (PROC) PROCTER & GAMBLE CO.
 Percent Similarity: 37.79%
 Best Local Similarity: 25.90%
 Query Match: 6.43%
 RESULT 1430
 ID ABR83959 standard; cDNA; 2487 BP.
 DE Human cDNA differentially expressed in granulocytic cells #530.
 PD WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 37.79%
 Best Local Similarity: 25.90%
 Query Match: 6.43%
 RESULT 1431
 ID ADP65508 standard; DNA; 2487 BP.
 DE Human bone morphogenetic protein 1 (BMP-1) mRNA DNA.
 PD WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Percent Similarity: 37.79%
 Best Local Similarity: 25.90%
 Query Match: 6.43%
 RESULT 1432
 ID ADP65019 standard; DNA; 2487 BP.
 DE Human bone morphogenetic protein 1 (BMP1), transcript DNA sequence.
 PD WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Percent Similarity: 37.79%
 Best Local Similarity: 25.90%
 Query Match: 6.43%
 RESULT 1433
 ID ADH11557 standard; cDNA; 2487 BP.
 DE Human bone morphogenetic protein (BMP) polynucleotide #6.
 PD US2003224501-A1.
 PD 04-DEC-2003.
 PA (YOUNG/) YOUNG P E.
 PA (RUBE/) RUBEN S M.
 Percent Similarity: 37.79%
 Best Local Similarity: 25.90%
 Query Match: 6.43%
 RESULT 1434
 ID ACN38772 standard; cDNA; 2487 BP.
 DE Tumour-associated antigenic target (TAT) cDNA DNA83022, SEQ ID NO:2495.
 PD WO2004030615-A2.

PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 37.79%
 Best Local Similarity: 25.90%
 Query Match: 6.43%
 RESULT 1435
 ID AAN80631 standard; DNA; 2500 BP.
 DE Human Bone Morphogenic Protein-1 cDNA in lambda U2OS-1.
 PD WO8800205-A.
 PD 14-JAN-1988.
 PA (GEMY) GENETICS INST INC.
 Percent Similarity: 37.79%
 Best Local Similarity: 25.90%
 Query Match: 6.43%
 RESULT 1436
 ID AAN82184 standard; DNA; 1575 BP.
 DE Modified tissue plasminogen activator lacking the G region and with G-183 DE and S-186 substd for S and T resp.
 PD JP632330084-A.
 PD 26-SEP-1988.
 PA (EISA) EISAI CO LTD.
 Percent Similarity: 37.21%
 Best Local Similarity: 23.85%
 Query Match: 6.41%
 RESULT 1437
 ID AAN81089 standard; DNA; 1680 BP.
 DE Tissue plasminogen activator analogue coding sequence.
 PD EP293934-A.
 PD 07-DEC-1988.
 PA (ZYMO) ZYMOGENETICS INC.
 PA (NOVO) NOVO IND AS.
 PA (EISA) EISA CO LTD.
 Percent Similarity: 38.46%
 Best Local Similarity: 24.18%
 Query Match: 6.41%
 RESULT 1438
 ID ACN42707 standard; cDNA; 1710 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1582.
 PD WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Percent Similarity: 41.81%
 Best Local Similarity: 26.76%
 Query Match: 6.41%
 RESULT 1439
 ID AAQ05534 standard; DNA; 2099 BP.
 DE Plasmid pLGTQTPA encoding novel mutant tissue plasminogen activator (tPA).
 PD EP379890-A.
 PD 01-AUG-1990.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 Percent Similarity: 37.59%
 Best Local Similarity: 24.29%
 Query Match: 6.41%
 RESULT 1440
 ID ABL04087 standard; cDNA; 4140 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 6743.
 PD WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 38.58%
 Best Local Similarity: 23.60%
 Query Match: 6.41%
 RESULT 1441
 ID ACF05073 standard; cDNA; 948 BP.
 DE Bovine recombinant prethrombin-2 nucleotide sequence.
 PD WO2003052059-A2.
 PD 26-JUN-2003.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 44.65%
 Best Local Similarity: 28.78%
 Query Match: 6.40%
 RESULT 1442

ID ACP05076 standard; cDNA; 956 BP.
 DE Bovine recombinant prethrombin-2 nucleotide sequence.
 PN WO2003052059-A2.
 PD 26-JUN-2003.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 44.65%
 Best Local Similarity: 28.78%
 Query Match: 6.40%
 RESULT 1443
 ID ACP05075 standard; cDNA; 1098 BP.
 DE Bovine recombinant prethrombin-2 nucleotide sequence.
 PN WO2003052059-A2.
 PD 26-JUN-2003.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 44.65%
 Best Local Similarity: 28.78%
 Query Match: 6.40%
 RESULT 1444
 ID AAN91133 standard; DNA; 1419 BP.
 DE Sequence of coding region in plasmid pmTQk112.
 PN EP302456-A.
 PD 08-FEB-1989.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 Percent Similarity: 35.91%
 Best Local Similarity: 22.98%
 Query Match: 6.40%
 RESULT 1445
 ID AAS00146 standard; cDNA; 2487 BP.
 DE Human cDNA clone HTPFG82 encoding IgSF protein #2.
 PN WO200118176-A1.
 PD 15-MAR-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 34.94%
 Best Local Similarity: 22.89%
 Query Match: 6.40%
 RESULT 1446
 ID AAN82185 standard; DNA; 1575 BP.
 DE Modified tissue plasminogen activator lacking F and G region and with S-DE 119 substd for M.
 PN JP63230084-A.
 PD 26-SEP-1988.
 PA (EISA) EISAI CO LTD.
 Percent Similarity: 36.92%
 Best Local Similarity: 24.42%
 Query Match: 6.39%
 RESULT 1447
 ID ADO09841 standard; cDNA; 10662 BP.
 DE Human NOV2b cDNA.
 PN US2004018970-A1.
 PD 29-JAN-2004.
 PA (SHIM/) SHIMKETS R A.
 PA (PATT/) PATTURAJAN M.
 PA (VERN/) VERNET C A M.
 PA (CASM/) CASMAN S J.
 PA (NALLY/) MALYANKAR U M.
 PA (SHEN/) SHENOY S G.
 PA (SPYT/) SPYTEK K A.
 PA (GANG/) GANGOLLI E A.
 PA (MILL/) MILLER C E.
 PA (BOLD/) BOLDOG F L.
 PA (LILL/) LI L.
 PA (TAUP/) TAUPIER R J.
 PA (KEKU/) KEKUDA R.
 PA (SMIT/) SMITHSON G.
 PA (ZERH/) ZERHUSEN B D.
 PA (LIUX/) LIU X.
 PA (COLM/) COLMAN S D.
 PA (TCHE/) TCHERNEV V T.
 PA (SIJG/) SI J.
 PA (EDIN/) EDINGER S R.
 PA (STON/) STONE D J.
 PA (SCIO/) SCORE P.

PA (MILL/) MILLET I.
 PA (ROTH/) ROTHENBERG M E.
 Percent Similarity: 33.48%
 Best Local Similarity: 21.42%
 Query Match: 6.39%
 RESULT 1448
 ID ACN38775 standard; cDNA; 2463 BP.
 DE Tumour-associated antigenic target (TAT) cDNA DNA325072, SEQ ID NO:2501.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 39.09%
 Best Local Similarity: 27.66%
 Query Match: 6.38%
 RESULT 1449
 ID ABK31781 standard; DNA; 3387 BP.
 DE DNA encoding novel human protease #38.
 PN WO200200860-A2.
 PD 03-JAN-2002.
 PA (SUGS-) SUGEN INC.
 Percent Similarity: 34.03%
 Best Local Similarity: 23.73%
 Query Match: 6.38%
 RESULT 1450
 ID ABK86141 standard; cDNA; 3711 BP.
 DE cDNA encoding human protease PRPS8.
 PN WO200238744-A2.
 PD 16-MAY-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 34.03%
 Best Local Similarity: 23.73%
 Query Match: 6.38%
 RESULT 1451
 ID AAO04962 standard; cDNA; 1506 BP.
 DE Sequence encoding glycosylated plasminogen activator.
 PN JP02049586-A.
 PD 19-FEB-1990.
 PA (KANF) KANEGAFUCHI CHEM KK.
 Percent Similarity: 35.82%
 Best Local Similarity: 22.87%
 Query Match: 6.36%
 RESULT 1452
 ID ADI30831 standard; cDNA; 2152 BP.
 DE Human cDNA #157.
 PN US6607879-B1.
 PD 19-AUG-2003.
 PA (INCY-) INCYTE CORP.
 Percent Similarity: 36.47%
 Best Local Similarity: 24.62%
 Query Match: 6.36%
 RESULT 1453
 ID AAZ88364 standard; cDNA; 1239 BP.
 DE Human prourokinase CT97 nucleotide sequence.
 PN WO200000624-A1.
 PD 06-JAN-2000.
 PA (CROP-) CROPTTECH DEV CORP.
 Percent Similarity: 37.11%
 Best Local Similarity: 23.44%
 Query Match: 6.35%
 RESULT 1454
 ID AAZ88363 standard; cDNA; 1305 BP.
 DE Patatin signal peptide and prourokinase CT111 nucleotide sequence.
 PN WO200000624-A1.
 PD 06-JAN-2000.
 PA (CROP-) CROPTTECH DEV CORP.
 Percent Similarity: 37.11%
 Best Local Similarity: 23.44%
 Query Match: 6.35%
 RESULT 1455
 ID AAN81069 standard; DNA; 1437 BP.
 DE Mutant no. 2600: tissue plasminogen activator homologue with finger and DE growth factor domain deletions.
 PN EP292009-A.

Percent Similarity: 32.20% Conservative: 101
 Best Local Similarity: 19.50% Mismatches: 278
 Query Match: 6.32% Indels: 261
 RESULT 1472
 ID AAD13115 standard; cDNA; 708 BP.
 DE Human membrane-type serine protease (MTSP) 4 cDNA.
 PN WO200157194-A2.
 PD 09-AUG-2001.
 PA (CORV-) CORVAS INT INC.
 Percent Similarity: 44.94% Conservative: 43
 Best Local Similarity: 28.84% Mismatches: 105
 Query Match: 6.31% Indels: 42
 RESULT 1473
 ID AD110374 standard; DNA; 708 BP.
 DE Human cell surface protease coding sequence #3.
 PN WO200295007-A2.
 PD 28-NOV-2002.
 PA (CORV-) CORVAS INT INC.
 Percent Similarity: 44.94% Conservative: 43
 Best Local Similarity: 28.84% Mismatches: 105
 Query Match: 6.31% Indels: 42
 RESULT 1474
 ID ADJ46898 standard; cDNA; 708 BP.
 DE Human transmembrane serine protease (MTSP) cDNA #3.
 PN US2004001801-A1.
 PD 01-JAN-2004.
 PA (CORV-) CORVAS INT INC.
 Percent Similarity: 44.94% Conservative: 43
 Best Local Similarity: 28.84% Mismatches: 105
 Query Match: 6.31% Indels: 42
 RESULT 1475
 ID ABK31780 standard; DNA; 792 BP.
 DE DNA encoding novel human protease #37.
 PN WO200200860-A2.
 PD 03-JAN-2002.
 PA (SUGE-) SUGEN INC.
 Percent Similarity: 44.79% Conservative: 47
 Best Local Similarity: 26.64% Mismatches: 95
 Query Match: 6.31% Indels: 48
 RESULT 1476
 ID ADJ95175 standard; DNA; 1869 BP.
 DE Novel NOVX gene sequence #202.
 PN WO2003040325-A2.
 PD 15-MAY-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 33.38% Conservative: 96
 Best Local Similarity: 20.30% Mismatches: 264
 Query Match: 6.31% Indels: 226
 RESULT 1477
 ID ADK51027 standard; DNA; 1869 BP.
 DE Human NOV11B gene sequence SeqID47.
 PN WO2003083046-A2.
 PD 09-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 33.38% Conservative: 96
 Best Local Similarity: 20.30% Mismatches: 264
 Query Match: 6.31% Indels: 226
 RESULT 1478
 ID ADK51031 standard; DNA; 1869 BP.
 DE Human NOV11D gene sequence SeqID51.
 PN WO2003083046-A2.
 PD 09-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 33.38% Conservative: 96
 Best Local Similarity: 20.30% Mismatches: 264
 Query Match: 6.31% Indels: 226
 RESULT 1479
 ID ADL56819 standard; cDNA; 2037 BP.
 DE Human NOVX cDNA #3.
 PN US2003215449-A1.
 PD 20-NOV-2003.
 PA (MEZE-) MEZES P D.
 PA (RAST-) RASTELLI L.

PA (HERR-) HERRMANN J L.
 PA (MACD-) MACDOUGALL J R.
 PA (ZHON-) ZHONG H.
 PA (CASM-) CASMAN S J.
 PA (BOLD-) BOLDOG F L.
 PA (SHIM-) SHIMKETS R A.
 PA (GORM-) GORMAN L.
 PA (EISE-) EISEN A J.
 PA (VERN-) SPADERNA S K.
 PA (BERG-) BERGHS C.
 PA (SPYT-) SPYTEK K A.
 PA (DIPP-) DIPPO V A.
 PA (ZERH-) ZERHUSEN B D.
 PA (PEYM-) PEYMAN J A.
 PA (ELLE-) ELLERMAN K.
 PA (STON-) STONE D J.
 PA (GROS-) GROSSE W M.
 PA (ALSO-) ALSOBROOK J P.
 PA (LEPL-) LEPLEY D M.
 PA (RIEG-) RIEGER D K.
 PA (BURG-) BURGESS C E.
 PA (EDIN-) EDINGER S R.
 PA (VOSS-) VOSS E Z.
 PA (MILL-) MILLER C E.
 Percent Similarity: 33.06% Conservative: 95
 Best Local Similarity: 20.19% Mismatches: 261
 Query Match: 6.31% Indels: 234
 RESULT 1480
 ID ASS59536 standard; cDNA; 2038 BP.
 DE Human cDNA, homologous to Kallikrein, designated NOV3.
 PN WO200255705-A2.
 PD 18-JUL-2002.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 33.06% Conservative: 95
 Best Local Similarity: 20.19% Mismatches: 261
 Query Match: 6.31% Indels: 234
 RESULT 1481
 ID ADJ95173 standard; DNA; 2038 BP.
 DE Novel NOVX gene sequence #201.
 PN WO2003040325-A2.
 PD 15-MAY-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 33.06% Conservative: 95
 Best Local Similarity: 20.19% Mismatches: 261
 Query Match: 6.31% Indels: 234
 RESULT 1482
 ID ADK51025 standard; DNA; 2038 BP.
 DE Human NOV11A gene sequence SeqID45.
 PN WO2003083046-A2.
 PD 09-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 33.06% Conservative: 95
 Best Local Similarity: 20.19% Mismatches: 261
 Query Match: 6.31% Indels: 234
 RESULT 1483
 ID ADO39203 standard; cDNA; 2038 BP.
 DE Human cDNA encoding novel protein NOV3.
 PN US2004018196-A1.
 PD 29-JAN-2004.
 PA (MEZE-) MEZES P D.
 PA (RAST-) RASTELLI L.
 PA (HERR-) HERRMANN J L.
 PA (MACD-) MACDOUGALL J R.
 PA (ZHON-) ZHONG H.
 PA (CASM-) CASMAN S J.
 PA (BOLD-) BOLDOG F L.
 PA (SHIM-) SHIMKETS R A.
 PA (GORM-) GORMAN L.
 PA (EISE-) EISEN A J.
 PA (SPAD-) SPADERNA S K.
 PA (VERN-) VERNET C A M.
 PA (BERG-) BERGHS C.

Query Match: 6.30% Indels: 142
RESULT 1498
ID AAN91117 standard; DNA; 1314 BP.
DE Sequence of coding region in plasmid pTQ1PA delta trp.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI) FUJISAWA PHARM CO LTD.
Percent Similarity: 37.32% Conservative: 64
Best Local Similarity: 23.90% Mismatches: 159
Query Match: 6.30% Indels: 142
RESULT 1499
ID AAN91127 standard; DNA; 1314 BP.
DE Sequence of coding region in plasmid pSTQ1trp.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI) FUJISAWA PHARM CO LTD.
Percent Similarity: 37.32% Conservative: 64
Best Local Similarity: 23.90% Mismatches: 159
Query Match: 6.30% Indels: 142
RESULT 1500
ID AAN91126 standard; DNA; 1314 BP.
DE Sequence of coding region in plasmid pSTQktrp.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI) FUJISAWA PHARM CO LTD.
Percent Similarity: 37.32% Conservative: 64
Best Local Similarity: 23.90% Mismatches: 159
Query Match: 6.30% Indels: 142

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 9, 2005, 20:40:48 ; Search time 5938 Seconds
(without alignments)
4615.405 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 3945

Sequence: 1 MELGCWTQLTFLQLLLIS.....LSTATKVLVLPKDWIERNMK 720

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cpn2.1/USPTO.spool/US10063692/runat_09052005.122254.4841/app_query.fasta_1.903
-DB=EST -QFMT=fstatap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcr -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10063692 @CEN 1 1 4352 @runat_09052005.122254.4841 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3936	99.8	3165	3	HSN806734
2	3813	96.7	2850	3	AF370388
3	3612	91.6	2746	3	AK088017
4	3489.5	88.5	2214	9	AY406074
5	3211.5	81.4	2214	9	AY406076
6	2480.5	62.9	2214	9	AY406075
7	1766	44.8	2184	3	AK031254
8	1578.5	40.0	1049	5	BX399905
9	1527	38.7	952	5	BX439313

10	1492	37.8	886	5	BX337781
11	1440	36.5	1158	4	BM461342
12	1436	36.4	879	6	CD514783
13	1341	34.0	795	6	CD655367
14	1258	31.9	718	7	CF125161
15	1226	31.1	785	7	CO397557
16	1156.5	29.3	742	5	BX350293
17	1150	29.2	697	2	BB620582
18	1128	28.6	711	7	CO733882
19	1107	28.1	630	4	BM724013
20	1104	28.0	693	7	CO880461
21	1100	27.9	773	4	BG403264
22	1097.5	27.8	715	1	AL048495
23	1086	27.5	660	7	CK359441
24	1081.5	27.4	711	5	BU253929
25	1077	27.3	830	7	CK474785
26	1065	27.0	626	5	BP381335
27	1058	26.8	635	2	BB632336
28	1055	26.7	584	5	BP205877
29	1005	25.5	595	4	BI346571
30	1004.5	25.5	891	6	CB204666
31	991.5	25.1	846	7	CO387203
32	990	25.1	566	5	BP289572
33	948	24.0	774	1	AU067539
34	940	23.8	500	6	CB712029
35	924	23.4	832	5	BP464936
36	917	23.2	593	2	AW918019
37	915	23.2	547	2	BE231795
38	909	23.0	546	4	BM254217
39	908	23.0	938	5	BU383403
40	904	22.9	557	4	BM106593
41	882	22.4	590	7	CK622160
42	877	22.2	660	6	BY745962
43	860	21.8	664	7	CN059249
44	859	21.8	476	5	BP282717
45	853	21.6	633	2	AW957662
46	843.5	21.4	1100	5	BX337780
47	834	21.1	492	7	CN296855
48	812	20.6	452	2	BE048236
49	803	20.4	520	4	BI346989
50	801	20.3	520	2	BE653376
51	794	20.1	687	4	BI526460
52	791	20.1	1008	5	BX399904
53	789	20.0	468	2	AM484384
54	786	19.9	519	2	BE683792
55	784	19.9	482	5	BX515589
56	776	19.7	584	5	BP312143
57	774	19.6	463	1	AA444868
58	772	19.6	483	4	BM088773
59	752	19.1	521	2	BE910833
60	735	18.6	428	1	BF197805
61	722	18.3	458	1	AI549757
62	710	18.0	583	5	BP216550
63	704	17.8	456	7	CO260289
64	704	17.8	594	7	CN061039
65	688	17.4	814	5	BU206384
66	686	17.4	422	2	AW323842
67	685	17.4	348	7	CN334668
68	675	17.1	570	1	AI536361
69	669	17.0	489	5	BY243636
70	662	16.8	897	5	BX434191
71	653.5	16.6	662	5	BU218794
72	650	16.5	419	4	BM484683
73	642	16.3	385	6	CD707019
74	634.5	16.1	382	5	BY275139
75	632	16.0	482	5	BY243643
76	621	15.7	378	4	BM090462
77	612	15.5	410	5	AX731559
78	599	15.2	435	6	CB793309
79	594.5	15.1	494	2	BE374037
80	594	15.1	378	2	AM426139
81	586	14.9	465	5	BY244862
82	576	14.6	907	5	BU358450

BX337781	BX337781
BM461342	AGENCOURT
CD514783	AGENCOURT
CD655367	AGENCOURT
CF125161	UI-HF-EL0
CO397557	AGENCOURT
BX350293	BX350293
BB620582	BB620582
CO733882	SILH03C07
BM724013	UI-E-BO1-
CO880461	BovGen.08
BG403264	602419419
AL048495	DXFZ8586L
CK359441	4100177 B
BU253929	603747035
CK474785	AGENCOURT
BP381335	BP381335
BB632336	BB632336
BP205877	BP205877
BI346571	375792 MA
CB204666	AGENCOURT
CO387203	AGENCOURT
BP289572	BP289572
AU067539	AU067539
CB712029	AMGNNUC:N
BP464936	BP464936
AW918019	EST349323
BE231795	136621 MA
BM254217	515580 MA
BU383403	60382549
BM106593	510508 MA
CK622160	m101D03.Y
BY745962	BY745962
CN059249	Salamande
BP282717	BP282717
AW957662	EST369732
BX337780	BX337780
CN296855	170004250
BE048236	tz48G03.Y
BI346989	376376 MA
BE653376	UI-M-AL1-
BI526460	60295024
BX399904	BX399904
AM484384	60496 MAR
BE683792	183732 MA
BX515589	BX515589
BP312143	BP312143
AA444868	va75f07.Y
BM088773	502333 MA
BE910833	601661905
BF197805	7P92F09.X
AI549757	va75f07.Y
BP216550	BP216550
CO260289	4131981 B
CN061039	AG20_P42-
BU206384	603951279
AW323842	u077D04.Y
CN334668	170005999
AI536361	ma97e11.Y
BY243636	BY243636
BX434191	BX434191
BU218794	603105534
BM484683	538615 MA
CD707019	EST23546
BY275139	BY275139
BY243643	BY243643
BM090462	505887 MA
AX731559	DXFZ8586L
CB793309	AMGNNUC:N
BE374037	601228074
AM426139	59708 MAR
BY244862	BY244862
BU358450	603477265

83	573	14.5	371	5	BY131558	BY131558	BY131558	156	312	7.9	3035	3	AK004939	Mus muscu
84	568	14.4	421	5	BY295210	BY295210	BY295210	157	309.5	7.8	1531	3	CR653493	Tetraodon
85	565.5	14.3	395	2	AW416537	AW416537	AW416537	158	306.5	7.8	1586	3	CR606412	full-leng
86	560	14.2	959	1	AU051031	AU051031	AU051031	159	302.5	7.7	1857	3	AK089402	Mus muscu
87	559	14.2	808	5	BU359706	BU359706	BU359706	160	301	7.6	3683	3	AK033582	Mus muscu
88	554	14.0	411	7	CU296856	CU296856	CU296856	161	300	7.6	621	4	BI387043	BFL26_001
89	553	14.0	416	6	CB768218	CB768218	CB768218	162	300	7.6	642	9	AG144714	Pan trogl
90	551	14.0	343	2	AW307893	AW307893	AW307893	163	298.5	7.6	1717	3	CR653983	Tetraodon
91	546	13.8	338	1	AA375185	AA375185	AA375185	164	298	7.6	1723	3	CR634742	Tetraodon
92	539	13.7	425	5	BY266233	BY266233	BY266233	165	297.5	7.5	2511	3	AK038356	Mus muscu
93	528.5	13.4	752	5	BM879710	BM879710	BM879710	C 166	296	7.5	722	5	BU742056	UI-E-BOL-
94	528	13.4	310	7	CU222781	CU222781	CU222781	167	292	7.4	163	7	BY035258	BY035258
95	525	13.3	416	5	BY238364	BY238364	BY238364	168	291	7.4	380	5	BY035258	BY035258
96	520	13.2	427	5	BY273129	BY273129	BY273129	169	289.5	7.3	2498	5	CR623908	full-leng
97	515	13.1	791	5	BU316123	BU316123	BU316123	C 170	289	7.3	722	5	BQ014522	UI-H-ED1-
98	510	12.9	348	7	RA74049	RA74049	RA74049	171	287	7.3	1618	3	CR725571	Tetraodon
99	510	12.9	756	7	CU334669	CU334669	CU334669	172	286	7.2	2076	3	CR652267	Tetraodon
100	508	12.9	404	5	BY271161	BY271161	BY271161	173	285.5	7.2	1679	3	CR637804	Tetraodon
101	501	12.7	851	7	CO394970	CO394970	CO394970	174	285	7.2	185	2	BF366351	IL2-NT009
102	493	12.5	643	8	BZ245624	BZ245624	BZ245624	C 175	285	7.2	1237	6	CD497665	CD497665
103	479	12.1	414	5	BY282746	BY282746	BY282746	176	285	7.2	1584	3	CR648830	Tetraodon
104	476.5	12.1	749	4	BM105355	BM105355	BM105355	177	284.5	7.2	807	4	BI834499	Tetraodon
105	476	12.1	482	4	BM105355	BM105355	BM105355	178	284	7.2	1438	3	CR639903	Tetraodon
106	475.5	12.1	427	5	BY265763	BY265763	BY265763	179	284	7.2	1538	3	CR634681	Tetraodon
107	471	11.9	410	5	BY287911	BY287911	BY287911	180	284	7.2	1559	3	CR634333	Tetraodon
108	471	11.9	714	7	CF525168	CF525168	CF525168	181	282.5	7.2	1706	3	CR634000	Tetraodon
109	470	11.9	386	2	BF451877	BF451877	BF451877	182	282.5	7.2	1707	3	CR639050	Tetraodon
110	470	11.9	504	1	AA199196	AA199196	AA199196	183	282	7.1	1966	3	CR638621	Tetraodon
C 111	466	11.8	817	7	CK775452	CK775452	CK775452	184	281.5	7.1	1056	5	BM919200	AGENCOURT
112	463.5	11.7	333	7	TS2085	TS2085	TS2085	185	280.5	7.1	795	5	AY414006	Homo sapi
113	460	11.7	381	7	CR772910	CR772910	CR772910	186	279.5	7.1	921	4	BI833975	full-leng
114	459.5	11.6	369	1	AA833210	AA833210	AA833210	187	278	7.0	1434	3	CR623031	full-leng
115	459	11.6	378	3	AK031598	AK031598	AK031598	188	278	7.0	1467	3	CR607773	full-leng
116	453	11.5	425	5	BY295062	BY295062	BY295062	189	276	7.0	264	2	BB585844	BB585844
117	447	11.3	423	5	BY259943	BY259943	BY259943	C 190	276	7.0	1066	8	CC229783	CC229783
118	435	11.0	262	2	AW431829	AW431829	AW431829	191	275.5	7.0	674	5	BU488601	BU488601
119	433	11.0	410	2	BF920134	BF920134	BF920134	192	275.5	7.0	746	5	BU540841	BU540841
120	432	11.0	297	2	AW483167	AW483167	AW483167	C 193	275.5	7.0	850	6	CD508999	CD493-H10
121	427	10.8	258	1	AL701986	AL701986	AL701986	C 194	275.5	7.0	855	6	CD507437	CD507437
122	421	10.7	358	5	BY128083	BY128083	BY128083	C 195	275.5	7.0	857	6	CD508602	CD508602
123	417	10.6	359	6	BY783505	BY783505	BY783505	C 196	275.5	7.0	859	6	CD496923	CD496923
124	417	10.6	2751	3	AK050052	AK050052	AK050052	C 197	275.5	7.0	860	6	CD504920	CD504920
125	416.5	10.6	757	5	BX884986	BX884986	BX884986	198	275.5	7.0	890	6	CD504919	CD504919
126	413	10.5	633	5	BY252479	BY252479	BY252479	199	275.5	7.0	890	6	CD508998	CD508998
127	408	10.3	357	5	BY339892	BY339892	BY339892	200	275.5	7.0	894	5	BU487901	BU487901
128	408	10.3	359	5	BY341239	BY341239	BY341239	201	275.5	7.0	1421	3	CR633905	CR633905
129	403.5	10.2	4266	3	CR749540	CR749540	CR749540	202	274	6.9	1429	3	CR732608	Tetraodon
130	392.5	9.9	445	5	BY289536	BY289536	BY289536	C 203	273.5	6.9	882	6	CB561012	AGENCOURT
131	392	9.9	327	2	AW353000	AW353000	AW353000	C 204	273.5	6.9	896	6	CD499146	CD499146
132	389	9.9	611	5	BU477941	BU477941	BU477941	C 205	273.5	6.9	1116	6	CD509741	CD509741
133	385	9.8	325	2	AG957673	AG957673	AG957673	C 206	273.5	6.9	1130	6	CD499724	CD499724
C 134	382	9.7	731	9	AW511653	AW511653	AW511653	C 207	273.5	6.9	1164	6	CD504975	CD504975
135	377	9.6	389	4	BM876043	BM876043	BM876043	C 208	273.5	6.9	1181	6	CD502179	CD502179
136	377	9.6	409	5	BY264071	BY264071	BY264071	C 209	273.5	6.9	1201	6	CD495483	CD495483
137	369	9.4	2876	3	AK087522	AK087522	AK087522	C 210	273.5	6.9	1212	6	CD498397	CD498397
C 138	367.5	9.3	569	7	CO631899	CO631899	CO631899	C 211	273.5	6.9	1215	6	CD504505	CD504505
139	365	9.3	399	1	AJ696577	AJ696577	AJ696577	C 212	273.5	6.9	1232	6	CD503870	CD503870
140	358	9.1	2386	3	BC046065	BC046065	BC046065	213	273.5	6.9	1409	3	CR608439	CR608439
C 141	357	9.0	539	9	CG991118	CG991118	CG991118	214	273.5	6.9	2686	3	CR749503	Homo sapi
C 142	352.5	8.9	776	9	CC530365	CC530365	CC530365	215	273	6.9	778	5	BX083127	BX083127
143	352	8.9	352	5	BY310228	BY310228	BY310228	216	273	6.9	797	5	BX081500	BX081500
144	350	8.9	373	1	AA126930	AA126930	AA126930	217	273	6.9	805	4	BJ714778	BJ714778
145	349.5	8.9	688	8	AZ794032	AZ794032	AZ794032	218	273	6.9	1571	7	CF110615	Shultzeomi
C 146	349	8.8	740	5	BQ009840	BQ009840	BQ009840	219	272.5	6.9	878	6	CD508601	CD508601
147	343	8.7	702	5	BW282919	BW282919	BW282919	220	271.5	6.9	925	3	CR636671	Tetraodon
148	337	8.5	188	5	BQ694586	BQ694586	BQ694586	221	271	6.9	838	7	CNI156901	CNI156901
149	333	8.4	506	1	AA266124	AA266124	AA266124	222	271	6.9	1423	3	CR654263	CR654263
150	327	8.3	382	3	AK081081	AK081081	AK081081	223	270	6.8	1201	3	CR639571	Tetraodon
C 151	323	8.2	723	5	BQ014545	BQ014545	BQ014545	224	270	6.8	1967	3	CR730923	CR730923
152	320	8.1	507	1	AA043793	AA043793	AA043793	225	269.5	6.8	840	7	CO528471	CO528471
153	318.5	8.1	3248	3	BC008514	BC008514	BC008514	226	269.5	6.8	968	3	CR651513	Tetraodon
154	318.5	8.1	4017	3	AK052738	AK052738	AK052738	227	269.5	6.8	1136	3	CR642844	Tetraodon
155	318	8.1	241	5	BU788909	BU788909	BU788909	228	269.5	6.8	2044	3	CR647409	Tetraodon

229	268.5	6.8	952	3	CR648349	Tetraodon	CR648349	Tetraodon	302	265.5	6.7	963	3	CR635040	Tetraodon
230	268.5	6.8	958	3	CR643383	Tetraodon	CR643383	Tetraodon	303	265.5	6.7	963	3	CR653362	Tetraodon
c 231	268.5	6.8	966	6	CD498092	CD431-F04	CD498092	CD431-F04	304	265.5	6.7	963	3	CR654376	Tetraodon
232	268.5	6.8	968	3	CR645716	Tetraodon	CR645716	Tetraodon	305	265.5	6.7	963	3	CR655625	Tetraodon
233	268.5	6.8	991	6	CD498091	CD431-F04	CD498091	CD431-F04	306	265.5	6.7	964	3	CR635805	Tetraodon
234	268.5	6.8	1024	6	CD506086	CD477-C09	CD506086	CD477-C09	307	265.5	6.7	964	3	CR652426	Tetraodon
235	268.5	6.8	1075	3	CR637860	Tetraodon	CR637860	Tetraodon	308	265.5	6.7	965	3	CR636493	Tetraodon
c 236	268.5	6.8	891	6	CD499332	CD438-H02	CD499332	CD438-H02	309	265.5	6.7	965	3	CR642503	Tetraodon
c 237	268.5	6.8	924	7	CK409299	AUF_IfLvr	CK409299	AUF_IfLvr	310	265.5	6.7	965	3	CR642503	Tetraodon
238	267.5	6.8	981	3	CR645650	Tetraodon	CR645650	Tetraodon	311	265.5	6.7	965	3	CR645376	Tetraodon
239	267.5	6.8	944	5	BM919892	AGENCOURT	BM919892	AGENCOURT	312	265.5	6.7	966	3	CR642902	Tetraodon
240	266.5	6.8	870	3	CR656477	Tetraodon	CR656477	Tetraodon	313	265.5	6.7	966	3	CR646996	Tetraodon
241	266.5	6.8	974	3	CR641480	Tetraodon	CR641480	Tetraodon	314	265.5	6.7	967	3	CR642781	Tetraodon
242	266.5	6.8	1741	3	BU488413	60412747	BU488413	60412747	315	265.5	6.7	967	3	CR648557	Tetraodon
243	266.5	6.7	749	3	CR636630	Tetraodon	CR636630	Tetraodon	316	265.5	6.7	967	3	CR653274	Tetraodon
244	266.5	6.7	801	7	CR636630	Tetraodon	CR636630	Tetraodon	317	265.5	6.7	968	3	CR655912	Tetraodon
245	265.5	6.7	843	3	CR638127	Tetraodon	CR638127	Tetraodon	318	265.5	6.7	968	3	CR655105	Tetraodon
246	265.5	6.7	906	3	CR656092	Tetraodon	CR656092	Tetraodon	319	265.5	6.7	971	3	CR638949	Tetraodon
247	265.5	6.7	907	3	CR640949	Tetraodon	CR640949	Tetraodon	320	265.5	6.7	971	3	CR639592	Tetraodon
248	265.5	6.7	915	3	CR641090	Tetraodon	CR641090	Tetraodon	321	265.5	6.7	971	3	CR643673	Tetraodon
249	265.5	6.7	919	3	CR644534	Tetraodon	CR644534	Tetraodon	322	265.5	6.7	971	3	CR643965	Tetraodon
250	265.5	6.7	919	3	CR647695	Tetraodon	CR647695	Tetraodon	323	265.5	6.7	971	3	CR653075	Tetraodon
251	265.5	6.7	920	3	CR646003	Tetraodon	CR646003	Tetraodon	324	265.5	6.7	972	3	CR649003	Tetraodon
252	265.5	6.7	924	3	CR649278	Tetraodon	CR649278	Tetraodon	325	265.5	6.7	973	3	CR634877	Tetraodon
253	265.5	6.7	927	3	CR649904	Tetraodon	CR649904	Tetraodon	326	265.5	6.7	973	3	CR642156	Tetraodon
254	265.5	6.7	929	3	CR641687	Tetraodon	CR641687	Tetraodon	327	265.5	6.7	974	3	CR654336	Tetraodon
255	265.5	6.7	932	3	CR644830	Tetraodon	CR644830	Tetraodon	328	265.5	6.7	975	3	CR651274	Tetraodon
256	265.5	6.7	938	3	CR646496	Tetraodon	CR646496	Tetraodon	329	265.5	6.7	975	3	CR656121	Tetraodon
257	265.5	6.7	938	3	CR655652	Tetraodon	CR655652	Tetraodon	330	265.5	6.7	976	3	CR637198	Tetraodon
258	265.5	6.7	939	3	CR653581	Tetraodon	CR653581	Tetraodon	331	265.5	6.7	977	3	CR642541	Tetraodon
259	265.5	6.7	941	3	CR638500	Tetraodon	CR638500	Tetraodon	332	265.5	6.7	977	3	CR648403	Tetraodon
260	265.5	6.7	943	3	CR645523	Tetraodon	CR645523	Tetraodon	333	265.5	6.7	978	3	CR735011	Tetraodon
261	265.5	6.7	943	3	CR649221	Tetraodon	CR649221	Tetraodon	334	265.5	6.7	981	3	CR646070	Tetraodon
262	265.5	6.7	943	3	CR646188	Tetraodon	CR646188	Tetraodon	335	265.5	6.7	1039	3	CR644082	Tetraodon
263	265.5	6.7	944	3	CR637521	Tetraodon	CR637521	Tetraodon	336	265.5	6.7	1197	3	CR640066	Tetraodon
264	265.5	6.7	945	3	CR643027	Tetraodon	CR643027	Tetraodon	337	265.5	6.7	1201	3	CR645235	Tetraodon
265	265.5	6.7	945	3	CR648151	Tetraodon	CR648151	Tetraodon	338	265.5	6.7	1209	3	CR729660	Tetraodon
266	265.5	6.7	948	3	CR633117	Tetraodon	CR633117	Tetraodon	339	265.5	6.7	1217	3	CR652649	Tetraodon
267	265.5	6.7	949	3	CR655908	Tetraodon	CR655908	Tetraodon	340	265.5	6.7	1390	3	CR649867	Tetraodon
268	265.5	6.7	950	3	CR643289	Tetraodon	CR643289	Tetraodon	341	265.5	6.7	1399	3	CR727544	Tetraodon
269	265.5	6.7	952	3	CR636594	Tetraodon	CR636594	Tetraodon	342	265.5	6.7	1988	3	CR592485	full-length
270	265.5	6.7	953	3	CR637521	Tetraodon	CR637521	Tetraodon	343	265.5	6.7	774	5	BX083148	BX083148
271	265.5	6.7	953	3	CR637531	Tetraodon	CR637531	Tetraodon	344	265.5	6.7	779	5	BX078970	BX078970
272	265.5	6.7	953	3	CR639263	Tetraodon	CR639263	Tetraodon	345	265.5	6.7	850	5	BX078970	BX078970
273	265.5	6.7	953	3	CR647021	Tetraodon	CR647021	Tetraodon	346	265.5	6.7	854	6	CR565651	AGENCOURT
274	265.5	6.7	953	3	CR653165	Tetraodon	CR653165	Tetraodon	c 347	265.5	6.7	854	6	CR565651	AGENCOURT
275	265.5	6.7	954	3	CR635344	Tetraodon	CR635344	Tetraodon	c 348	265.5	6.7	1106	3	CR645231	Tetraodon
276	265.5	6.7	954	3	CR655952	Tetraodon	CR655952	Tetraodon	349	264.5	6.7	774	7	CV488433	AGENCOURT
277	265.5	6.7	955	3	CR635542	Tetraodon	CR635542	Tetraodon	350	264.5	6.7	877	7	CV406791	AUF_IfLvr
278	265.5	6.7	955	3	CR644574	Tetraodon	CR644574	Tetraodon	351	264.5	6.7	959	3	CR637196	Tetraodon
279	265.5	6.7	956	3	CR635540	Tetraodon	CR635540	Tetraodon	352	264.5	6.7	964	3	CR655278	Tetraodon
280	265.5	6.7	956	3	CR637602	Tetraodon	CR637602	Tetraodon	353	264.5	6.7	966	3	CR645072	Tetraodon
281	265.5	6.7	957	3	CR635227	Tetraodon	CR635227	Tetraodon	354	264.5	6.7	2073	3	AK007987	MUS MUSCU
282	265.5	6.7	957	3	CR640159	Tetraodon	CR640159	Tetraodon	355	263.5	6.7	798	5	BX074786	BX074786
283	265.5	6.7	957	3	CR646990	Tetraodon	CR646990	Tetraodon	356	263.5	6.7	832	7	KN180066	AGENCOURT
284	265.5	6.7	958	3	CR638822	Tetraodon	CR638822	Tetraodon	357	263.5	6.7	881	7	CK409600	AUF_IfLvr
285	265.5	6.7	958	3	CR639620	Tetraodon	CR639620	Tetraodon	358	263.5	6.7	894	7	CK402317	AUF_IfLvr
286	265.5	6.7	958	3	CR653201	Tetraodon	CR653201	Tetraodon	359	263.5	6.7	925	7	CK406767	Tetraodon
287	265.5	6.7	959	3	CR637270	Tetraodon	CR637270	Tetraodon	360	263.5	6.7	939	3	CR638380	Tetraodon
288	265.5	6.7	959	3	CR643681	Tetraodon	CR643681	Tetraodon	361	263.5	6.7	942	3	CD363253	AGENCOURT
289	265.5	6.7	959	3	CR650507	Tetraodon	CR650507	Tetraodon	362	263.5	6.7	967	6	CD363253	AGENCOURT
290	265.5	6.7	959	3	CR651405	Tetraodon	CR651405	Tetraodon	363	263.5	6.7	1450	3	CR603372	full-length
291	265.5	6.7	959	3	CR651712	Tetraodon	CR651712	Tetraodon	364	263.5	6.7	1502	3	CR649600	Tetraodon
292	265.5	6.7	959	3	CR652069	Tetraodon	CR652069	Tetraodon	c 365	263	6.7	760	7	CV484847	AGENCOURT
293	265.5	6.7	960	3	CR635690	Tetraodon	CR635690	Tetraodon	c 366	263	6.7	850	7	CF284554	AGENCOURT
294	265.5	6.7	960	3	CR643347	Tetraodon	CR643347	Tetraodon	367	263	6.7	963	7	KN17696	AGENCOURT
295	265.5	6.7	960	3	CR653969	Tetraodon	CR653969	Tetraodon	368	262.5	6.7	957	3	CR635563	Tetraodon
296	265.5	6.7	961	3	CR636815	Tetraodon	CR636815	Tetraodon	369	262.5	6.7	1018	6	CD507436	CD485-A11
297	265.5	6.7	961	3	CR654102	Tetraodon	CR654102	Tetraodon	370	262.5	6.7	1476	6	CR644996	Tetraodon
298	265.5	6.7	962	3	CR635908	Tetraodon	CR635908	Tetraodon	c 371	262	6.6	570	9	CR841478	GR0AA75D
299	265.5	6.7	962	3	CR636196	Tetraodon	CR636196	Tetraodon	372	261.5	6.6	853	7	CK407561	AUF_IfLvr
300	265.5	6.7	962	3	CR637964	Tetraodon	CR637964	Tetraodon	373	261.5	6.6	853	7	CO960318	AGENCOURT
301	265.5	6.7	962	3	CR641763	Tetraodon	CR641763	Tetraodon	374	261.5	6.6	855	5	BQ733682	AGENCOURT

375	261.5	6.6	954	3	CR633957	CR633957 Tetraodon	448	255	6.5	860	3	CR644603	CR644603 Tetraodon
376	261.5	6.6	959	3	CR645823	CR645823 Tetraodon	449	255	6.5	863	3	CR654851	CR654851 Tetraodon
377	261.5	6.6	965	3	CR718326	CR718326 Tetraodon	450	255	6.5	864	3	CR642012	CR642012 Tetraodon
378	261.5	6.6	1051	4	BM547198	BM547198 AGENCOURT	451	255	6.5	864	3	CR655196	CR655196 Tetraodon
379	261.5	6.6	1138	3	CR636401	CR636401 Tetraodon	452	255	6.5	874	3	CR655656	CR655656 Tetraodon
380	261.5	6.6	1567	3	CR645935	CR645935 Tetraodon	453	255	6.5	877	3	CR653848	CR653848 Tetraodon
381	260.5	6.6	795	9	AY414007	Pan trogl	c 454	255	6.5	886	7	CF375630	CF375630 AGENCOURT
382	260.5	6.6	815	4	BJ714978	BJ714978	455	255	6.5	928	7	CR864509	CR864509 AGENCOURT
383	260.5	6.6	820	5	BM081126	BM081126	456	255	6.5	977	3	CR720946	CR720946 Tetraodon
384	260.5	6.6	822	5	BM079673	BM079673	457	255	6.5	1046	3	CR633733	CR633733 Tetraodon
385	260.5	6.6	926	3	CR643380	CR643380 Tetraodon	458	255	6.5	1086	6	CD499351	CD499351 CDA38-H02
386	260.5	6.6	957	3	CR639412	CR639412 Tetraodon	459	255	6.5	1114	3	CR647072	CR647072 Tetraodon
387	260.5	6.6	974	3	CR650791	CR650791 Tetraodon	460	255	6.5	1126	3	CR637589	CR637589 Tetraodon
388	260.5	6.6	1188	3	CR727891	CR727891 Tetraodon	461	255	6.5	1200	3	CR640466	CR640466 Tetraodon
c 389	260	6.6	676	7	CV491738	CV491738 AGENCOURT	462	254.5	6.5	807	7	CV484837	CV484837 AGENCOURT
390	260	6.6	771	5	BM073544	BM073544	463	254.5	6.5	971	3	CR636724	CR636724 Tetraodon
391	260	6.6	787	5	BM073699	BM073699	464	254.5	6.5	1085	5	BM919045	BM919045 AGENCOURT
392	260	6.6	829	7	CO250114	AGENCOURT	465	254.5	6.5	1210	3	CR647865	CR647865 Tetraodon
393	259.5	6.6	768	5	BM077913	BM077913	466	254.5	6.5	1519	3	CR641286	CR641286 Tetraodon
394	259.5	6.6	782	7	CF347656	AGENCOURT	467	254	6.4	506	8	AQ150311	AQ150311 HS 3178_B
395	259.5	6.6	786	5	BM072919	BM072919	468	254	6.4	738	5	BM083513	BM083513 BX083513
396	259.5	6.6	848	7	CO915858	AGENCOURT	469	254	6.4	763	5	BM083864	BM083864 BX083864
397	259.5	6.6	882	3	CR650843	CR650843 Tetraodon	470	254	6.4	794	5	BU487543	BU487543 604126191
398	259.5	6.6	2041	3	CR598482	full-leng	471	254	6.4	817	5	BM076781	BM076781 BX076781
399	259	6.6	645	4	BJ498457	BJ498457	472	254	6.4	860	3	CF225589	CF225589 AGENCOURT
400	259	6.6	822	5	BM081087	BM081087	473	254	6.4	878	7	CF225589	CF225589 AGENCOURT
401	259	6.6	844	5	BM078668	BM078668	474	254	6.4	995	3	CR644564	CR644564 Tetraodon
402	259	6.6	1223	3	AK014645	Mus muscu	475	254	6.4	1065	3	CR651738	CR651738 Tetraodon
403	259	6.6	1869	3	CR633979	CR633979 Tetraodon	476	253.5	6.4	749	5	BU486703	BU486703 604127811
404	258.5	6.6	812	7	CV491817	AGENCOURT	477	253.5	6.4	797	5	BU076220	BU076220 BX076220
c 405	258	6.5	717	7	CV491804	AGENCOURT	478	253.5	6.4	801	5	BU417196	BU417196 603671644
406	258	6.5	752	5	BM077057	BM077057	479	253.5	6.4	809	5	BU417370	BU417370 603671273
407	258	6.5	770	7	CF998216	AGENCOURT	480	253.5	6.4	853	5	BU487073	BU487073 604126372
408	258	6.5	788	5	BM077756	BM077756	c 481	253.5	6.4	917	7	CF582693	CF582693 AGENCOURT
409	258	6.5	793	5	BU488539	604124870	482	253.5	6.4	922	3	CR652681	CR652681 Tetraodon
410	258	6.5	818	5	BM076890	BM076890	483	253.5	6.4	1152	3	CR658453	CR658453 Tetraodon
411	258	6.5	824	7	CN322770	AGENCOURT	484	253	6.4	1152	3	BU416681	BU416681 603671141
412	258	6.5	876	3	CR635090	Tetraodon	485	253	6.4	782	4	BJ715033	BJ715033 BX715033
413	258	6.5	1477	3	CR643003	Tetraodon	486	253	6.4	866	3	CR642780	CR642780 Tetraodon
414	257.5	6.5	830	5	BM075027	BM075027	487	253	6.4	883	3	CR654193	CR654193 Tetraodon
415	257.5	6.5	848	7	CO959111	AGENCOURT	488	253	6.4	998	3	CR643074	CR643074 Tetraodon
416	257.5	6.5	954	3	CR642576	Tetraodon	489	253	6.4	5901	9	AY407075	AY407075 Mus muscu
c 417	257.5	6.5	1106	6	CD509145	CDA94-G02	490	252.5	6.4	693	5	BM189458	BM189458 BW189458
418	257.5	6.5	1136	3	CR645632	Tetraodon	491	252.5	6.4	805	5	BU417083	BU417083 603671453
419	257.5	6.5	1218	3	CR644124	Tetraodon	492	252.5	6.4	892	3	CR643850	CR643850 Tetraodon
420	257	6.5	767	6	CA350208	620902_NC	493	252.5	6.4	901	3	CR645646	CR645646 Tetraodon
421	257	6.5	782	7	CK026016	AGENCOURT	494	252.5	6.4	904	3	CR640189	CR640189 Tetraodon
422	257	6.5	823	5	BM074929	BM074929	495	252.5	6.4	904	3	CR642568	CR642568 Tetraodon
423	256.5	6.5	795	9	AY414008	Mus muscu	496	252.5	6.4	905	3	CR639582	CR639582 Tetraodon
424	256.5	6.5	868	3	AK009019	Mus muscu	497	252.5	6.4	906	3	CR637481	CR637481 Tetraodon
425	256.5	6.5	2742	3	BC044626	Homo sapi	498	252.5	6.4	909	3	CR655333	CR655333 Tetraodon
426	256	6.5	716	5	BM074928	BM074928	499	252.5	6.4	909	3	CR655881	CR655881 Tetraodon
427	256	6.5	723	5	BM073538	BM073538	500	252.5	6.4	911	3	CR644035	CR644035 Tetraodon
428	256	6.5	727	5	BM078251	BM078251	501	252.5	6.4	911	3	CR645585	CR645585 Tetraodon
429	256	6.5	733	5	BM084289	BM084289	502	252.5	6.4	911	3	CR650663	CR650663 Tetraodon
430	256	6.5	768	5	BM078667	BM078667	503	252.5	6.4	912	3	CR654453	CR654453 Tetraodon
431	256	6.5	775	5	BM076322	BM076322	504	252.5	6.4	913	3	CR652478	CR652478 Tetraodon
432	256	6.5	779	5	BM079925	BM079925	505	252.5	6.4	915	3	CR655403	CR655403 Tetraodon
433	256	6.5	825	5	BM073854	BM073854	506	252.5	6.4	916	3	CR633664	CR633664 Tetraodon
434	256	6.5	831	7	CN322308	AGENCOURT	507	252.5	6.4	917	3	CR639740	CR639740 Tetraodon
c 435	256	6.5	858	7	CF284556	AGENCOURT	508	252.5	6.4	919	3	CR639446	CR639446 Tetraodon
436	256	6.5	908	7	CN156107	943469_MA	509	252.5	6.4	919	3	CR650874	CR650874 Tetraodon
437	256	6.5	1082	3	CR655570	Tetraodon	510	252.5	6.4	920	3	CR635099	CR635099 Tetraodon
438	256	6.5	1174	3	CR729399	Tetraodon	511	252.5	6.4	920	3	CR635994	CR635994 Tetraodon
439	255.5	6.5	833	7	CO960543	AGENCOURT	512	252.5	6.4	920	3	CR641802	CR641802 Tetraodon
440	255.5	6.5	939	3	CR634185	Tetraodon	513	252.5	6.4	920	3	CR646673	CR646673 Tetraodon
441	255.5	6.5	967	3	CR710965	Tetraodon	514	252.5	6.4	920	3	CR646862	CR646862 Tetraodon
442	255	6.5	701	5	BU417312	603670839	515	252.5	6.4	922	3	CR640332	CR640332 Tetraodon
443	255	6.5	711	5	BM083229	BM083229	516	252.5	6.4	923	3	CR635331	CR635331 Tetraodon
444	255	6.5	759	7	CF522916	AGENCOURT	517	252.5	6.4	923	3	CR643185	CR643185 Tetraodon
445	255	6.5	772	5	BU416382	603670632	518	252.5	6.4	924	3	CR645044	CR645044 Tetraodon
c 446	255	6.5	774	7	CV483748	AGENCOURT	519	252.5	6.4	924	3	CR650125	CR650125 Tetraodon
447	255	6.5	816	5	BM078622	BM078622	520	252.5	6.4	925	3	CR634177	CR634177 Tetraodon

521	252.5	6.4	925	3	CR638868	Tetraodon	CR638868	594	249.5	6.3	871	3	CR728114	Tetraodon	CR728114
522	252.5	6.4	926	3	CR642728	Tetraodon	CR642728	595	249.5	6.3	901	3	CR642443	Tetraodon	CR642443
523	252.5	6.4	927	3	CR649071	Tetraodon	CR649071	596	249.5	6.3	905	5	BU488572	Tetraodon	BU488572
524	252.5	6.4	928	3	CR644693	Tetraodon	CR644693	597	249.5	6.3	906	3	CR636996	Tetraodon	CR636996
525	252.5	6.4	927	3	CR649839	Tetraodon	CR649839	598	249.5	6.3	908	3	CR641726	Tetraodon	CR641726
526	252.5	6.4	927	3	CR650861	Tetraodon	CR650861	599	249.5	6.3	920	3	CR645319	Tetraodon	CR645319
527	252.5	6.4	929	3	CR650703	Tetraodon	CR650703	600	249.5	6.3	924	3	CR633589	Tetraodon	CR633589
528	252.5	6.4	929	3	CR651331	Tetraodon	CR651331	601	249.5	6.3	925	3	CR651690	Tetraodon	CR651690
529	252.5	6.4	930	3	CR653042	Tetraodon	CR653042	602	249.5	6.3	928	3	CR641657	Tetraodon	CR641657
530	252.5	6.4	930	3	CR656522	Tetraodon	CR656522	603	249.5	6.3	929	3	CR652631	Tetraodon	CR652631
531	252.5	6.4	931	3	CR643809	Tetraodon	CR643809	604	249.5	6.3	931	3	CR639501	Tetraodon	CR639501
532	252.5	6.4	932	3	CR639229	Tetraodon	CR639229	605	249.5	6.3	932	3	CR639294	Tetraodon	CR639294
533	252.5	6.4	933	3	CR652196	Tetraodon	CR652196	606	249.5	6.3	1141	5	BM918816	Tetraodon	BM918816
534	252.5	6.4	934	3	CR635034	Tetraodon	CR635034	607	249.5	6.3	693	7	CF778907	AGENCY	CF778907
535	252.5	6.4	934	3	CR639892	Tetraodon	CR639892	608	249.5	6.3	728	4	BJ714567	Tetraodon	BJ714567
536	252.5	6.4	939	3	CR644641	Tetraodon	CR644641	609	249.5	6.3	729	4	BJ707845	Tetraodon	BJ707845
537	252.5	6.4	940	3	CR651400	Tetraodon	CR651400	610	249.5	6.3	730	4	BJ709178	Tetraodon	BJ709178
538	252.5	6.4	941	3	CR646689	Tetraodon	CR646689	611	249.5	6.3	731	4	BJ708245	Tetraodon	BJ708245
539	252.5	6.4	944	3	CR655890	Tetraodon	CR655890	612	249.5	6.3	731	4	BJ711604	Tetraodon	BJ711604
540	252.5	6.4	1049	5	BM919345	Tetraodon	BM919345	613	249.5	6.3	732	4	BJ709989	Tetraodon	BJ709989
541	252.5	6.4	1200	3	CR635412	Tetraodon	CR635412	614	249.5	6.3	732	4	BJ710455	Tetraodon	BJ710455
542	252.5	6.4	1458	3	CR641256	Tetraodon	CR641256	615	249.5	6.3	732	4	BJ713493	Tetraodon	BJ713493
543	252.5	6.4	735	4	BJ707169	Tetraodon	BJ707169	616	249.5	6.3	736	4	BJ708003	Tetraodon	BJ708003
544	252.5	6.4	818	6	CB560134	AGENCY	CB560134	617	249.5	6.3	740	4	BJ708327	Tetraodon	BJ708327
545	252.5	6.4	834	7	CF376371	AGENCY	CF376371	618	249.5	6.3	776	6	CA771814	Tetraodon	CA771814
546	252.5	6.4	838	5	BM975937	Tetraodon	BM975937	619	249.5	6.3	798	6	CA777464	Tetraodon	CA777464
547	252.5	6.4	860	3	CR635188	Tetraodon	CR635188	620	249.5	6.3	827	5	BM771814	Tetraodon	BM771814
548	252.5	6.4	862	3	CR638045	Tetraodon	CR638045	621	249.5	6.3	847	6	CD508696	Tetraodon	CD508696
549	252.5	6.4	1058	7	CF591286	AGENCY	CF591286	622	249.5	6.3	856	7	CF581209	Tetraodon	CF581209
550	251.5	6.4	830	5	BU492586	Tetraodon	BU492586	623	249.5	6.3	874	6	BY708812	Tetraodon	BY708812
551	251.5	6.4	855	7	CK407980	Tetraodon	CK407980	624	249.5	6.3	876	3	AK007765	Tetraodon	AK007765
552	251.5	6.4	888	5	BU417435	Tetraodon	BU417435	625	249.5	6.3	877	3	AK003079	Tetraodon	AK003079
553	251.5	6.4	907	3	CR645594	Tetraodon	CR645594	626	249.5	6.3	877	3	AK007815	Tetraodon	AK007815
554	251.5	6.4	920	3	CR656598	Tetraodon	CR656598	627	249.5	6.3	877	3	AK008729	Tetraodon	AK008729
555	251.5	6.4	923	7	CF348030	Tetraodon	CF348030	628	249.5	6.3	877	3	AK008927	Tetraodon	AK008927
556	251.5	6.4	797	7	CF348030	Tetraodon	CF348030	629	249.5	6.3	879	3	AK008888	Tetraodon	AK008888
557	251.5	6.4	845	7	CF374141	AGENCY	CF374141	630	249.5	6.3	882	7	CF581178	AGENCY	CF581178
558	251.5	6.4	856	7	CF378642	AGENCY	CF378642	631	249.5	6.3	891	3	AK008644	Tetraodon	AK008644
559	251.5	6.4	860	3	CR642136	Tetraodon	CR642136	632	249.5	6.3	892	7	CF580743	AGENCY	CF580743
560	251.5	6.4	902	4	BI752107	Tetraodon	BI752107	633	249.5	6.3	909	7	CF581329	AGENCY	CF581329
561	251.5	6.4	1037	3	CR639656	Tetraodon	CR639656	634	249.5	6.3	910	7	CF586044	AGENCY	CF586044
562	251.5	6.4	1515	3	CR645042	Tetraodon	CR645042	635	249.5	6.3	916	7	CF580742	AGENCY	CF580742
563	251.5	6.4	4379	3	BC053923	Tetraodon	BC053923	636	249.5	6.3	943	5	BQ222778	AGENCY	BQ222778
564	250.5	6.3	722	7	CO882996	Tetraodon	CO882996	637	249.5	6.3	2487	3	CR590439	AGENCY	CR590439
565	250.5	6.3	768	7	CK173303	Tetraodon	CK173303	638	248.5	6.3	568	4	BI341226	Tetraodon	BI341226
566	250.5	6.3	783	5	BM707378	Tetraodon	BM707378	639	248.5	6.3	669	7	CN563024	Tetraodon	CN563024
567	250.5	6.3	788	3	CR646057	Tetraodon	CR646057	640	248.5	6.3	769	5	BM960661	Tetraodon	BM960661
568	250.5	6.3	804	5	BU417486	Tetraodon	BU417486	641	248.5	6.3	852	7	CO936690	AGENCY	CO936690
569	250.5	6.3	811	7	CK176944	Tetraodon	CK176944	642	248.5	6.3	1305	6	CD502467	AGENCY	CD502467
570	250.5	6.3	814	7	CK175861	Tetraodon	CK175861	643	248.5	6.3	643	4	BJ492843	Tetraodon	BJ492843
571	250.5	6.3	818	7	CK190772	Tetraodon	CK190772	644	248.5	6.3	732	4	BJ709656	Tetraodon	BJ709656
572	250.5	6.3	839	7	CO249929	AGENCY	CO249929	645	248.5	6.3	732	4	BJ709656	Tetraodon	BJ709656
573	250.5	6.3	844	5	BU416522	Tetraodon	BU416522	646	248.5	6.3	749	5	BU487405	Tetraodon	BU487405
574	250.5	6.3	844	7	CO933077	AGENCY	CO933077	647	248.5	6.3	798	5	BU707512	Tetraodon	BU707512
575	250.5	6.3	889	7	CK409575	Tetraodon	CK409575	648	248.5	6.3	846	6	CD497919	Tetraodon	CD497919
576	250.5	6.3	900	7	CK409575	Tetraodon	CK409575	649	248.5	6.3	919	6	BY708787	Tetraodon	BY708787
577	250.5	6.3	908	7	CK408339	Tetraodon	CK408339	650	248.5	6.3	931	7	CF577601	AGENCY	CF577601
578	250.5	6.3	912	3	CR641542	Tetraodon	CR641542	651	247.5	6.3	738	6	CA345943	Tetraodon	CA345943
579	250.5	6.3	920	7	CR651608	Tetraodon	CR651608	652	247.5	6.3	741	7	CV487080	AGENCY	CV487080
580	250.5	6.3	920	7	CK407536	Tetraodon	CK407536	653	247.5	6.3	744	5	BM981286	Tetraodon	BM981286
581	250.5	6.3	925	3	CR653117	Tetraodon	CR653117	654	247.5	6.3	770	5	BM972759	Tetraodon	BM972759
582	250.5	6.3	928	7	CF581264	AGENCY	CF581264	655	247.5	6.3	780	4	BJ720412	Tetraodon	BJ720412
583	250.5	6.3	932	7	CK408003	Tetraodon	CK408003	656	247.5	6.3	784	5	BM974176	Tetraodon	BM974176
584	250.5	6.3	935	7	CK407783	Tetraodon	CK407783	657	247.5	6.3	790	7	CK173411	Tetraodon	CK173411
585	250.5	6.3	1000	1	AL532786	Tetraodon	AL532786	658	247.5	6.3	808	5	BM974661	Tetraodon	BM974661
586	250.5	6.3	1035	3	CK50808X	Tetraodon	CK50808X	659	247.5	6.3	823	5	BM979297	Tetraodon	BM979297
587	250.5	6.3	1883	3	CR641415	Tetraodon	CR641415	660	247.5	6.3	828	5	CK180142	Tetraodon	CK180142
588	250.5	6.3	679	4	BJ502290	Tetraodon	BJ502290	661	247.5	6.3	836	5	BM979926	Tetraodon	BM979926
589	249.5	6.3	973	3	CR716391	Tetraodon	CR716391	662	247.5	6.3	849	6	CD496157	Tetraodon	CD496157
590	249.5	6.3	748	4	BI836955	Tetraodon	BI836955	663	247.5	6.3	908	3	CR644464	Tetraodon	CR644464
591	249.5	6.3	749	4	BJ726902	Tetraodon	BJ726902	664	247.5	6.3	917	3	CR648546	Tetraodon	CR648546
592	249.5	6.3	818	5	BM979902	Tetraodon	BM979902	665	247.5	6.3	920	3	CR654011	Tetraodon	CR654011
593	249.5	6.3	820	5	BU416925	Tetraodon	BU416925	666	247.5	6.3	944	6	CD796235	Tetraodon	CD796235

C 667	247	6.3	614	7	CF101857	CF101857 hac32c10.	C 740	245.5	6.2	773	4	BJ726614	BJ726614
C 668	247	6.3	647	6	CD015434	CD015434 hac21f03.	C 741	245.5	6.2	774	4	BJ715378	BJ715378
C 669	247	6.3	648	6	CD014428	CD014428 hac31n09.	C 742	245.5	6.2	776	4	BJ718243	BJ718243
C 670	247	6.3	770	5	BU490853	BU490853 604129946	C 743	245.5	6.2	776	5	EX074785	EX074785
C 671	247	6.3	844	7	CF581226	CF581226 AGENCOURT	C 744	245.5	6.2	777	4	BJ717871	BJ717871
C 672	247	6.3	848	7	CF586043	CF586043 AGENCOURT	C 745	245.5	6.2	779	4	BJ716216	BJ716216
C 673	247	6.3	870	6	CD506832	CD506832 CDA81-E08	C 746	245.5	6.2	794	4	BJ719963	BJ719963
C 674	247	6.3	874	7	CF581314	CF581314 AGENCOURT	C 747	245.5	6.2	798	4	BJ720317	BJ720317
C 675	247	6.3	882	6	CD500632	CD500632 CDA46-B04	C 748	245.5	6.2	852	7	CO933440	CO933440
C 676	247	6.3	893	7	CF580422	CF580422 AGENCOURT	C 749	245.5	6.2	893	3	CR645057	CR645057
C 677	247	6.3	915	7	CF580726	CF580726 AGENCOURT	C 750	245.5	6.2	911	3	CR646918	CR646918
C 678	247	6.3	1008	3	CNS098PT	BU047002 Single re	C 751	245.5	6.2	911	3	CR649923	CR649923
C 679	247	6.3	1051	3	CR655901	CR655901 Tetraodon	C 752	245.5	6.2	912	3	CR644026	CR644026
C 680	247	6.3	1070	6	CD505254	CD505254 CDA72-F12	C 753	245.5	6.2	912	3	CR655471	CR655471
C 681	246.5	6.2	779	5	BU416569	BU416569 603671624	C 754	245.5	6.2	913	3	CR639696	CR639696
C 682	246.5	6.2	783	7	CO915425	CO915425 AGENCOURT	C 755	245.5	6.2	913	3	CR650510	CR650510
C 683	246.5	6.2	817	5	BU489309	BU489309 604129260	C 756	245.5	6.2	914	3	CR644712	CR644712
C 684	246.5	6.2	820	5	BU417081	BU417081 603671152	C 757	245.5	6.2	915	3	CR642478	CR642478
C 685	246.5	6.2	888	7	AK007333	Mus muscu	C 758	245.5	6.2	916	3	CR633670	CR633670
C 686	246.5	6.2	888	7	CNS11336	CNS11336 AGENCOURT	C 759	245.5	6.2	916	3	CR635159	CR635159
C 687	246.5	6.2	908	3	CR639515	CR639515 Tetraodon	C 760	245.5	6.2	917	3	CR641924	CR641924
C 688	246.5	6.2	916	3	CR644691	CR644691 Tetraodon	C 761	245.5	6.2	917	3	CR652850	CR652850
C 689	246.5	6.2	916	3	CR652423	CR652423 Tetraodon	C 762	245.5	6.2	918	3	CR637918	CR637918
C 690	246.5	6.2	918	3	CR650862	CR650862 Tetraodon	C 763	245.5	6.2	918	3	CR642059	CR642059
C 691	246.5	6.2	919	3	CR645747	CR645747 Tetraodon	C 764	245.5	6.2	918	3	CR646866	CR646866
C 692	246.5	6.2	919	3	CR732093	CR732093 Tetraodon	C 765	245.5	6.2	920	3	CR640305	CR640305
C 693	246.5	6.2	925	3	CR636483	CR636483 Tetraodon	C 766	245.5	6.2	920	3	CR646500	CR646500
C 694	246.5	6.2	926	3	CR642894	CR642894 Tetraodon	C 767	245.5	6.2	921	3	CR634303	CR634303
C 695	246.5	6.2	927	3	CR638224	CR638224 Tetraodon	C 768	245.5	6.2	921	3	CR646833	CR646833
C 696	246.5	6.2	927	3	CR653272	CR653272 Tetraodon	C 769	245.5	6.2	921	3	CR647938	CR647938
C 697	246.5	6.2	928	3	CR638651	CR638651 Tetraodon	C 770	245.5	6.2	921	3	CR648374	CR648374
C 698	246.5	6.2	929	3	CR643837	CR643837 Tetraodon	C 771	245.5	6.2	922	3	CR639603	CR639603
C 699	246.5	6.2	930	3	CR649255	CR649255 Tetraodon	C 772	245.5	6.2	923	3	CR646823	CR646823
C 700	246.5	6.2	935	3	CR655306	CR655306 Tetraodon	C 773	245.5	6.2	923	3	CR651452	CR651452
C 701	246.5	6.2	936	3	CR637185	CR637185 Tetraodon	C 774	245.5	6.2	924	3	CR634150	CR634150
C 702	246.5	6.2	936	3	CR639122	CR639122 Tetraodon	C 775	245.5	6.2	925	3	CR633696	CR633696
C 703	246.5	6.2	1020	3	CR655414	CR655414 Tetraodon	C 776	245.5	6.2	925	3	CR638053	CR638053
C 704	246.5	6.2	1052	5	BM255522	BM255522 AGENCOURT	C 777	245.5	6.2	925	3	CR643848	CR643848
C 705	246.5	6.2	1473	3	CR655736	CR655736 Tetraodon	C 778	245.5	6.2	925	3	CR645030	CR645030
C 706	246	6.2	741	5	BX540472	BX540472 BX540472	C 779	245.5	6.2	925	3	CR651356	CR651356
C 707	246	6.2	744	5	BU416638	BU416638 603671357	C 780	245.5	6.2	925	3	CR653755	CR653755
C 708	246	6.2	799	5	BX076088	BX076088 BX076088	C 781	245.5	6.2	926	3	CR635794	CR635794
C 709	246	6.2	811	5	BU417493	BU417493 603671392	C 782	245.5	6.2	926	3	CR642588	CR642588
C 710	246	6.2	817	4	BJ716525	BJ716525 BJ716525	C 783	245.5	6.2	926	3	CR643840	CR643840
C 711	246	6.2	826	6	CD506833	CD506833 CDA81-E08	C 784	245.5	6.2	926	3	CR648762	CR648762
C 712	246	6.2	876	3	AK007566	AK007566 Mus muscu	C 785	245.5	6.2	926	3	CR649853	CR649853
C 713	246	6.2	885	5	BX707387	BX707387 BX707387	C 786	245.5	6.2	927	3	CR637181	CR637181
C 714	246	6.2	900	6	BY703467	BY703467 BY703467	C 787	245.5	6.2	927	3	CR638875	CR638875
C 715	246	6.2	907	7	CF581371	CF581371 AGENCOURT	C 788	245.5	6.2	927	3	CR649174	CR649174
C 716	246	6.2	913	7	CF581274	CF581274 AGENCOURT	C 789	245.5	6.2	928	3	CR655117	CR655117
C 717	246	6.2	914	7	CF578058	CF578058 AGENCOURT	C 790	245.5	6.2	928	3	CR634111	CR634111
C 718	246	6.2	923	7	CF581324	CF581324 AGENCOURT	C 791	245.5	6.2	928	3	CR637946	CR637946
C 719	245.5	6.2	686	4	BJ706506	BJ706506 BJ706506	C 792	245.5	6.2	928	3	CR639510	CR639510
C 720	245.5	6.2	731	4	BJ723231	BJ723231 BJ723231	C 793	245.5	6.2	928	3	CR652215	CR652215
C 721	245.5	6.2	735	1	AV906915	AV906915 AV906915	C 794	245.5	6.2	929	3	CR635930	CR635930
C 722	245.5	6.2	744	4	BJ724325	BJ724325 BJ724325	C 795	245.5	6.2	929	3	CR639664	CR639664
C 723	245.5	6.2	747	4	BJ720611	BJ720611 BJ720611	C 796	245.5	6.2	929	3	CR642856	CR642856
C 724	245.5	6.2	747	4	BJ724412	BJ724412 BJ724412	C 797	245.5	6.2	929	3	CR653731	CR653731
C 725	245.5	6.2	747	4	BJ726569	BJ726569 BJ726569	C 798	245.5	6.2	930	3	CR636527	CR636527
C 726	245.5	6.2	748	4	BJ716014	BJ716014 BJ716014	C 799	245.5	6.2	930	3	CR642584	CR642584
C 727	245.5	6.2	748	4	BJ716963	BJ716963 BJ716963	C 800	245.5	6.2	932	3	CR633598	CR633598
C 728	245.5	6.2	748	4	BJ721670	BJ721670 BJ721670	C 801	245.5	6.2	932	3	CR635120	CR635120
C 729	245.5	6.2	750	4	BJ724827	BJ724827 BJ724827	C 802	245.5	6.2	932	3	CR647728	CR647728
C 730	245.5	6.2	751	4	BJ721319	BJ721319 BJ721319	C 803	245.5	6.2	932	3	CR649884	CR649884
C 731	245.5	6.2	751	4	BJ721860	BJ721860 BJ721860	C 804	245.5	6.2	932	3	CR640933	CR640933
C 732	245.5	6.2	752	4	BJ725497	BJ725497 BJ725497	C 805	245.5	6.2	933	3	CR647323	CR647323
C 733	245.5	6.2	757	4	BJ723169	BJ723169 BJ723169	C 806	245.5	6.2	933	3	CR651528	CR651528
C 734	245.5	6.2	760	4	BJ726635	BJ726635 BJ726635	C 807	245.5	6.2	933	3	CR656731	CR656731
C 735	245.5	6.2	765	4	BJ715465	BJ715465 BJ715465	C 808	245.5	6.2	934	3	CR653273	CR653273
C 736	245.5	6.2	771	4	BJ719672	BJ719672 BJ719672	C 809	245.5	6.2	935	3	CR652266	CR652266
C 737	245.5	6.2	772	4	BJ719248	BJ719248 BJ719248	C 810	245.5	6.2	935	3	CR653488	CR653488
C 738	245.5	6.2	773	4	BJ717746	BJ717746 BJ717746	C 811	245.5	6.2	937	3	CR654770	CR654770
C 739	245.5	6.2	773	4	BJ718606	BJ718606 BJ718606	C 812	245.5	6.2	938	3	CR647700	CR647700

813	245.5	6.2	939	3	CR653655	Tetraodon	CR653655	886	243	6.2	847	7	CO960123	AGENCYCOURT
814	245.5	6.2	940	3	CR634548	Tetraodon	CR634548	887	243	6.2	908	3	CR638917	Tetraodon
815	245.5	6.2	940	3	CR654861	Tetraodon	CR654861	888	243	6.2	1115	5	BM918560	AGENCYCOURT
816	245.5	6.2	943	3	CR656736	Tetraodon	CR656736	889	243	6.2	1630	3	CR648863	Tetraodon
817	245.5	6.2	943	3	CR640353	Tetraodon	CR640353	c 890	242.5	6.1	776	4	BJ716484	BJ716484
818	245.5	6.2	943	3	CR649462	Tetraodon	CR649462	891	242.5	6.1	799	7	CO936831	AGENCYCOURT
819	245.5	6.2	945	3	CR635020	Tetraodon	CR635020	892	242.5	6.1	890	3	CR644201	Tetraodon
820	245.5	6.2	961	3	CR644090	Tetraodon	CR644090	893	242.5	6.1	901	3	CR655134	Tetraodon
821	245.5	6.2	1013	3	CNS08SVR	Single re	CR626851	894	242.5	6.1	918	3	CR653996	Tetraodon
822	245.5	6.2	1203	3	CR641198	Tetraodon	CR641198	895	242.5	6.1	1238	9	AY408326	Mus muscu
823	245.5	6.2	1207	3	CR647047	Tetraodon	CR647047	896	242.5	6.1	1848	3	CR654394	Tetraodon
824	245.5	6.2	1726	3	CR653279	Tetraodon	CR653279	897	242	6.1	797	5	BU417007	Tetraodon
825	245.5	6.2	1894	3	CR626692	full-leng	CR626692	898	242	6.1	806	7	CO927000	AGENCYCOURT
826	245	6.2	727	4	BJ712430	BJ712430	BJ712430	899	242	6.1	811	5	BU417059	Tetraodon
827	245	6.2	730	4	BJ708144	BJ708144	BU492581	900	242	6.1	819	5	BU416369	Tetraodon
828	245	6.2	781	5	BU492581	604130334	CR662498	901	242	6.1	871	5	EX077714	EX077714
829	245	6.2	789	7	CF662498	CGLL02a06	BU486885	c 902	242	6.1	1144	6	CD507354	CD507354
830	245	6.2	874	5	BU486885	603972212	CD497918	903	242	6.1	1253	3	CR592280	full-leng
831	245	6.2	880	6	CD497918	CD430-F03	CD505684	904	242	6.1	6030	9	AY407073	Homo sapi
832	245	6.2	909	6	CD505684	CD475-A11	CR644892	905	241.5	6.1	708	4	BJ705989	BJ705989
833	245	6.2	918	3	CR644892	Tetraodon	CR734060	906	241.5	6.1	709	4	BJ705756	BJ705756
834	245	6.2	942	3	CR734060	Tetraodon	AK016509	907	241.5	6.1	709	4	BJ706011	BJ706011
835	245	6.2	1089	3	AK016509	Mus muscu	BI757320	908	241.5	6.1	710	4	BJ706306	BJ706306
836	245	6.2	1128	4	BI757320	603029535	CR638750	909	241.5	6.1	710	4	BJ714703	BJ714703
837	245	6.2	1139	3	CR638750	Tetraodon	AY411207	910	241.5	6.1	711	4	BJ704593	BJ704593
838	244.5	6.2	3048	9	AY411207	Homo sapi	BJ706958	911	241.5	6.1	711	4	BJ705039	BJ705039
839	244.5	6.2	725	4	BJ706958	BJ706958	CK873031	912	241.5	6.1	712	4	BJ714674	BJ714674
840	244.5	6.2	777	7	CK873031	AGENCYCOURT	EX081322	913	241.5	6.1	722	4	BJ712631	BJ712631
841	244.5	6.2	781	5	EX081322	EX081322	BU491739	914	241.5	6.1	724	4	BJ714304	BJ714304
842	244.5	6.2	790	5	BU491739	604128370	CD498003	915	241.5	6.1	726	4	BJ712324	BJ712324
843	244.5	6.2	797	6	CD498003	CD431-B05	BU498003	916	241.5	6.1	730	4	BJ708039	BJ708039
844	244.5	6.2	810	5	BU492339	604129362	CR644892	917	241.5	6.1	735	5	BU486806	BU486806
845	244.5	6.2	884	7	CNS07659	AGENCYCOURT	CF581269	918	241.5	6.1	792	5	EX914864	EX914864
846	244.5	6.2	897	7	CF581269	AGENCYCOURT	CR633827	c 919	241.5	6.1	794	5	BM388081	BM388081
847	244.5	6.2	905	3	CR733827	Tetraodon	CR651501	920	241.5	6.1	820	5	BU487247	BU487247
848	244.5	6.2	909	3	CR651501	Tetraodon	CR650208	921	241.5	6.1	852	3	CNS09M01	Single re
849	244.5	6.2	925	3	CR650208	Tetraodon	CR644791	922	241.5	6.1	868	7	CK015897	AGENCYCOURT
850	244.5	6.2	943	3	CR644791	Tetraodon	EX073443	c 923	241.5	6.1	876	6	CB562993	AGENCYCOURT
851	244	6.2	695	5	EX073443	EX073443	EX076323	924	241.5	6.1	915	3	CR656100	Tetraodon
852	244	6.2	734	5	EX076323	EX076323	EX076323	925	241.5	6.1	916	3	CR646536	Tetraodon
853	244	6.2	740	7	CN169918	AGENCYCOURT	BU490424	926	241.5	6.1	921	3	CR635696	Tetraodon
854	244	6.2	750	5	EX076323	EX076323	BU490424	927	241.5	6.1	929	3	CR655848	Tetraodon
855	244	6.2	764	4	BJ724595	BJ724595	CA774808	928	241.5	6.1	961	3	CR644045	Tetraodon
856	244	6.2	774	6	CA774808	ip12f10.x	BU490424	c 930	241	6.1	595	7	CF101863	Single re
857	244	6.2	799	5	BU490424	604131761	CF581361	c 931	241	6.1	595	7	CF102254	hac34d01.
858	244	6.2	895	3	AK003060	Mus muscu	CF581361	c 932	241	6.1	735	7	CO882924	BoVGen.11
859	244	6.2	908	7	CF581361	AGENCYCOURT	CR650638	933	241	6.1	756	7	CO574502	AGENCYCOURT
860	244	6.2	928	3	CR650638	Tetraodon	BG712830	934	241	6.1	821	7	CO595905	AGENCYCOURT
861	244	6.2	1480	3	CR650638	Tetraodon	CK176945	935	241	6.1	874	7	CF374140	AGENCYCOURT
862	243.5	6.2	650	4	BG712830	pqlin.pk0	BJ726859	936	241	6.1	887	3	CR648357	Tetraodon
863	243.5	6.2	757	7	CK176945	EST766265	CK029489	c 937	241	6.1	920	7	CF581286	AGENCYCOURT
864	243.5	6.2	764	4	BJ726859	BJ726859	BJ718142	c 938	240.5	6.1	740	4	BJ724753	BJ724753
865	243.5	6.2	775	7	CK029489	AGENCYCOURT	EX914956	939	240.5	6.1	757	5	EX858890	EX858890
866	243.5	6.2	784	4	BJ718142	BJ718142	CF266485	940	240.5	6.1	807	7	CN321900	AGENCYCOURT
867	243.5	6.2	816	5	EX914956	EX914956	CK406949	941	240.5	6.1	814	7	CN323058	AGENCYCOURT
868	243.5	6.2	852	7	CF266485	AGENCYCOURT	CK406949	c 942	240.5	6.1	829	4	BI521986	603081617
869	243.5	6.2	879	7	CK406949	AUF_iflvr	CK407045	943	240.5	6.1	832	5	BU416693	BU416693
870	243.5	6.2	879	7	CK407045	AUF_iflvr	CR634091	944	240.5	6.1	835	5	BU489163	BU489163
871	243.5	6.2	904	3	CR634091	Tetraodon	CR734219	945	240.5	6.1	901	3	CR640301	Tetraodon
872	243.5	6.2	905	3	CR734219	Tetraodon	CK406448	946	240.5	6.1	903	3	CR635831	Tetraodon
873	243.5	6.2	905	7	CK406448	AUF_iflvr	CR649458	947	240.5	6.1	907	3	CR649952	Tetraodon
874	243.5	6.2	910	3	CR649458	Tetraodon	CR641262	948	240.5	6.1	911	3	CR636786	Tetraodon
875	243.5	6.2	916	3	CR641262	Tetraodon	CR647064	949	240.5	6.1	912	3	CR649775	Tetraodon
876	243.5	6.2	927	3	CR647064	Tetraodon	CR635918	950	240.5	6.1	915	3	CR647813	Tetraodon
877	243.5	6.2	934	3	CR635918	Tetraodon	CR638649	951	240.5	6.1	918	3	CR638345	Tetraodon
878	243.5	6.2	934	3	CR638649	Tetraodon	CR646129	952	240.5	6.1	921	3	CR656065	Tetraodon
879	243.5	6.2	935	7	CR646129	Tetraodon	CK408890	953	240.5	6.1	921	3	CR647144	Tetraodon
880	243.5	6.2	957	7	CK408890	AUF_iflvr	BI838552	954	240.5	6.1	925	3	CR653326	Tetraodon
881	243	6.2	689	5	EX083735	EX083735	EX083163	955	240.5	6.1	932	3	CR641267	Tetraodon
882	243	6.2	780	4	BI838552	603086213	CF346385	956	240.5	6.1	935	3	CNS09688	Single re
883	243	6.2	786	5	EX083163	EX083163	CF346385	957	240.5	6.1	940	3	CR646211	Tetraodon
884	243	6.2	822	5	CF346385	AGENCYCOURT		958	240.5	6.1	944	3	CR651701	Tetraodon
885	243	6.2	842	7	CF346385	AGENCYCOURT								

959	240.5	6.1	946	3	CR652182	Tetraodon	CR652182	1032	238.5	6.0	940	3	CR731036	Tetraodon	CR731036
960	240.5	6.1	947	3	CR646891	Tetraodon	CR646891	1033	238.5	6.0	969	3	CNS0954U	Single re	BM042730
961	240.5	6.1	948	3	CR641038	Tetraodon	CR641038	1034	238.5	6.0	975	3	CNS09CN0	Single re	BM052456
962	240.5	6.1	958	3	CR642655	Tetraodon	CR642655	1035	238.5	6.0	1172	6	CD508404	CD490-F11	CD508404
963	240.5	6.1	961	3	CR649860	Tetraodon	CR649860	1036	238.5	6.0	2873	9	AW411208	Pan trogl	AY411208
964	240.5	6.1	964	3	CNS093BK	Single re	BM040488	1037	238	6.0	698	5	BM437706	BM437706	BM437706
965	240.5	6.1	970	3	CR656705	Tetraodon	CR656705	1038	238	6.0	701	6	CB492844	omykrbnas	CB492844
966	240.5	6.1	3368	3	AK004995	Mus muscu	AK004995	1039	238	6.0	746	5	BM431504	BM431504	BM431504
967	240	6.1	749	5	BM076018	Mus muscu	BM076018	1040	238	6.0	756	4	BM431504	BM431504	BM431504
968	240	6.1	754	5	BM233608	BM233608	BM233608	1041	238	6.0	788	5	BM487936	BM487936	BM487936
969	240	6.1	791	5	BU416654	603671252	BU416654	1042	238	6.0	788	7	CO925483	CO925483	CO925483
970	240	6.1	832	4	BI521033	603081617	BI521033	1043	238	6.0	884	7	CF580474	CF580474	CF580474
971	240	6.1	883	6	CD508695	CD492-C07	CD508695	1044	238	6.0	908	3	CR646073	Tetraodon	CR646073
972	240	6.1	1407	3	CR683082	Tetraodon	CR683082	1045	238	6.0	1156	3	CR601602	full-leng	CR601602
973	240	6.1	1985	3	AK075718	Mus muscu	AK075718	1046	238	6.0	2348	9	AY419858	Mus muscu	AY419858
974	240	6.1	2487	9	AY419858	Homo sapi	AY419858	1047	237.5	6.0	658	5	BM671526	BM671526	BM671526
975	239.5	6.1	732	4	BM708107	BM708107	BM708107	1048	237.5	6.0	749	4	BM705582	BM705582	BM705582
976	239.5	6.1	738	6	CD781033	EST652394	CD781033	1049	237.5	6.0	708	4	BM725221	BM725221	BM725221
977	239.5	6.1	753	7	CK631172	AM2-AE001	CK631172	1050	237.5	6.0	758	5	BM083792	BM083792	BM083792
978	239.5	6.1	758	5	BM081136	BM081136	BM081136	1051	237.5	6.0	762	7	CV486958	AGENCY	CV486958
979	239.5	6.1	790	5	BM078252	BM078252	BM078252	1052	237.5	6.0	774	4	BM715933	BM715933	BM715933
980	239.5	6.1	811	7	CNS326143	AGENCY	CNS326143	1053	237.5	6.0	789	5	BU416643	BU416643	BU416643
981	239.5	6.1	839	5	BU417215	603671003	BU417215	1054	237.5	6.0	794	5	BM082383	BM082383	BM082383
982	239.5	6.1	854	5	BU416893	603671026	BU416893	1055	237.5	6.0	807	7	CK192378	EST781693	CK192378
983	239.5	6.1	889	7	CK408000	AUF Iflvr	CK408000	1056	237.5	6.0	881	7	CF581181	AGENCY	CF581181
984	239.5	6.1	896	7	CF589938	AGENCY	CF589938	1057	237.5	6.0	908	7	CN324016	AGENCY	CN324016
985	239.5	6.1	907	7	CK423429	AUF Iflvr	CK423429	1058	237.5	6.0	916	3	CR643509	Tetraodon	CR643509
986	239.5	6.1	917	7	CR653217	Tetraodon	CR653217	1059	237.5	6.0	920	3	CR633793	Tetraodon	CR633793
987	239.5	6.1	930	3	CR646196	Tetraodon	CR646196	1060	237.5	6.0	932	7	CF581205	AGENCY	CF581205
988	239.5	6.1	1042	5	BM426922	BM426922	BM426922	1061	237.5	6.0	935	7	CF581228	AGENCY	CF581228
989	239.5	6.1	1155	3	CR645634	Tetraodon	CR645634	1062	237.5	6.0	979	3	CNS093DT	AGENCY	CNS093DT
990	239.5	6.1	1323	3	CR615568	full-leng	CR615568	1063	237	6.0	660	4	BM101561	Single re	BM101561
991	239.5	6.1	1326	3	CR596989	full-leng	CR596989	1064	237	6.0	719	5	BM489337	BM489337	BM489337
992	239.5	6.1	1333	3	CR592814	full-leng	CR592814	1065	237	6.0	731	4	BM724119	BM724119	BM724119
993	239.5	6.1	1334	3	CR622783	full-leng	CR622783	1066	237	6.0	752	7	CK031058	AGENCY	CK031058
994	239.5	6.1	1342	3	CR601129	full-leng	CR601129	1067	237	6.0	769	5	BM081610	BM081610	BM081610
995	239.5	6.1	1345	3	CR613780	full-leng	CR613780	1068	237	6.0	784	5	BM082097	BM082097	BM082097
996	239.5	6.1	1347	3	CR591153	full-leng	CR591153	1069	237	6.0	790	6	BM078713	BM078713	BM078713
997	239.5	6.1	1352	3	CR611613	full-leng	CR611613	1070	237	6.0	796	5	BM078187	BM078187	BM078187
998	239.5	6.1	1353	3	CR622185	full-leng	CR622185	1071	237	6.0	804	5	BM076361	BM076361	BM076361
999	239.5	6.1	1354	3	CR593594	full-leng	CR593594	1072	237	6.0	810	5	BM079786	BM079786	BM079786
1000	239.5	6.1	1355	3	CR597047	full-leng	CR597047	1073	237	6.0	810	5	BM084214	BM084214	BM084214
1001	239.5	6.1	1358	3	CR599000	full-leng	CR599000	1074	237	6.0	811	5	BM078725	BM078725	BM078725
1002	239.5	6.1	1360	3	CR608843	full-leng	CR608843	1075	237	6.0	822	5	BM074166	BM074166	BM074166
1003	239.5	6.1	1365	3	CR601475	full-leng	CR601475	1076	237	6.0	831	4	BI832541	603082155	BI832541
1004	239.5	6.1	1367	3	CR615236	full-leng	CR615236	1077	237	6.0	849	7	CK866915	AGENCY	CK866915
1005	239.5	6.1	1369	3	CR611617	full-leng	CR611617	1078	237	6.0	852	5	BM079209	AGENCY	BM079209
1006	239.5	6.1	1983	3	CR602253	full-leng	CR602253	1079	237	6.0	868	5	BM078626	BM078626	BM078626
1007	239	6.1	594	7	CF101840	hac32b04	CF101840	1080	237	6.0	878	7	CF581364	AGENCY	CF581364
1008	239	6.1	701	5	BM917087	BM917087	BM917087	1081	237	6.0	914	7	CF587070	AGENCY	CF587070
1009	239	6.1	737	5	BM922269	BM922269	BM922269	1082	237	6.0	936	7	CK866304	AGENCY	CK866304
1010	239	6.1	751	4	BM722875	BM722875	BM722875	1083	237	6.0	1917	9	AY400074	Homo sapi	AY400074
1011	239	6.1	751	4	BM91755	604128508	BM91755	1084	237	6.0	2841	3	AK046385	BM05385	AK046385
1012	239	6.1	847	7	CK407116	AUF Iflvr	CK407116	1085	237	6.0	544	2	BE030820	129027 MA	BE030820
1013	239	6.1	890	7	CF581438	AGENCY	CF581438	1086	236.5	6.0	597	7	CF737811	UI-M-HD0-	CF737811
1014	239	6.1	1239	3	CR654513	Tetraodon	CR654513	1087	236.5	6.0	706	4	BM707939	BM707939	BM707939
1015	239	6.1	1842	3	CR653520	Tetraodon	CR653520	1088	236.5	6.0	750	5	BM268384	BM268384	BM268384
1016	238.5	6.0	687	5	BM036510	BM036510	BM036510	1089	236.5	6.0	753	7	CV491657	AGENCY	CV491657
1017	238.5	6.0	690	5	BM079128	BM079128	BM079128	1090	236.5	6.0	763	7	CV286181	UI-M-HD0-	CV286181
1018	238.5	6.0	707	6	BM714071	BM714071	BM714071	1091	236.5	6.0	775	5	BU416319	603670926	BU416319
1019	238.5	6.0	707	6	BM244706	UI-M-PY0-	BM244706	1092	236.5	6.0	783	5	BM073267	BM073267	BM073267
1020	238.5	6.0	762	4	BM726029	BM726029	BM726029	1093	236.5	6.0	792	5	BM379560	BM379560	BM379560
1021	238.5	6.0	764	4	BM719808	BM719808	BM719808	1094	236.5	6.0	912	3	CR635692	Tetraodon	CR635692
1022	238.5	6.0	764	4	BM726180	BM726180	BM726180	1095	236.5	6.0	912	3	CF581325	AGENCY	CF581325
1023	238.5	6.0	773	7	CK142650	AGENCY	CK142650	1096	236.5	6.0	613	6	CD014827	hac25405	CD014827
1024	238.5	6.0	775	7	CV510879	CV510879	CV510879	1097	236	6.0	682	5	BM081125	BM081125	BM081125
1025	238.5	6.0	796	4	BM714839	BM714839	BM714839	1098	236	6.0	744	5	BM084290	BM084290	BM084290
1026	238.5	6.0	861	7	CF586989	AGENCY	CF586989	1099	236	6.0	752	5	BM078569	BM078569	BM078569
1027	238.5	6.0	865	7	CF591847	AGENCY	CF591847	1100	236	6.0	775	4	BM715927	BM715927	BM715927
1028	238.5	6.0	918	7	CK409444	AUF Iflvr	CK409444	1101	236	6.0	786	7	CO934370	AGENCY	CO934370
1029	238.5	6.0	920	7	CF581372	AGENCY	CF581372	1102	236	6.0	848	5	BU489306	604129359	BU489306
1030	238.5	6.0	922	3	CR639360	Tetraodon	CR639360	1103	236	6.0	873	7	CF581179	AGENCY	CF581179
1031	238.5	6.0	923	3	CR654160	Tetraodon	CR654160	1104	236	6.0					

1105	236	6.0	901	7	CF581310	CF581310	AGENCOURT	C1178	234.5	5.9	783	5	BW381901	BW381901
C1106	236	6.0	920	7	CF581281	AGENCOURT	CF581281	AGENCOURT	1179	234.5	798	5	BU416406	BU416406
1108	235.5	6.0	778	7	CK846337	968823 MA	CK846337	1180	234.5	5.9	802	5	BU488019	BU488019
1109	235.5	6.0	791	5	CK328977	AGENCOURT	CK328977	1181	234.5	5.9	808	5	BU416766	BU416766
1110	235.5	6.0	816	5	CK085069	CK085069	CK085069	1182	234.5	5.9	808	5	BU489614	BU489614
C1111	235.5	6.0	843	6	CF346384	AGENCOURT	CF346384	1183	234.5	5.9	811	7	CK026585	CK026585
1112	235.5	6.0	847	5	CD495456	CD495456	CD495456	1184	234.5	5.9	812	6	CD497616	CD497616
1113	235.5	6.0	852	7	BU486913	604126437	BU486913	1185	234.5	5.9	816	5	BU416324	BU416324
1114	235.5	6.0	887	5	CK084717	CK084717	CK084717	1186	234.5	5.9	830	7	CF577942	CF577942
1115	235.5	6.0	887	7	CO919178	AGENCOURT	CO919178	1187	234.5	5.9	831	7	CF577942	CF577942
1116	235.5	6.0	888	7	CK407348	AUF_IFLVR	CK407348	1188	234.5	5.9	831	7	CO350417	CO350417
1117	235.5	6.0	910	7	CK407839	AUF_IFLVR	CK407839	1189	234.5	5.9	835	7	CF581323	CF581323
1118	235.5	6.0	958	7	CK421858	AUF_IPSPN	CK421858	1190	234.5	5.9	851	5	BU417208	BU417208
C1119	235.5	6.0	973	1	AL532541	AL532541	AL532541	C1191	234.5	5.9	855	6	CD507088	CD507088
1120	235.5	6.0	976	3	CNS092520	Single re	CK039352	1192	234.5	5.9	857	7	CF578099	CF578099
1121	235	6.0	668	5	CK076087	CK076087	CK076087	C1193	234.5	5.9	864	6	CD503222	CD503222
1122	235	6.0	692	5	CK083245	CK083245	CK083245	C1194	234.5	5.9	864	6	CD508294	CD508294
C1123	235	6.0	696	4	CK0719517	CK0719517	CK0719517	1195	234.5	5.9	874	7	CF581293	CF581293
C1124	235	6.0	716	4	CK0724290	CK0724290	CK0724290	1196	234.5	5.9	879	7	CF581242	CF581242
1125	235	6.0	734	5	BU489873	604130802	BU489873	1197	234.5	5.9	884	7	CK407570	CK407570
C1126	235	6.0	739	4	CK0720668	CK0720668	CK0720668	1198	234.5	5.9	885	6	CD503390	CD503390
1127	235	6.0	741	4	CK0709342	CK0709342	CK0709342	1199	234.5	5.9	889	3	CNS0955C	CNS0955C
C1128	235	6.0	741	4	CK0716386	CK0716386	CK0716386	1200	234.5	5.9	890	7	CK507648	CK507648
C1129	235	6.0	741	4	CK0716629	CK0716629	CK0716629	1201	234.5	5.9	891	6	CD507087	CD507087
1130	235	6.0	743	4	CK0726389	CK0726389	CK0726389	1202	234.5	5.9	895	6	CD503221	CD503221
C1131	235	6.0	743	4	CK0726813	CK0726813	CK0726813	1203	234.5	5.9	907	7	CF581237	CF581237
C1132	235	6.0	743	4	CK0726935	CK0726935	CK0726935	1204	234.5	5.9	912	7	CF581384	CF581384
1133	235	6.0	744	4	CK0710738	CK0710738	CK0710738	1205	234.5	5.9	924	7	CK422293	CK422293
C1134	235	6.0	744	4	CK0715838	CK0715838	CK0715838	1206	234.5	5.9	927	3	CR634480	CR634480
C1135	235	6.0	745	4	CK0720093	CK0720093	CK0720093	1207	234.5	5.9	928	3	CR734879	CR734879
1136	235	6.0	747	4	CK0709201	CK0709201	CK0709201	1208	234.5	5.9	951	7	CF581439	CF581439
C1137	235	6.0	747	4	CK0720444	CK0720444	CK0720444	1209	234.5	5.9	953	7	CF581207	CF581207
C1138	235	6.0	748	4	CK0717972	CK0717972	CK0717972	1210	234.5	5.9	1452	3	CR616676	CR616676
1139	235	6.0	749	4	CK0719140	CK0719140	CK0719140	1211	234.5	5.9	246	5	AK005546	AK005546
C1140	235	6.0	754	4	CK0723286	CK0723286	CK0723286	1212	234	5.9	754	5	CK082451	CK082451
C1141	235	6.0	758	4	CK0717755	CK0717755	CK0717755	1213	234	5.9	757	5	CK082451	CK082451
C1142	235	6.0	759	4	CK0718064	CK0718064	CK0718064	1214	234	5.9	760	5	BU487758	BU487758
C1143	235	6.0	760	4	CK0719011	CK0719011	CK0719011	C1215	234	5.9	763	4	CK0723745	CK0723745
C1144	235	6.0	760	4	CK0725468	CK0725468	CK0725468	1216	234	5.9	769	7	CF348317	CF348317
C1145	235	6.0	761	4	CK0719652	CK0719652	CK0719652	1217	234	5.9	774	5	BU416308	BU416308
C1146	235	6.0	766	4	CK0722152	CK0722152	CK0722152	1218	234	5.9	783	7	CK0936234	CK0936234
C1147	235	6.0	770	4	CK0720324	CK0720324	CK0720324	1219	234	5.9	825	4	CK0936234	CK0936234
C1148	235	6.0	770	4	CK0722144	CK0722144	CK0722144	1220	234	5.9	840	7	CF581456	CF581456
C1149	235	6.0	771	4	CK0718099	CK0718099	CK0718099	1221	234	5.9	842	7	CK0916767	CK0916767
C1150	235	6.0	773	4	CK0719394	CK0719394	CK0719394	1222	234	5.9	860	7	CK0916767	CK0916767
C1151	235	6.0	774	4	CK0725643	CK0725643	CK0725643	1223	234	5.9	897	3	CK090900P	CK090900P
C1152	235	6.0	776	4	CK0721985	CK0721985	CK0721985	1224	234	5.9	920	7	CK406808	CK406808
C1153	235	6.0	777	4	CK0717147	CK0717147	CK0717147	1225	234	5.9	922	7	CF581452	CF581452
C1154	235	6.0	778	4	CK0721208	CK0721208	CK0721208	1226	234	5.9	948	2	BF314703	BF314703
C1155	235	6.0	785	4	CK0726255	CK0726255	CK0726255	1227	234	5.9	1050	3	AK006271	AK006271
C1156	235	6.0	787	4	CK0718273	CK0718273	CK0718273	1228	233.5	5.9	606	7	CV023565	CV023565
C1157	235	6.0	787	4	CK0718450	CK0718450	CK0718450	1229	233.5	5.9	631	5	CK072216	CK072216
C1158	235	6.0	787	4	CK0720814	CK0720814	CK0720814	1230	233.5	5.9	674	5	CK07263618	CK07263618
C1159	235	6.0	788	4	CK0721988	CK0721988	CK0721988	1231	233.5	5.9	689	2	BE314082	BE314082
C1160	235	6.0	791	4	CK0715849	CK0715849	CK0715849	1232	233.5	5.9	737	7	CK867609	CK867609
C1161	235	6.0	794	7	CF285235	AGENCOURT	CF285235	1233	233.5	5.9	750	7	CF999911	CF999911
1162	235	6.0	794	7	CF285235	AGENCOURT	CF285235	1234	233.5	5.9	759	5	BU489998	BU489998
1163	235	6.0	819	6	CA588481	hnb6407	CA588481	1235	233.5	5.9	759	5	BU486571	BU486571
1164	235	6.0	835	5	BU416582	BU416582	BU416582	1236	233.5	5.9	774	4	CK862841	CK862841
C1165	235	6.0	835	6	CD500955	CD500955	CD500955	1237	233.5	5.9	790	5	BU490314	BU490314
1166	235	6.0	845	7	CF581283	AGENCOURT	CF581283	1238	233.5	5.9	792	5	BU492574	BU492574
1167	235	6.0	846	5	BU490789	604129350	BU490789	1239	233.5	5.9	814	5	BU491344	BU491344
1168	235	6.0	855	7	CF581183	AGENCOURT	CF581183	1240	233.5	5.9	839	7	CK407549	CK407549
1169	235	6.0	856	6	CA778232	ip15g12.y	CA778232	1241	233.5	5.9	848	3	CNS0932D	CNS0932D
1170	235	6.0	958	6	CD508293	CD508293	CD508293	1242	233.5	5.9	855	7	CF578057	CF578057
1171	235	6.0	1386	6	CD013940	CD013940	CD013940	1243	233.5	5.9	858	3	CNS0808C	CNS0808C
1172	234.5	5.9	723	5	CK873612	CK873612	CK873612	1244	233.5	5.9	872	2	CF379487	CF379487
C1173	234.5	5.9	727	4	CK0718156	CK0718156	CK0718156	1245	233.5	5.9	884	7	CF375629	CF375629
C1174	234.5	5.9	729	4	CK0720948	CK0720948	CK0720948	1246	233.5	5.9	886	7	CK407770	CK407770
1175	234.5	5.9	735	7	CF523551	AGENCOURT	CF523551	1247	233.5	5.9	899	7	CK402522	CK402522
1176	234.5	5.9	758	6	CA371410	651831 NC	CA371410	1248	233.5	5.9	906	7	CK407031	CK407031
1177	234.5	5.9	777	5	CK073284	CK073284	CK073284	1249	233.5	5.9	913	7	CK408663	CK408663

1251	233.5	5.9	936	3	CR650622	CR650622 Tetraodon	c1324	231	5.9	759	4	BJ720597	BJ720597
1252	233.5	5.9	942	7	CK407882	AUF_Iflvr	1325	231	5.9	759	5	BU489621	BU489621
1253	233.5	5.9	949	7	CK409345	AUF_Iflvr	1326	231	5.9	777	5	BU492087	BU492087
1254	233.5	5.9	953	7	CK408923	AUF_Iflvr	1327	231	5.9	777	5	BU484985	BU484985
1255	233.5	5.9	993	3	BQ278177	AGENCYCOURT	1328	231	5.9	785	5	BX082093	BX082093
1256	233.5	5.9	1838	5	CR651108	Tetraodon	1329	231	5.9	808	7	CF581449	CF581449
Q1257	233	5.9	681	6	CA044889	seaplbn85	1330	231	5.9	906	3	CR645466	CR645466
1258	233	5.9	769	5	BU490592	AGENCYCOURT	1331	231	5.9	912	3	CR649827	CR649827
1259	233	5.9	811	7	CV480267	AGENCYCOURT	1332	231	5.9	1580	3	CR731118	CR731118
1260	233	5.9	823	7	CO580622	ILLUMIGEN	1333	231	5.9	3042	9	AY411209	AY411209
1261	233	5.9	861	7	CK407019	AUF_Iflvr	1334	230.5	5.8	544	2	BE012596	BE012596
1262	233	5.9	873	2	BF313551	601900179	1335	230.5	5.8	593	4	BI900802	BI900802
Q1263	233	5.9	916	7	CF581227	AGENCYCOURT	1336	230.5	5.8	661	4	BJ706475	BJ706475
1264	233	5.9	921	3	CR728740	Tetraodon	1337	230.5	5.8	691	4	BG270309	BG270309
1265	233	5.9	1110	3	CR728740	Tetraodon	1338	230.5	5.8	693	6	CB888497	CB888497
1266	232.5	5.9	578	4	BI715986	ic64b09.y	1339	230.5	5.8	696	4	BJ711817	BJ711817
1267	232.5	5.9	592	4	BI713261	ic86b11.y	1340	230.5	5.8	704	4	BJ713184	BJ713184
1268	232.5	5.9	710	5	BU487317	604125540	1341	230.5	5.8	704	4	BJ714577	BJ714577
1269	232.5	5.9	757	7	CF999621	AGENCYCOURT	1342	230.5	5.8	705	4	BJ708106	BJ708106
1270	232.5	5.9	768	5	BU489088	604131220	1343	230.5	5.8	706	4	BJ705779	BJ705779
1271	232.5	5.9	771	5	BU487650	604124925	1344	230.5	5.8	707	4	BJ706274	BJ706274
1272	232.5	5.9	774	5	BU417316	603671161	1345	230.5	5.8	707	4	BJ708473	BJ708473
1273	232.5	5.9	775	7	CV512147	kc80d09.y	1346	230.5	5.8	707	4	BJ708855	BJ708855
1274	232.5	5.9	779	5	EX082553	EX082553	1347	230.5	5.8	707	4	BJ711151	BJ711151
1275	232.5	5.9	792	7	CF270725	AGENCYCOURT	1348	230.5	5.8	707	4	BJ713645	BJ713645
1276	232.5	5.9	821	7	CN758375	ID0AAA22A	1349	230.5	5.8	707	4	BJ713772	BJ713772
1277	232.5	5.9	824	5	BU489024	604126211	1350	230.5	5.8	707	4	BJ713836	BJ713836
1278	232.5	5.9	854	5	BU417063	603671230	1351	230.5	5.8	707	4	BJ713851	BJ713851
Q1279	232.5	5.9	912	7	CF375008	AGENCYCOURT	1352	230.5	5.8	707	4	BJ714430	BJ714430
1280	232.5	5.9	915	7	CK416684	AUF_IpInt	1353	230.5	5.8	708	4	BJ708894	BJ708894
1281	232.5	5.9	926	3	CR649141	Tetraodon	1354	230.5	5.8	708	4	BJ708974	BJ708974
1282	232.5	5.9	929	3	CR638742	Tetraodon	1355	230.5	5.8	708	4	BJ711651	BJ711651
1283	232.5	5.9	969	3	CNS09CY0	Single re	1356	230.5	5.8	709	4	BJ708560	BJ708560
1284	232.5	5.9	984	3	CNS08F60	Single re	1357	230.5	5.8	709	4	BJ713958	BJ713958
1285	232	5.9	614	6	CA330127	haa91b07.y	1358	230.5	5.8	709	4	BJ714247	BJ714247
1286	232	5.9	718	5	BU491697	604127982	1359	230.5	5.8	710	4	BJ708338	BJ708338
1287	232	5.9	730	4	EG142368	is62h02.y	1360	230.5	5.8	711	4	BJ708298	BJ708298
1288	232	5.9	767	5	EX084213	EX084213	1361	230.5	5.8	713	4	BJ710718	BJ710718
Q1289	232	5.9	768	4	BJ719858	AGENCYCOURT	1362	230.5	5.8	713	4	BJ713222	BJ713222
1290	232	5.9	774	7	CO935600	AGENCYCOURT	1363	230.5	5.8	730	5	EX261809	EX261809
Q1291	232	5.9	779	4	BJ716761	BJ716761	1364	230.5	5.8	739	5	EX261809	EX261809
1292	232	5.9	781	5	BU490303	604130876	1365	230.5	5.8	740	5	BU491763	BU491763
1293	232	5.9	831	7	CF577959	AGENCYCOURT	1366	230.5	5.8	752	7	CO924856	CO924856
1294	232	5.9	912	7	CF581342	AGENCYCOURT	1367	230.5	5.8	766	7	CO924856	CO924856
1295	232	5.9	981	3	CNS092N7	Single re	1368	230.5	5.8	800	5	BU490078	BU490078
1296	232	5.9	983	3	CF587272	AGENCYCOURT	1369	230.5	5.8	804	5	BU489089	BU489089
1297	231.5	5.9	731	5	EX264456	EX264456	1370	230.5	5.8	817	5	BU487270	BU487270
1298	231.5	5.9	754	5	BU416465	603671427	1371	230.5	5.8	822	5	BU487088	BU487088
1299	231.5	5.9	769	4	CA384091	664487 NC	1372	230.5	5.8	822	5	BU416609	BU416609
1300	231.5	5.9	769	5	BU487648	604125581	1373	230.5	5.8	847	5	BU416609	BU416609
1301	231.5	5.9	773	4	BJ714981	BJ714981	1374	230.5	5.8	859	5	BU416746	BU416746
1302	231.5	5.9	773	4	BJ714981	BJ714981	1375	230.5	5.8	911	3	CNS08SQV	CNS08SQV
1303	231.5	5.9	774	5	EX083929	EX083929	1376	230.5	5.8	914	7	CK407280	CK407280
Q1304	231.5	5.9	776	5	BM378954	BM378954	1377	230.5	5.8	945	3	CNS090YX	CNS090YX
1305	231.5	5.9	778	4	BJ715008	BJ715008	1378	230.5	5.8	945	3	CNS090YX	CNS090YX
1306	231.5	5.9	779	4	BJ715139	BJ715139	1379	230.5	5.8	946	7	CF580421	CF580421
Q1307	231.5	5.9	791	6	CD494377	CD494377	1380	230.5	5.8	955	3	CNS09Q7K	CNS09Q7K
1308	231.5	5.9	810	5	BU417231	603671259	1381	230.5	5.8	966	4	BJ502595	BJ502595
1309	231.5	5.9	857	7	CN331197	AGENCYCOURT	1382	230	5.8	704	4	BJ720127	BJ720127
1310	231.5	5.9	871	3	CNS09J0L	Single re	1383	230	5.8	720	4	BJ722245	BJ722245
1311	231.5	5.9	897	7	CK408034	AGENCYCOURT	1384	230	5.8	734	5	BM441827	BM441827
1312	231.5	5.9	916	7	CK406443	AUF_Iflvr	1385	230	5.8	734	5	BM441827	BM441827
1313	231.5	5.9	924	3	CNS09KAG	Single re	1386	230	5.8	746	4	BJ722650	BJ722650
1314	231.5	5.9	941	3	CNS08QZ2	Single re	1387	230	5.8	750	4	BJ725876	BJ725876
1315	231.5	5.9	1539	3	CR725733	Tetraodon	1388	230	5.8	751	4	BJ717470	BJ717470
1316	231	5.9	675	5	BM327101	BM327101	1389	230	5.8	754	4	BJ722243	BJ722243
1317	231	5.9	737	4	BJ710889	BJ710889	1390	230	5.8	755	4	BJ722598	BJ722598
1318	231	5.9	738	4	BJ710881	BJ710881	1391	230	5.8	756	4	BJ724115	BJ724115
1319	231	5.9	740	4	BJ707972	BJ707972	1392	230	5.8	757	4	BJ723154	BJ723154
1320	231	5.9	740	4	BJ708681	BJ708681	1393	230	5.8	759	5	BM427883	BM427883
1321	231	5.9	741	4	BJ709131	BJ709131	1394	230	5.8	765	4	BJ716105	BJ716105
1322	231	5.9	742	4	BJ709994	BJ709994	1395	230	5.8	765	4	BJ723675	BJ723675
1323	231	5.9	756	5	EX072958	EX072958	1396	230	5.8	766	4	BJ717821	BJ717821

C1397	230	5.8	766	4	BJ724646	BJ724646	BJ724646	1470	229	5.8	769	5	BU489923	604131753
C1398	230	5.8	766	4	BJ726594	BJ726594	BJ726594	1471	229	5.8	785	5	BU492931	603972510
C1399	230	5.8	773	4	BJ718339	BJ718339	BJ718339	1472	229	5.8	805	5	BU488819	604126315
1400	230	5.8	777	5	BU488575	604126425	BU488575	1473	229	5.8	815	5	BU474411	60704411
C1401	230	5.8	779	4	BJ720882	BJ720882	BJ720882	1474	229	5.8	819	5	BU488246	603972114
1402	230	5.8	780	7	CV180969	ta166c02.	CV180969	1475	229	5.8	832	5	BU488645	604126615
C1403	230	5.8	781	4	BJ721886	BJ721886	BJ721886	1476	229	5.8	856	5	BU417033	603671642
C1404	230	5.8	781	4	BJ724145	BJ724145	BJ724145	1477	229	5.8	886	6	BY707818	BY707818
C1405	230	5.8	782	4	BJ720619	BJ720619	BJ720619	1478	229	5.8	892	7	CF583919	CF583919
C1406	230	5.8	784	4	BJ719077	BJ719077	BJ719077	1479	229	5.8	920	7	CF581252	AGNSCOURT
1407	230	5.8	787	5	BM052636	BM052636	BM052636	1480	229	5.8	948	7	CF580501	AGNSCOURT
1408	230	5.8	862	5	BM078364	BM078364	BM078364	1481	229	5.8	1167	6	CD505685	CD505685
C1409	230	5.8	862	7	CF578104	AGNSCOURT	CF578104	1482	229	5.8	1258	6	CD505711	CD505711
1410	230	5.8	869	3	CR654860	Tetraodon	CR654860	1483	229	5.8	1917	9	AY400075	AY400075
1411	230	5.8	875	3	CR656008	Tetraodon	CR656008	1484	228.5	5.8	698	6	CA384684	CA384684
1412	230	5.8	877	3	CR656219	Tetraodon	CR656219	1485	228.5	5.8	717	7	CV514474	CV514474
1413	230	5.8	885	3	CR637306	Tetraodon	CR637306	1486	228.5	5.8	725	4	BJ719060	BJ719060
1414	230	5.8	885	3	CR639406	Tetraodon	CR639406	1487	228.5	5.8	737	5	EX076672	EX076672
1415	230	5.8	890	3	CR648278	Tetraodon	CR648278	1488	228.5	5.8	759	5	EX074459	EX074459
1416	230	5.8	891	3	CR642487	Tetraodon	CR642487	1489	228.5	5.8	765	5	BM502043	BM502043
1417	230	5.8	891	3	CR651505	Tetraodon	CR651505	1490	228.5	5.8	765	5	EX079152	EX079152
1418	230	5.8	895	3	CR637212	Tetraodon	CR637212	1491	228.5	5.8	767	7	CK142895	CK142895
1419	230	5.8	895	3	CR643996	Tetraodon	CR643996	1492	228.5	5.8	816	6	CA363014	CA363014
1420	230	5.8	896	3	CR641041	Tetraodon	CR641041	1493	228.5	5.8	821	3	CNS09DMH	CNS09DMH
1421	230	5.8	896	3	CR643450	Tetraodon	CR643450	1494	228.5	5.8	821	3	CNS09DZO	CNS09DZO
1422	230	5.8	902	3	CR640950	Tetraodon	CR640950	1495	228.5	5.8	825	7	CNS23091	CNS23091
1423	230	5.8	903	3	CR636383	Tetraodon	CR636383	1496	228.5	5.8	835	6	CD503391	CD503391
1424	230	5.8	904	3	CR643834	Tetraodon	CR643834	1497	228.5	5.8	847	7	CNS331424	CNS331424
1425	230	5.8	906	3	CR655428	Tetraodon	CR655428	1498	228.5	5.8	849	5	EX078383	EX078383
1426	230	5.8	907	3	CR640257	Tetraodon	CR640257	1499	228.5	5.8	851	7	CNS28087	CNS28087
1427	230	5.8	907	3	CR644595	Tetraodon	CR644595	1500	228.5	5.8	857	5	EX078781	EX078781
1428	230	5.8	907	3	CR648453	Tetraodon	CR648453							
1429	230	5.8	909	3	CR643119	Tetraodon	CR643119							
1430	230	5.8	910	3	CR655271	Tetraodon	CR655271							
1431	230	5.8	911	3	CR634729	Tetraodon	CR634729							
1432	230	5.8	911	3	CR636801	Tetraodon	CR636801							
1433	230	5.8	912	3	CR643658	Tetraodon	CR643658							
1434	230	5.8	925	5	BQ228286	AGNSCOURT	BQ228286							
1435	230	5.8	930	7	CNS017567	AGNSCOURT	CNS017567							
1436	230	5.8	958	7	CF581199	AGNSCOURT	CF581199							
1437	230	5.8	966	3	CNS09EUG	Single re	EX055316							
1438	230	5.8	1170	3	CR647251	Tetraodon	CR647251							
1439	229.5	5.8	695	5	BU487609	604127783	BU487609							
C1440	229.5	5.8	708	7	CO039157	UT-M-ALL	CO039157							
C1441	229.5	5.8	720	7	CK175862	EST765182	CK175862							
C1442	229.5	5.8	720	7	CV482430	AGNSCOURT	CV482430							
C1443	229.5	5.8	725	7	CK173410	EST762730	CK173410							
1444	229.5	5.8	727	5	BU482926	604131325	BU482926							
C1445	229.5	5.8	728	4	CV286212	ta154e05.	CV286212							
C1446	229.5	5.8	743	4	BJ722376	BJ722376	BJ722376							
1447	229.5	5.8	745	5	EX082188	EX082188	EX082188							
1448	229.5	5.8	757	5	EX082187	EX082187	EX082187							
1449	229.5	5.8	762	6	CA346591	677514 NC	CA346591							
C1450	229.5	5.8	781	5	BM407764	BM407764	BM407764							
1451	229.5	5.8	786	5	BU417143	603671493	BU417143							
C1452	229.5	5.8	794	6	CD493976	CD493976	CD493976							
1453	229.5	5.8	801	5	EX076450	EX076450	EX076450							
1454	229.5	5.8	804	5	EX084332	EX084332	EX084332							
1455	229.5	5.8	805	5	EX078419	EX078419	EX078419							
1456	229.5	5.8	818	5	BU417349	603670957	BU417349							
1457	229.5	5.8	820	5	EX076451	EX076451	EX076451							
1458	229.5	5.8	827	7	CO957859	AGNSCOURT	CO957859							
1459	229.5	5.8	841	5	BU490897	603972517	BU490897							
1460	229.5	5.8	892	7	CF581454	AGNSCOURT	CF581454							
C1461	229.5	5.8	901	7	CK186284	EST775599	CK186284							
1462	229.5	5.8	920	3	CNS09608	Single re	EX044328							
1463	229.5	5.8	946	3	CNS018454	AGNSCOURT	CNS018454							
1464	229.5	5.8	952	3	CNS09PEA	Single re	EX068990							
1465	229.5	5.8	975	3	CNS09CUN	Single re	EX052731							
1466	229	5.8	670	7	CK686546	ZF101-P00	CK686546							
C1467	229	5.8	707	4	BJ725706	BJ725706	BJ725706							
1468	229	5.8	730	4	BJ713520	BJ713520	BJ713520							
1469	229	5.8	742	5	EX083323	EX083323	EX083323							

RESULTS

RESULT 1
HSM806734

LOCUS
Homo sapiens mRNA; cDNA DKFZp686N24154 (from clone DKFZp686N24154).

DEFINITION
Homo sapiens mRNA; cDNA DKFZp686N24154 (from clone DKFZp686N24154).

ACCESSION
BX640676.1

VERSION
BX640676.1

KEYWORDS
Homo sapiens (human)

SOURCE
Homo sapiens

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 3165)
Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS
Fobo, G., Han, M. and Wiemann, S.

CONSRMT
The German cDNA Consortium

TITLE
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764

JOURNAL
Neuberberg, GERMANY

COMMENT
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the
Heinrich-Heine-University, Dueseldorf/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp686N24154) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686N24154
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES
Location/Qualifiers
1..3165
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="RZPD:DKFZp686N24154Q"
/db_xref="taxon:9606"
/clone="DKFZp686N24154"
/tissue_type="colon endothel, primary cell culture"
/clone_lib="686 (synonym: hlcc3). Vector psportl_sfi; host


```

DH10B; sites SfiIIA + SfiIIB"
/dev_stage="adult"
/notes="hypothetical protein"
1. .3165
/gene="DKFZp686N24154"
447. 2609
/gene="DKFZp686N24154"
/codon_start=1
/product="hypothetical protein"
/protein_id="CAE45808.1"
/db_xref="GI:34364726"
/db_xref="UniProt/TREMBL:Q6N062"
/translation="MELGCTWQLGLTFLLQLLLLSLPREYTVINEACPAENWIMCRE
CEYDQIECVCPKREVVGTYTPCCRNEENECDSLIHPGCTIFENKSCRNNGGT
LDDFYKGYCAECAGWYGGMRQGVQLRAPKGQILLESYPLNAHCETTHAKPGF
VTQLRFLMSLDFDYCYDVEVDRDNRDQIIRKVCNERPAPIOSIGSSLHLVF
HSDGKNFGFTHAIYBEITACSSPCFHDGTCVLDKAGSYKCACLAGYTGRCENLLE
ENCSDPGGPVNGYOKITGGPGLINGRHAKIGTVVSFFCNNSYVLSSGNEKRTCCQNGE
WSGKQPICIKACREPKISDLVRRVLPMQVQSRFPLHQLYSAATSKOKLOSAPTKKP
ALPFGDLPMGYQHLHTLOLEYECISPFYRLGLSSRRKTLRTGWSGRAPSCVPIGKIE
NITAPKTOGLRPMQAAIYRTSGVHDSLRKGMFLVCSGALVNERTVVAACHVTD
LGKVTMIKTADLVKLVKGFYRDDRDDEKTIQSLRISAIILHPNYPDPLDADIALKL
LQKARTSTRVQPICLAASRDLSFOESHIIVAGWNVLDVRSPPGFKNIDLRSGVVSFV
VDSLLCEOEHDHGIPIVSVTDNMFCAWSEPTAPSDICTAEAGGIAAASFPGRASPEPR
WHLMLGLVSYSDKTCSHRLSTAFATKVLFPKDIERNMK"
ORIGIN
```

```

Alignment Scores:
Pred. No.: 0 Length: 3165
Score: 3936.00 Matches: 718
Percent Similarity: 99.86% Conservative: 1
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 99.77% Indels: 0
DB: 3 Gaps: 0

US-10-063-692-38 (1-720) x HSM806734 (1-3165)

QY 1 MetGluLeuGlyCysTrpThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuSer 20
Db 447 ATGGAGCTGGGTTCGTGGAGCGAGTGGGGCTCACTTTCTTCAGCTCCTTCATCTCG 506
QY 21 SerLeuProArgGluThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40
Db 507 TCCTTCGCAAGAGAGTACACAGTCATTATATGAAGCTGCCCTGAGCAGAGTGGAATATC 566
QY 41 MetCysArgGluCysCysGluThrYAspGlnIleGluCysValCysProGlyLysArgGlu 60
Db 567 ATGTGTCGGGAGTGTGTGAATATGATCATGATTGAGTGGCTCTGCCCGGAAAGAGGAA 626
QY 61 ValValGlyThrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
Db 627 GTCTGGGTATACCATCCCTTCCTGTCAGGAATGAGGAAATGAGTGTGACTCCTGCCTG 686
QY 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100
Db 687 ATCCACCCAGGTGTACCATCTTTTGAAAACCTGCAAGAGCTGCCGAAATGGCTCATGGGG 746
QY 101 GlyThrLeuAspAspPheThrValLysGlyPheThrCysAlaGluCysArgAlaGlyTrp 120
Db 747 GGTACCTTGGATTCATATGATGAGGGGTTCCTACTGTGCAGAGTGCAGAGCAGGCTGG 806
QY 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu 140
Db 807 TACGGAGGAGACTGCATCGCATGTGGCCAGGTTCTGCGAGCCCCCAAGGGTCAGATTTTG 866
QY 141 LeuGluSerTyrProLeuAsnAlaHisCysGluTrpThrIleHisAlaLysProGlyPhe 160
Db 867 TTGGAAAGCTATCCCTTAAATGCTCACTGTGAATGGHCCATTATGCTAAACCTGGGTTT 926
QY 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp 180
Db 927 GTCATCAACTAAGATTTTGTCATGTTGAGCCTTGAGCTTGAGTTGACTACATGTGCCAGTATGAC 986
```

```

181 TyrValGluValArgAspGlyAspAenArgAspGlyGlnIleIleLysArgValCysGly 200
Db 987 TATGTTGAGTTCGTGATGGAGAACCCGCGATGCCAGATCATCAAGGCTGCTCTGTGGC 1046
QY 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220
Db 1047 AAGGAGCGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCCAGCTCCTCTTCCACTCC 1106
QY 221 AspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer 240
Db 1107 GATGGCTCCAGAAATTTTGACGGTTTCCATGTCATTTATGAGGAGATCAGCATGCTCC 1166
QY 241 SerSerProCysPheHisaspGlyThrCysValLeuAspLysAlaGlySerTyrLysCys 260
Db 1167 TCATCCCTTGTTTCATGACCGCACGTCGCTCCTTGACAGCTGGATCTTACAAGTGT 1226
QY 261 AlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuLeuGluGluArgAsnCys 280
Db 1227 GCCTGCTGGCAGGCTATATCTGGCGAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGC 1286
QY 281 SerAspProGlyGlyProValAsnGlyTyrGlnLysIleThrGlyGlyProGlyLeuIle 300
Db 1287 TCAGACCCCTGGGGGCCCACTCAATGGGTACCAAGAAATAACAGGGGGGCTGGGGCTTATC 1346
QY 301 AsnGlyArgHisAlaLysIleGlyThrValValSerPhePheCysAsnAsnSerTyrVal 320
Db 1347 AACGGAGCGCATCTTAAATTTGGCACCGTGGTGTCTTCTTTTGTAACTCCTATGTT 1406
QY 321 LeuSerGlyAsnGluLysArgThrCysGlnGlnAsnGlyGluTrpSerGlyLysGlnPro 340
Db 1407 CTTAGTGGCAATGAGAAAAGAACTTGCACAGCAGAGATGGAGTGGTCAGGGAACAGCCC 1466
QY 341 IleCysIleLysAlaCysArgGluProLysIleSerAspLeuValArgArgValLeu 360
Db 1467 ATCTGCATAAAAGCCCTGCCGAGAACCAAGATTTTCAGACCTGGTGAGAGGAGAGTCTT 1526
QY 361 ProMetGlnValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSer 380
Db 1527 CCGATGCAGTTCAGTCAAGGGAGACACCATTTACACAGCTATATCTCAGGGGCTTCAGC 1586
QY 381 LysGlnLysLeuGlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuPro 400
Db 1587 AAGCAGAAACTGCAGAGTGCCTTACCAAGAAAGCCAGCCCTTCCCTTTGGAGATCTGCC 1646
QY 401 MetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysLysSerProPheTyrArg 420
Db 1647 ATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGTGACATCTCACCTTCTACCC 1706
QY 421 ArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTrpSerGlyArgAlaPro 440
Db 1707 CGCTGGGAGCAGCAGGAGGACATGCTTGAGGACTGGGAAGTGGAGTGGCGGGCAGCCA 1766
QY 441 SerCysIleProIleCysGlyLysIleGluAsnIleThrAlaProLysThrGlnGlyLeu 460
Db 1767 TCCTGCATCCCTATCTCGCGGAAAAATTGAGAACATCACTGCTCCAAAGACCCCAAGGGT 1826
QY 461 ArgTrpProTrpGlnAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeu 480
Db 1827 CGTGGCCGCTGGCAGCAGCCATCTACAGAGAGACCAGCGGGGTGATGACGAGCAGCCTA 1886
QY 481 HisLysGlyValAlaTrpPheLeuValCysSerGlyValAlaLeuValAsnGluArgThrVal 500
Db 1887 CACNAGGGAGCGTGGTTCCTAGTCTGACGGGTGCCCTGGTGAATGAGCGCACTGTGGTG 1946
QY 501 ValAlaAlaHisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeu 520
Db 1947 GTGGCTGCCCATCTGTACTGACCTGGGGAAGTCAACATGATCAAGACAGCAGACCTG 2006
QY 521 LysValValLeuGlyLysPheTyrArgAspAspArgAspGluLysThrIleGlnSer 540
Db 2007 AAAGTTGTTTGGGGAATTTCTACCGGGATGATGACCGGGATGAGAGACCATCCAGAGC 2066
QY 541 LeuGlnIleSerAlaIleIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAsp 560
```


Db 2067 CTACGATTCTCTCTATCATCTTGCATCCCACTATGACCCCATCTCTGCTTGTGATCTGC 2126
QY 561 IleAlaileLeuLysLeuLeuAspLysAlaAArgileSerThrArgValGlnProIleCys 580
Db 2127 ATGCCATCTGAAGCTCTAGACAGGCCGCTATCAGCACCCGAGTCCAGCCCATCTGC 2186
QY 581 LeuAlaAAserArgAspLeuSerThrSerPheGlnGluSerHisIleThrValAlaGly 600
Db 2187 CTGCGTCCAGTCGGATCTTCAGCACTTCTTCCAGAGTCCCACTCATCTGCTGGCTGGC 2246
QY 601 TrpAsnValLeuAlaAspValArgSerProGlyPheIleAsnAspThrLeuArgSerGly 620
Db 2247 TGGATGTCTGCGACAGTGGAGGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGG 2306
QY 621 ValValSerValValAspSerLeuLeuCysGluGluGlnHisGluAspHisGlyIlePro 640
Db 2307 GTGGTCAGTGTGGTGCAGTCTGCTGTGTGAGGAGCAGCATGAGGACCATGCCATCCCA 2366
QY 641 ValSerValThrAspAsnMetPheCysAlaSerTirpGluProThrAlaProSerAspIle 660
Db 2367 GTGAGTGTCTACTATACATGTTCTGTGCGAGCTGGGAACCCACTGCCCTTCTGATATC 2426
QY 661 CysThrAlaGluThrGlyIleAlaAlaValSerPheProGlyArgAlaSerProGlu 680
Db 2427 TGCACTGCAGAGCAGGAGCATCGCGCTGTGTCTTCCGGGAGCAGCATCTCTGAG 2486
QY 681 ProArgTirpHisLeuMetGlyLeuValSerTirpSerTirpAspLysThrCysSerHisArg 700
Db 2487 CCACGCTGGCACTGATGGAGCTGTGCTGAGCTGAGTATGATTAACATGAGCACCACAGG 2546
QY 701 LeuSerThrAlaPheThrLysValLeuProPheLysAspTirpIleGluArgAsnMetLys 720
Db 2547 CTCTCCACTGCCCTTCCACCAAGGTGCTGCTTTTAAAGACTGGATTGAAAGAAATATGAAA 2606
RESULT 2
AF370388
LOCUS Homo sapiens FP938 mRNA, complete cds. linear HTC 31-DEC-2003
DEFINITION
ACCESSION AF370388
VERSION AF370388.1 GI:33341705
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Huang, Y., Zhou, X.M., Zhang, P.P., Jiang, H.Q., Qin, W.X., Zhao, X.T.,
Wan, D.F., and Gu, J.R.
TITLE Novel human cDNA clones with function of inhibiting cancer cell
growth
JOURNAL Unpublished
REFERENCE
AUTHORS Qin, W.X., Wan, D.F., Zhou, X.M., Zhang, P.P., Jiang, H.Q., Huang, Y.,
Zhao, X.T., and Gu, J.R.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2001) National Laboratory for Oncogenes & Related
Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie-Tu Road, Shanghai
200032, P. R. China
FEATURES
source Location/Qualifiers
1..2650
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
845..2098
/codon_start=1
/product="FP938"
/protein_id="AAQ15224.1"
/db_xref="GI:33341706"
/translation="MLKAPMCISFVTTWFLVAMEKELASRMERWSKQICIKACR
EPKISLVRRLVPMQVQSRETFPLHLYSNAFSKQLQSAPTKKPAFPGLDPMGYQH
LHTQLQECISPPYRLGSSRRKTLRTGKWSRAPSCIPICIKENITAPKTQGLRWP
WQAAIYRTSGVDGSLHKGAWFLVCSGALVNERTVVAHCVTDLIGKVTMIKTADLK

ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 2650
Score: 3813.00 Matches: 697
Percent Similarity: 99.86% Conservative: 0
Best Local Similarity: 99.86% Mismatches: 0
Query Match: 96.65% Indels: 1
DB: 3 Gaps: 0
US-10-063-692-38 (1-720) x AF370388 (1-2650)
QY 24 ArgGluTyrThrValIleAsnGluAlaCysProGlyValaGluTirpAsnIleMetCysArg 43
Db 4 AGAGGTACACAGTCATTAAATGAGCTGCTCCCTGGAGCAGAGTGGAAATATCATGTGTCGG 63
QY 44 GluCysCysGluTyrAspGlnIleGluCysValCysProGlyLysArgGluValValGly 63
Db 64 GAGTGTGTGAATATGATCAGATTGAGTGGCTGCTCCCGGAAAGAGGAGTGTGGGT 123
QY 64 TyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeuIleHisPro 83
Db 124 TATACCATCCCTTGTGTCAGGAATGAGGAGAAATGAGTGTGACTCTCTCCCTGTATCCACCA 183
QY 84 GlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTirpGlyGlyThrLeu 103
Db 184 GGTGTGATACCATCTTTGAAATGCAAGAGCTGCGGAAATGGCTCATGGGGGGGTACCTTG 243
QY 104 AspAspPheTyrValLysGlyPheTyrCysAlaGluCysArgAlaGlyTirpTyrGlyGly 123
Db 244 GATGACTTCTATGTGAGGGGTTCTACTGTGCAGAGTGCAGAGGCTGGTACGAGGA 303
QY 124 AspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeuLeuGluSer 143
Db 304 GACTGCATCGATGTGGCAGGTTCTGCGAGGCCCAAGGGTTCAGATTTTGTGGAAAGC 363
QY 144 TyrProLeuAsnAlaHisCysGluTirpThrIleHisAlaLysProGlyPheValIleGln 163
Db 364 TATCCCTAAATGCTCAGTGTGAATGACCATTCATGCTAAACCTGGTTGTATCCAA 423
QY 164 LeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAspTyrValGlu 183
Db 424 CTAAGATTGTCTATGTTGAGCTGGAGTTTGACTACATGTGCCAGTATGACTATGTAG 483
QY 184 ValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGlyAsnGluArg 203
Db 484 GTTCGTGATGAGAGACAACCGCATGGCCAGATCATCAAGCGTGTCTGTGCAACGAGCGG 543
QY 204 ProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSerAspGlySer 223
Db 544 CAGGCTCTTATCAGAGCATAGATGCTCCTCCTCCAGCTCTCTTTCACCTCCGATGCTCC 603
QY 224 LysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSerSerPro 243
Db 604 AGAATTTTGAAGTTTCCATGCCATTATGAGGAGATCAGCAGCATGCTCTCATCCCT 663
QY 244 CysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCysAlaCysLeu 263
Db 664 TGTTCATGACGCGCAGTGGCTCTTGTACAAGGCTGGATCTTACAAGTGTGCTGCTG 723
QY 264 AlaGlyTyrThrGlyGlnArgCysGluAsnLeuLeuGluArgAsnCysSerAspPro 283
Db 724 GCAGGCTATACTGGGCGCGCTGTGAAATCTCTTTGAAGAAGAACTGCTCAGACCT 783
QY 284 GlyGlyProValAsnGlyTyrGlnLysIleThrGlyGlyProGlyLeuIleAsnGlyArg 303
Db 784 GGGGGCCCAAGTCAATGGGTACCAAAAATTAACAGGGGGCCCTGGGGCTTATCAACGAGCG 843
QY 304 HisAlaLysIleGlyThrValValSerPhePheCysAsnAsnSerTyrValLeuSerGly 323

Db 844 CATGCTAAATTTGGCACCGTGGTGTCTTCTTTGTAAACAATCTCTATGTC 903
QY 324 AenGluLysArgThrCysGlnGlnAenGlyGlu-TrpSerGlyLysGlnProIleCysI 343
Db 904 AATGAGAAAAGAACTTGCAGCAGAAATGAGAGGTGGTTCAGGAGAAACAGCCCATCTGCAT 963
QY 343 elysAlaCysArgGluProIysIleSerAspIleValArgArgValLeuProMetG 363
Db 964 AAAGCCTCCGAGAACCAAGATTTTCAGACCTGGTGAGAGAGAGATCTTCCGATGCA 1023
QY 363 nValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSerLysGlnly 383
Db 1024 GGTTCAGTCAGGGAGACACCATACACAGCTATACTCAGCGGCTTCAGCAGCAGAA 1083
QY 383 sLeuGlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuProMetGlyTy 403
Db 1084 ACTGCAGAGTGGCCCTTACCAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGATA 1143
QY 403 rGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArgArgLeuGl 423
Db 1144 CCAACATCTGCATACCAGCTCCAGTATGAGTGATCTCACCCCTTCTACCGCGCGCTGGG 1203
QY 423 ySerSerArgArgThrCysLeuArgThrGlyLysTrpSerGlyValArgAlaProSerCysI 443
Db 1204 CAGCAGCAGAGACATCTGAGGACTGGAGTGGAGTGGCGGGCCACCATCTGTCAT 1263
QY 443 eProIleCysGlyLysIleGluAsnIleThrAlaProLysThrGlnGlyLeuArgTrpPr 463
Db 1264 CCCTATCTCGGGGAAATTTGAGAACTCACTGCTCCAAAGACCCAAAGGTTGCGCTGGGC 1323
QY 463 oTrpGlnAlaAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeuHisLysGl 483
Db 1324 GTGGCAGGAGCCATCTACAGGAGACCCAGCGGGTGCATGACGGCAGCTACACAGGG 1383
QY 483 yAlaTrpPheLeuValCysSerGlyAlaLeuValAenGluArgThrValValAlaAla 503
Db 1384 AGCGTGTTCTTACTGTCGACGGTGGCTGGTGAATGAGCGACACTGTGTGTGGCTGC 1443
QY 503 aHisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeuLysValVa 523
Db 1444 CCACCTGTGTACTGACCTGGGGAAGTTCACCATGATCAAGACAGCAGACCTGAAAGTTGT 1503
QY 523 lLeuGlyLysPheTyrArgAspAspArgAspGluLysThrIleGlnSerLeuGlnI 543
Db 1504 TTTGGGGAATTTCTACCGGGATGATACCGGGATGAGAGACCATCCAGAGCCTCAGAT 1563
QY 543 eSerAlaIleIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAspIleAla 563
Db 1564 TTCTGCTATCATTTCTGCATCCCACTATGACCCCATCTGCTGTGATGCTGACATCGCCAT 1623
QY 563 eLeuLysLeuLeuAspLysAlaArgIleSerThrArgValGlnProIleCysLeuAla 583
Db 1624 CCTGAAGCTCCTAGACAAAGCCCGTATCAGACCCCGAGTCCAGCCCATCTGCTCGCTGC 1683
QY 583 aSerArgAspLeuSerThrPheGlnGlnSerHisIleThrValAlaGlyTrpAsnVa 603
Db 1684 CAGTCGGGATCTCAGCAGCTTCTTCCAGGAGTCCCATCATCCTGCTGGCTGGGATGT 1743
QY 603 lLeuAlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSe 623
Db 1744 CTTGGCAGAGCTGAGGAGCCCTGGCTTCAGACGACGACATCGGCTCTGGGCTGTGCAG 1803
QY 623 rValValAspSerLeuLeuCysGluGlnGlnHisGluAspHisGlyIleProValSerVa 643
Db 1804 TGTGGTGGACTCGCTGCTGTGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1863
QY 643 lThrAspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAl 663
Db 1864 CACTGATAACATGTTCTGTGCCAGCTGGGAACCCAGCTGCCCTTCTGATATCTGCATCTGC 1923
QY 663 aGluThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTr 683

Db 1924 AGAGACAGGAGGCATCGGGCTGTGTCTCTCCGGGAGCAGCATCTCTCAGCACGCTG 1983
QY 683 phi.sleuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHisArgLeuSerTh 703
Db 1984 GCATCTGATGGGACTGGTCAGCTGAGCTATATAAACAATGAGCCAGCAGGCTCTCCAC 2043
QY 703 rAlaPheThrLysValLeuProPheLysAspTrpIleGluArgAsnMetLys 720
Db 2044 TGCCCTCCACCAAGGTGCTGCTTTTAAGACTGGATTGAAGAAATATGAA 2095
RESULT 3
AK088017
LOCUS
DEFINITION
Mus musculus 2 days neonate thymus cells cDNA, RIKEN
full-length enriched library, clone:8430002G05 product:hypothetical
EGF-like domain, CUB domain, Sushi domain / SCR repeat / CCP module
and Serine proteases, trypsin family domain containing protein,
full insert sequence.
AK088017
AK088017.1 GI:26352935
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Rodentia; Sciurognathi; Muridae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-Format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 695-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2746)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayaashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozawa, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC Building Adenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

Location/Qualifiers

FEATURES

source

1. .2746
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="FANTOM DB:E430002G05"
/db_xref="taxon:10090"
/clone="E430002G05"
/cell_type="thymic cells"
/tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="2 days neonate"
71. .2233

CDS

/note="unnamed protein product; hypothetical EGF-like
domain, CUB domain, Sushi domain / SCR repeat / CCP module
and Serine proteases, trypsin family domain containing
protein (InterPro|IPR000561, evidence: InterPro)
putative"
/codon_start=1
/protein_id="BAC40098.1"
/db_xref="GI:26352936"

/translation="MELDRWAQLGLVFLQLLLISLPREYTVINEAPCAEWNIMCRE
CEYDQIECLCPGKEVGYTIPCCRNEDNECDCLIHFGCTIFENCKSCRNSRGST
LDDFYKGYACACRAGWGGDMRCQGVLRASKQILLESYPLNAHCWTHIARPGP
IILQRFMLSLFDYMCQYDVEVRDGNDSPIIKRFGNERPAPIRFTSGSLHLVLF
HSDGKNDFGHAFVEETIACSSPFFHDGTCLLDTTGSFKACLAGYTGQRCELLE
ERNCDLGGPVNGYKKTIEGGLNHHVKIGTVVFFCNGSYVLSGNEKRKTCQNGE
WSGKQPCMKACREPKISDLVRRVLSMOVQSRPTLHOLYSTAFSKOLQDASTKKP
ALPFGDLPPGYOHLTVQVECI SPYRELGSRRCTLRGTGKWSGRAPSCI PCGKIE
STPSPKQTGRNFWQAAIYRRTSGVHDGSLHKGAFVLCSGALVNERTVVAACVTE
LGRKTIITADUKVGLKFRDDEKSIQNLRVSAIILHPNYDPIILDTIDIAVLK
LDKARISTRVQICLATTDLSTFSQESITVAGWNI LADVRSFGFNDLTHYGMVRV
VDPMLCEQHEHDGIPVSVTDNMFCASKDPSTPSDICTAETGTGIAALSPPGRASPEPR
WHLVGLVSNYSYDKTCSNGLSTAFKVLVLPKDWIERNMK"
2718. .2723
/note="putative"
2746
/note="putative"

polya_signal

polya_site

ORIGIN

Alignment Scores:

Pred. No.:	0	Length:	2746
Score:	3612.00	Matches:	649
Percent Similarity:	94.72%	Conservative:	33
Best Local Similarity:	90.14%	Mismatches:	38
Query Match:	91.56%	Indels:	0
DB:	3	Gaps:	0

US-10-063-692-38 (1-720) x AK088017 (1-2746)

QY	1	MetGluLeuGlyCysTrpThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuSer	20
DB	71	ATGGAGCTAGACAGATGGCGCGCGTGGTCTCTGCAGCTCTCTTCATCTCA	130
QY	21	SerLeuProArgGluTyrThrValIleAenGluAlaCysProGlyIleGluTrpAsnIle	40
DB	131	TCGTTGCCAAGAGAGTACACGGTCATTAAATGAAGCCTGTCGGAGCTGAGTGAACATC	190
QY	41	MetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysProGlyIleYsArgGlu	60
DB	191	ATGTGTAGAGATGTTGTGAATATGATCAGATGAATGCTCTGCCAGGAAGAGAA	250
QY	61	ValValGlyTyrThrIleProCysCysArgAenGluGluAenGluCysAspSerCysLeu	80
DB	251	GTGGTGGGTACACCATCCATCCATGTCAGGAATGAGGAATGAATGAATGCTCTCTCTA	310
QY	81	IleHisProGlyCysThrIlePheGluAenCysLysSerCysArgAenGlySerTrpGly	100
DB	311	ATTACCCCAAGTGTACCATCTTTGAAACTGCAAGAGCTGCGGCAATGGCTCTCTGGGC	370
QY	101	GlyThrLeuAspAspPheTyrValIysGlyPheTyrCysAlaGluCysArgAlaGlyTrp	120
DB	371	GGAACTCTGGATGACTTCTACGTGAAGGATTTCTACTGCGAGAGTGCAGGGCAGCTGG	430
QY	121	TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProIysGlyGlnIleLeu	140
DB	431	TACGGAGGAGACTGTCATGCGATGTGCGCAGGTTCTTCGAGCCTCAAAAGGTCAGATCTT	490
QY	141	LeuGluSerTyrProLeuAsnAlaHisCysGluTyrThrIleHisAlaIysProGlyPhe	160
DB	491	TTGGAGAGCTATCCCTTAAACGCTCCTGTGAATGGACTATTTCATCCAGAGCTGGGTT	550
QY	161	ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp	180
DB	551	ATCATCCAGTTGAGGTTTGGTATGTGAGCTAGAGCTTAGATGATCATGTCGCATATGAC	610
QY	181	TyrValGluValArgAspGlyAspAenArgAspGlyGlnIleIleIysArgValCysGly	200
DB	611	TACGTGGAGTCCGCGATGGGATAAATAGTAGACAGCCCTATCATCAAGCTTTCTCTGGC	670
QY	201	AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer	220
DB	671	AACGAGAGCCAGCTCCCATCAGGAGCACTGGCTCTTCACTCCATGTCCTTTTCCATTCT	730
QY	221	AspGlySerLysAenPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer	240
DB	731	GATGCTCCAGAACTTCATGCTTCCAGCTTCCAGCTTCTTTGAGAGATCAAGCTGCTCC	790
QY	241	SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCys	260
DB	791	TCATCCCTTTGTTTCCATGTCGACATGCTCTTGCACACCATGGCTCTTCAAGTGT	850
QY	261	AlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAenLeuGluGluArgAenCys	280
DB	851	GCCTCCCTGGCTGGCTTACATGGGAGCGCTGTGAAATCTACTTTGAAGAAAGAACTGC	910
QY	281	SerAspProGlyGlyProValAenGlyTyrGlnIleValIleThrGlyGlyProGlyLeuIle	300
DB	911	TCAGACCTTGGGGGCCAGTCAATGGGTACAGAAATACAGAGGCTCTGGAGCTTCTC	970
QY	301	AsnGlyArgHisAlaIleGlyThrValValSerPhePheCysAenAenSerTyrVal	320
DB	971	AATGAGCACCATGTAAATAATTGGCACGGTTGTCTTTCTTTTAAACGGCTCATACGTT	1030
QY	321	LeuSerGlyAenGluIleArgThrCysGlnGlnAenGlyGluTrpSerGlyLysGlnPro	340
DB	1031	CTGAGTGGCAATGAGAAACGAACTTGGCAGCAGAAATGGAGAGTGGTTCAGAAAGCACT	1090
QY	341	IleCysIleLeuAlaCysArgGluProIysIleSerAspLeuValArgArgValLeu	360
DB	1091	GTCTGCATGAAAGCCTGCCGGAACCGAAGATCTCAGACCTGTCGAGAGGAGAGTCTT	1150
QY	361	ProMetGlnValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSer	380

```
Db      1151 TCATGTCAGGTTTCAGTCAAGGAGGAGACCATATACATCAGCTTATTCACGCGCTTCAGC 1210
Qy      381 LysGlnLysLeuGlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuPro 400
Db      1211 AAGCAGMAATTGCAGGATGCTCTACCAAAAGCCAGCCCTTCATTTGGAGACCTGGCC 1270
Qy      401 MetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArg 420
Db      1271 CTTGGATACCAACATCTGCACACCCCAAGTCCAGTAGTGCATCTCGCCCTTCTACCGC 1330
Qy      421 ArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTrpSerGlyArgAlaPro 440
Db      1331 CCGCTGGGAAGCAGCAGGAGGACATGCTTGAGACTGGGAAGTGGAGTGGGGGGCCCG 1390
Qy      441 SerCysIleProIleCysGlyLysIleGluAsnIleThrAlaProLysThrGlnGlyLeu 460
Db      1391 TCTGTATCCCAATCTGTGGAAAATCGAGAGCACTCTCTCCAAAGACCCCAAGGCACC 1450
Qy      461 ArgTrpProTrpGlnAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeu 480
Db      1451 CGTGTGCCATGGCAGCAGCCCATCTACCGAGGACCAAGTGGTGTACACGATGGTGTCTG 1510
Qy      481 HisLysGlyValatTrpPheLeuValCysSerGlyAlaLeuValAsnGluArgThrValVal 500
Db      1511 CACAAGGTGCATGGTCTTGCTGCATGGTGGCCCTGGTGAATGAACGGACTGGTT 1570
Qy      501 ValAlaAlaHisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeu 520
Db      1571 GTGGCTGCCACTGTGTGACTGAGTGGGGAAGGCCACCATCATCAAGCAGCAGACCTC 1630
Qy      521 LysValValLeuGlyLysPheTyrArgAspAspAspAspAspGluLysThrIleGlnSer 540
Db      1631 AAGGTGTCTTGGGAAAATTTACAGGAGCCGATGATCGGAGTGAGAGGACATCCAGAAT 1690
Qy      541 LeuGlnIleSerAlaIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAsp 560
Db      1691 TTACGGGTTTCTGCTATCAATCTGCACCCCACTATGACCTTCTCTGTGACACTGAC 1750
Qy      561 IleAlaIleLeuLysLeuLeuAspLysAlaArgIleSerThrArgValGlnProIleCys 580
Db      1751 ATCGCTGTTCTGAAGCTCTAGACAAAGCTCGCATCAGTACCGTTCCTCAACCATCTGC 1810
Qy      581 LeuAlaAlaSerArgAspLeuSerThrSerPheGlnGluSerHisIleThrValAlaGly 600
Db      1811 CTGGCTACCACCTCGGACCTCAGCACCTCTTTCCAGGAATCCCAATCATCTGTGGCTGC 1870
Qy      601 TrpAsnValLeuAlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGly 620
Db      1871 TGGACATCTCTGCAGATGTGAGGAGCCCTGGCTTTAAGNATGATACCTTACATTTATGA 1930
Qy      621 ValValSerValValAspSerLeuCysGluGlnHisGluAspHisGlyIlePro 640
Db      1931 ATGTTTCAGAGTGTGTAGACCAATGCTTTGTGAGGAACAGCATGAAGACCATGCAATCCA 1990
Qy      641 ValSerValThrAspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIle 660
Db      1991 GTTAGTGTCACTGACACCAATGTTCTGTGCCAGCAAAAGATCCCAAGTACCCCTCTGACATC 2050
Qy      661 CysThrAlaGluThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGlu 680
Db      2051 TGCACCTGCAGAGACAGGGGGCATCGTGTCTTTGCTCTCCAGCCGAGCATCCCGAG 2110
Qy      681 ProArgTrpHisLeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHisArg 700
Db      2111 CCACGCTGGCATTTGGTGGGCTGGTGCAGCTGAGCTATGACAAGACATGTAGCAATGGC 2170
Qy      701 LeuSerThrAlaPheThrLysValLeuProPheIysAspTrpIleGluArgAsnMetLys 720
Db      2171 CTATCCACAGCCCTTCAAAAGGTGTTGCCGTTCAAGAGACTGGATTGAGAGAAACATGAAA 2230
```

RESULT 4
AY406074

```
LOCUS      AY406074                      2214 bp      DNA      linear      GSS 12-DEC-2003
DEFINITION Homo sapiens HCM2436 gene, VIRTUAL TRANSCRIPT, partial sequence,
             genomic survey sequence.
ACCESSION   AY406074
VERSION     AY406074.1  GI:39762048
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2214)
AUTHORS     Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
            Adams,M.D. and Cargill,M.
            Adams,M.D. and Cargill,M.
TITLE       Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL     Science 302 (5652), 1960-1963 (2003)
PUBMED     14671302
REFERENCE   2 (bases 1 to 2214)
AUTHORS     Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
            Adams,M.D. and Cargill,M.
            Adams,M.D. and Cargill,M.
TITLE       Direct Submission
JOURNAL     Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES    Location/Qualifiers
            source
            1..2214
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                <1..>2214
                /locus_tag="HCM2436"
            gene
            1..2214
            ORIGIN
            Alignment Scores:
            Pred. No.:      0      Length:      2214
            Score:          3489.50      Matches:      654
            Percent Similarity: 87.70%      Conservative: 2
            Best Local Similarity: 87.43%      Mismatches: 53
            Query Match:       88.45%      Indels:      39
            DB:                9      Gaps:        2
            US-10-063-692-38 (1-720) x AY406074 (1-2214)
            Qy      1 MetGluLeuGlyCysTrpThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuSer 20
            Db      1 ATGGAGCTGGTTCGTGGAGCGAGTTGGGGCTCACATTTTCTTCAGCTCTCTCATCTCG 60
            Qy      21 SerLeuProArgGluTyrThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40
            Db      61 TCTTCCCAAGAGAGTACACAGTCATTAAATGAAGCCTGCCCTGGAGCAGAGTGGAAATATC 120
            Qy      41 MetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysProGlyLysArgGlu 60
            Db      121 ATGTGTGGGAGTGTGTGAATATGATGATGATGAGTTCGCTCTGCCCGGAAAGAGGAA 180
            Qy      61 ValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
            Db      181 GTCTGGGTTTATACCATCCCTTGTCTCAGGAATGAGAGAAATGAGTGTGACTCTCTGCTG 240
            Qy      81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100
            Db      241 ATCCACCCAGGTGTGTACCATCTTTTGAATACTGCAAGAGCTGCCGAAATGGCTCATGGGG 300
            Qy      101 GlyThrLeuAspAspPheTyrValLysGlyPheTyrCysAlaGluCysArgAlaGlyTrp 120
            Db      301 GGTACCTTGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGCAGGAGCGCTGG 360
            Qy      121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu 140
```


JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 2214)
 AUTHORS Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
 Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES
 source
 1..2214
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 gene
 <1..>2214
 /locus_tag="HMC2436"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.25e-300 Length: 2214
 Score: 3211.50 Matches: 594
 Percent Similarity: 82.94% Conservative: 33
 Best Local Similarity: 78.57% Mismatches: 74
 Query Match: 81.41% Indels: 55
 DB: 9 Gaps: 3
 US-10-063-692-38 (1-720) x AY406076 (1-2214)
 QY 1 MetGluLeuGlyCysTrpThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuSer 20
 DB 1 ATGGAGCTAGACAGATGGCGCAGTTGGGGCTGGTGTCTCTGCAGCTCTCTCATCTCA 60
 QY 21 SerLeuProArgGluTyrThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40
 DB 61 TCGTTCGCCAAGAGAGTACAGGTCATTAATGAAGCTGTCCCGAGAGTGAAGTGAACATC 120
 QY 41 MetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysProGlyIysArgGlu 60
 DB 121 ATGTGTAGAGATGTTGTGAATATGATCAGATTGAATGCTCTGCCCAGGAAAGAGAA 180
 QY 61 ValValGlyTyrThrIleProCysCysArgAsnGluAsnGluCysAspSerCysLeu 80
 DB 181 GTGGTGGGTGTACACCATCCATGCTGCAGGAATGAGGATAATGAATGTGACTCCTGTCTA 240
 QY 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100
 DB 241 ATTCACCCAGGTGTGTACCATCTTTGAAACTGCAAGAGCTGCCGCAATGGCTCTCGGGC 300
 QY 101 GlyThrLeuAspAspPheTyrValIysGlyPheTyrCysAlaGluCysArgAlaGlyTrp 120
 DB 301 GGAACCTGGATGACTTCTACGTGAAGGGATTCTACTCGCAGAGTGCAGGGCAGGCTGG 360
 QY 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProIysGlyGlnIleLeu 140
 DB 361 TACCGAGGAGACTGCAATGCGATGTGCCAGGTTCTTCGAGCCCTCAAAGGGTCAATCTTG 420
 QY 141 LeuGluSerTyrProLeuAsnAlaHisCysGluTrpThrIleHisAlaIysProGlyPhe 160
 DB 421 TTGGAGAGCTATCCCTTAACCGTCACTGTGAATGGACTATTCATGCCAGCTCGGGTTT 480
 QY 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp 180
 DB 481 ATCATCCAGTTGAGGTTTGGTATGCTGAGCTAGAGTTTGAATGATGATGATGATGATG 540
 QY 181 TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleIleIysArgValCysGly 200
 DB 541 TATGTGAGGATCGCGATGGGATAATAGTGAAGCCCTATCATCAAGCCGTTCTTGTGGC 600
 QY 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220

DB 601 AACGAGAGGCCAGCTCCCATCAGGAGCACTGGCTCTTCACTCCATGTCTCTTTTCCATTCT 660
 QY 221 AspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer 240
 DB 661 GATGCTCCAAAGACTTCATGGCTTCACGCTGTCTTTTGAGGAGATACAGGCTGCTCC 720
 QY 241 SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCys 260
 DB 721 TCATCCCTTGTTCATGATGCACATGCCTCTTGACACCATGGGTCCTTCAAGTGT 780
 QY 261 AlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuGluGluArgAsnCys 280
 DB 781 GCCTGCTGGCTGGCTACACTGGCAGCGCTGTGAAAATCTTCTGAGGCTGGGAAGTGC 840
 QY 281 SerAspProGlyGlyProValAsnGlyTyrGlnIysIleThrGlyGlyProGlyLeuIle 300
 DB 841 AAG-----GTCAAGGTGGTG----- 855
 QY 301 AsnGlyArgHisAlaLysIleGlyThr----- 309
 DB 856 -----GCAGAGTTAGGCTCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 903
 QY 309 ----- 309
 DB 904 NNN 963
 QY 310 -----ValValSerPhePheCysAsnAsnSerTyrValLeuSerGlyAsn 324
 DB 964 NNN 1023
 QY 325 GluLysArgThrCysGlnGlnAsnGlyGluTrpSerGlyLysGlnProIleCysIleLys 344
 DB 1024 NNN 1083
 QY 345 AlaCysArgGluProIysIleSerAspLeuValArgArgValLeuProMetGlnVal 364
 DB 1084 NCCTGCGCGGAAACCGAAGATCTCAGACCTGGTGGTGAAGAGAGTCTCTTCGATGCAAGTT 1143
 QY 365 GlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSerLysGlnLysLeu 384
 DB 1144 CAGTCAAGGAGACACCATTCATCAGCTTTATTCACGCTTTTCAGCAAGCAGAAATTTG 1203
 QY 385 GlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuProMetGlyTyrGln 404
 DB 1204 CAGGATGCTCTACCAAAGCCAGCCCTTCCATTTGGAGACCTGCCCTCGATACCAA 1263
 QY 405 HisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArgArgLeuGlySer 424
 DB 1264 CATCTGCACACCAAGTCCAGTATGATGTCATCTCGCCCTTCTACCGCCGCTGGGAAGC 1323
 QY 425 SerArgArgThrCysLeuArgThrGlyLysTyrSerGlyValArgAlaProSerCysIlePro 444
 DB 1324 AGCAGAGGACATGCTCGAAGTGGGAAGTGGAGTGGGGGGCCCCCGTCTCTGTATCCCA 1383
 QY 445 IleCysGlyLysIleGluAsnIleThrAlaProLysThrGlnGlyLeuArgTrpProTrp 464
 DB 1384 ATCTGTGGAATAATCAGAGCACTCTCTCCAAAGACCCAGGACCCGCTGGCCATGG 1443
 QY 465 GlnAlaAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeuHisLysGlyAla 484
 DB 1444 CAGGACGACCATCTACCGGAGGACAGTGGTGTATACAGATGGTGTCTGCAAAAGGTGCA 1503
 QY 485 TrpPheLeuValCysSerGlyAlaLeuValAsnGluArgThrValValAlaAlaHis 504
 DB 1504 TGTGTTCTGTCTGCAAGTGGTCCCTCGGTAATGAACGAGCTGTGTGTGGCTGCCAC 1563
 QY 505 CysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeuLysValValLeu 524
 DB 1564 TGTGTGACTGAGCTGGGGAGGCCACCATCATCAAGACAGCAGACCTCAAGTTGTCTTG 1623
 QY 525 GlyLysPheTyrArgAspAspArgAspGluLysThrIleGlnSerLeuGlnIleSer 544
 DB 1624 GGAAAAATTTCTACAGGACGATGATCGGGATGAGAGAGCATCCAGAAATTTACGGGTTTCT 1683

6 (bases 1 to 2184)
REFERENCE
AUTHORS
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tonaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE
JOURNAL
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
FEATURES
 Location/Qualifiers
 1..2184
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM DB:5930437L24"
 /db_xref="taxon:10090"
 /clone="5930437L24"
 /tissue_type="forelimb"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="13 days embryo"
 misc_feature
 1..2184
 /notes="hypothetical EGF-like domain, CUB domain, Sushi domain / SCR repeat / CCP module and Serine proteases, trypsin family domain containing protein (InterPro|IPR00561, evidence: InterPro)"
ORIGIN
 Alignment Scores:
 Pred. No.: 5e-160 Length: 2184
 Score: 1766.00 Matches: 311
 Percent Similarity: 94.77% Conservative: 15
 Best Local Similarity: 90.41% Mismatches: 18
 Query Match: 44.77% Indels: 1
 DB: 3 Gaps: 0
 US-10-063-692-38 (1-720) x AK031254 (1-2184)
 QY 1 MetGluLeuGlyCysTrpThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuSer 20
 Db ATGGAGCTAGACAGATGGCGGAGTTGGGCTGGTCTCTGAGCTCTCTCTCACTCA 104
 QY 21 SerLeuProArgGluTrpThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40
 Db TCGTTGCCAAGAGAGTACACGGTCAATTAAGAGCTGTCCCGAGCTGAGTGAACATC 164
 QY 41 MetCysArgGluCysCysGluTrpAspGlnIleGluCysValCysProGlyIleArgGlu 60
 Db ATGTGTGAGAGAAATGTTGTGAATATGATCATGATGATGATGATGATGATGATGAT 224
 QY 61 ValValGlyTrpThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
 Db GTGGTGGGTACCACTCCATCTGCTGAGGATGAGGATGAGGATGAGGATGAGGATGAG 284

QY 81 IleHisProGlyCysThrIlePheGluAsnCysGlySerCysArgAsnGlySerTrpGly 100
 Db ATTCAACCCAGGTTGTACCATCTTTGAACATGCAAGAGCTGCGCAATGCTCTCTGGGC 344
 QY 101 GlyThrLeuAspAspPheTrpValIleGlyPheTrpCysAlaGluCysArgAlaGlyTrp 120
 Db GGAACCTCTGGATGACTTCTACGTGAAGGATTTCTATGCCAGAGTGTCAGGGCAGGCTGG 404
 QY 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProIleGlyGlnIleLeu 140
 Db TACGGAGGAGACTGTCATGCGATGCGCCAGTTCTTCGAGCCTC-AAGGGTCAGATCTTG 463
 QY 141 LeuGluSerTyrProLeuAsnAlaHisCysGluTrpThrIleHisAlaIleProGlyPhe 160
 Db TTGAGAGAGCTATCCCTTAAACGCTCACTGTGAATGAGCTATTATGTCAGACCTGGGTTT 523
 QY 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTrpAsp 180
 Db ATCATCCAGTTGAGGTTTGGTATGCTGAGCTTAGAGTTTGACTACATGTCCTTTTCCATTCT 583
 QY 181 TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleIleIleIleIleValCysGly 200
 Db TATGTGAGGTCGCGCATGGGATATAGTGACAGCCCTATCATCAAGCGTTTCTGTGGC 643
 QY 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220
 Db AACGAGAGGCCAGCTCCCATCAGGAGCACTGGGCTCTTCACTCCATGTCCTTTTCCATTCT 703
 QY 221 AspGlySerIleAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer 240
 Db GAAGGCTCCAGAACTTCGATGCTTCCAGCTTCTTTGAGGAGATGACAGGCTGTCTCC 763
 QY 241 SerSerProCysPheHisAspGlyThrCysValLeuAspIleValAlaGlySerTrpIleCys 260
 Db TCATCCCTTGTTCCTCATGTCGACATGCTCTTGGACCACTGGTCTTTTCAAGTGT 823
 QY 261 AlaCysLeuAlaGlyTrpThrGlyGlnArgCysGluAsnLeuGluGluArgAsnCys 280
 Db GCTGTGCTGGCTGGCTACACTGGGAGCGCTGTGAAATCTACTTGAAGAAAGAAATGTC 883
 QY 281 SerAspProGlyCysProValAsnGlyTyrGlnIleValIleThrGlyGlyProGlyLeuIle 300
 Db TCAGACTTGGGGGGCGGCGAGTCAATGGGTACAGAAATACAGAAAGTCTCTGAGCTTCTC 943
 QY 301 AsnGlyArgHisAlaIleGlyThrValValSerPhePheCysAsnAsnSerTrpVal 320
 Db AATGAGCGCCATGTAATAAATGGACGGTTGTCTCTTTTGTAAACGGCTCATAGCTT 1003
 QY 321 LeuSerGlyAsnGluIleArgThrCysGlnGlnAsnGlyGluTrpSerGlyIleGlnPro 340
 Db CTGAGTGGCAATGAGAAACGAACTTGCACAGAGATGAGAGTGGTTCAGGAAAGCAACCT 1063
 QY 341 IleCysIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 360
 Db GTCTGCATGAAA 1075
RESULT 8
 BX399905
 LOCUS
 DEFINITION
 BX399905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0D1086Y021 5-PRIME, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 1049)
 AUTHORS
 Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE
 Full-length cDNA libraries and normalization
 JOURNAL
 Unpublished (2001)
 COMMENT
 On May 13, 2003 this sequence version replaced gi:30622029.

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5757.r

For more information about this cluster, see <http://www.genoscope.cns.fr/cdna?s=CS0DI086AH1LOP1&c=5757.r>.

FEATURES

source

```

1. 1049
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cloned="CS0D108Y031"
/tissue_type="PLACENTA C
/clone_lib="Homo sapiens
/notes="1st strand cDNA w
primer. Five prime end e
digested with Not I and
sites of the pCMVSPORT 6

ORIGIN

Alignment Scores:
Pred. No.: 2.58e-142
Score: 1578.50
Percent Similarity: 92.09%
Best Local Similarity: 92.09%
Query Match: 40.01%
DB: 5

```

Score: 1527.00 Matches: 283
 Percent Similarity: 91.40% Conservativity: 4
 Best Local Similarity: 90.13% Mismatches: 17
 Query Match: 38.71% Indels: 12
 DB: 5 Gaps: 2

US-10-063-692-38 (1-720) x BX439313 (1-952)

QY 1 MetGluLeuGlyCysTrpThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuSer 20
 DB 13 ATGGAGCTGGTGGTGGAGCA-TTGGGCTCACCTTTCTTCAGCTCTCTTCATCTCG 71

QY 21 SerLeuProArgGluThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40
 DB 72 TCTTCCCAAGAGATACACAGTCATTAATGAAGCTGCGCTGGAGCAGAGTGAATATC 131

QY 41 MetCysArgGluCysGluThrAspGlnIleGluCysValCysProGlyLysArgGlu 60
 DB 132 ATGTGTGGGAGTGTGTGANTATGATCAGATTGAGTGGCTGTGCCCGGAAGAGGAA 191

QY 61 ValValGlyThrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
 DB 192 GTCGTGGTATTACCATCCCTCTGTCGAGGAATGAGGAGATGAGTGTGACTCTCTGCTG 251

QY 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100
 DB 252 ATCCACCCAGGTGTACCATCTTTGAAACTGCAAGAGCTGCCGAAATGCTCATGGGG 311

QY 101 GlyThrLeuAspPheThrValLysGlyPheThrCysAlaGluCysArgAlaGlyTrp 120
 DB 312 GGTACCTTGATGACTTCTATGTGAAGGGTCTTACTGTGACAGTGCAGAGCTGG 371

QY 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu 140
 DB 372 TACGGAGGAGCTGATGCGATGCGCAGTCTCGAGGCCCAAGGCTCAGATTTCG 431

QY 141 LeuGluSerTyrProLeuAsnAlaHisCysGluTrpThrIleHisAlaLysProGlyPhe 160
 DB 432 TTGGAAGCTATCCCTAAATGCTCACTGTGAATGAGCAATTCATGTAACCTGGGTTT 491

QY 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp 180
 DB 492 GTATCCAACTAAGATTGTGATGTTGAGCTGGAGTTGACTACATGTGCCAGTATGAC 551

QY 181 TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGly 200
 DB 552 TATGTTGAGTTCGTGATGAGACACCCGATGGCCAGATCATCAAGCGTGTCTGTGGC 611

QY 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220
 DB 612 AACGAGCGCCAGCTCTATCCAGACATAGGATCTCACTCCAGCTCTCTTCCACTCC 671

QY 221 AspGlySerIleAsnPheAspGlyPheHisAlaIleTyrGluIleThrAlaCysSer 240
 DB 672 GATGGCTCCAAGAATTTTACCGGTTTCCATGCGCATTTATGAGAGATACAGATGCTCC 731

QY 241 SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCys 260
 DB 732 TCATCCCTTGTTCATGACGCGACGTGGTCTTTGACAGCGTGGATCTTACAGTGT 791

QY 261 AlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuGluGluArgAsnCys 280
 DB 792 GCTGCTGGCAGCTAATACTGGGCGCGCTGTGAAATCGATTAAAGATAC-GAATGT 850

QY 281 SerAspProGlyGlyProValAsnGlyTyrGlnLysIle----- 293
 DB 851 ACAGAC-----ACCGTGGTGGCACCAGAGTGTGATCAACACCTTGGATGAGT 901

QY 294 ThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaLysIle 307
 DB 902 TCTGGAGGCTTGGGAAGTCCAGATCAAGCGTCAGAGATT 943

RESULT 10

BX337781
 LOCUS
 DEFINITION
 BX337781 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
 clone CSODI051YA20 5-PRIME, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 886)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 JOURNAL
 COMMENT
 On May 2, 2003 this sequence version replaced gi:30333640.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 5757.r

For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CSODI051BA10QP1&c=5757.r.

FEATURES
 source

1..886
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODI051YA20"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 5,07e-134 Length: 886
 Score: 1492.00 Matches: 270
 Percent Similarity: 98.90% Conservativity: 0
 Best Local Similarity: 98.90% Mismatches: 2
 Query Match: 37.82% Indels: 3
 DB: 5 Gaps: 0

US-10-063-692-38 (1-720) x BX337781 (1-886)

QY 1 MetGluLeuGlyCysTrpThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuSer 20
 DB 63 ATGGAGCTGGTGGTGGAGCA-TTGGGCTCACCTTTCTTCAGCTCTCTTCATCTCG 122

QY 21 SerLeuProArgGluThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40
 DB 123 TCTTCCCAAGAGATACACAGTCATTAATGAAGCTGCGCTGGAGCAGAGTGAATATC 182

QY 41 MetCysArgGluCysCysGluThrAspGlnIleGluCysValCysProGlyLysArgGlu 60
 DB 183 ATGTGTGGGAGTGTGTGANTATGATCAGATTGAGTGGCTGTGCCCGGAAGAGGAA 242

QY 61 ValValGlyThrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
 DB 243 GTCGTGGTATTACCATCCCTCTGTCGAGGAATGAGGAGATGAGTGTGACTCTCTGCTG 302

QY 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100
 DB 303 ATCCACCCAGGTGTACCATCTTTGAAACTGCAAGAGCTGCCGAAATGCTCATGGGG 362

QY 101 GlyThrLeuAspPheThrValLysGlyPheThrCysAlaGluCysArgAlaGlyTrp 120

```
|||||
363 GGTACCTTGGATGACTTCTTCTGTGAAGGGTTCTACTGTGCAGAGTGCAGAGCGCTGG 422
|||||
121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuAlaProLysGlyGlnLeu 140
|||||
423 TACGGAGGAGACTGTCATGCATGCTGTGGCCAGGTTCTCGAGAGCCCAAGAGGTCAGATTTTG 482
|||||
141 LeuGluSerTyProLeuAlaHisCysGluTyrThrIleHisAlaLysPro-GlyPh 160
|||||
483 TTGAAAGCTATCCCTTAATGCTCACTGTGAATGAGCACCATTTCATCAACCTGGGGTT 542
|||||
160 eValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAs 180
|||||
543 TGTCAATCAACCTAAGATTGTTCATGTTGAGCCTGGAGTTTGACTACATGTGCCATATGA 602
|||||
180 pTyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGl 200
|||||
603 CTATGTTGAGTTTCGTGATGGAGACCAACCGCATGCCAGATCATCAAGCGTGTCTGTGG 662
|||||
200 yAsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSe 220
|||||
663 CAACGAGCGGCCAGCTCCCTATCCAGAGCATAGGATCCTCACTCCAGCTCTCTTCACATC 722
|||||
220 rAspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSe 240
|||||
723 CGATGGCTCCAGAAATTTGACGGTTTCCATGCCATTATGAGGAGATCACAGCATGCTC 782
|||||
240 rSerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCy 260
|||||
783 CTCATCCCTTTGTTCCATGACGGCAGCTGGTGGTCTTGACAGGCTGGATCTTACAAATG 842
|||||
260 sAlaCysLeuAlaGlyTyrThrGlyGlnArgCysGlu 272
|||||
843 TGCTCTGTTGGCAGC-TATACCTGGGCGAGCS-TGTGAA 877
|||||

BM461342 1158 bp mRNA linear EST 05-FEB-2002
AGENCOURT 6419728 NCI_CGAP_Ov44 Mus musculus cDNA clone
IMAGE:5504093 5', mRNA sequence.
BM461342
BM461342.1 GI:18510382
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgi.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Aaron Hueh
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM2144 row: o column: 06
High quality sequence stop: 709.
Location/Qualifiers
1. .1158
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:5504093"
/lab_host="DRI0B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Ov44"
/notes="Organ: ovary, FMSG-treated; Vector: pCMV-SPORT6.1;
Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Average insert size 2.2 kb. Library
```

```
constructed by Life Technologies. Note: this is a NCI_CGAP
Library."

ORIGIN
Alignment Scores:
Pred. No.: 9,02e-129 Length: 1158
Score: 1440.00 Matches: 285
Percent Similarity: 85.34% Conservative: 12
Best Local Similarity: 81.90% Mismatches: 41
Query Match: 36.50% Indels: 12
DB: Gaps: 3

US-10-063-692-38 (1-720) x BM461342 (1-1158)
QY 1 MetGluLeuGlyCysTyrThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuSer 20
|||||
Db 101 ATGGAGCTAGACAGATGGGCGCAGTTGGGGCTGGTTCCTGCAGCTCCTTCTCATCTCA 160
|||||
QY 21 SerLeuProArgGluTyrThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40
|||||
Db 161 TCGTTGCCAAGAGAGTACACGGTCATTATGAAGCCTGTCCCGAGCTGAGTGAACATC 220
|||||
QY 41 MetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysProGlyLysArgGlu 60
|||||
Db 221 ATGTGTAGAGAGTGTGTGATATGATCAGATTGAATGCTCTGCCCAGGAAAGAGAA 280
|||||
QY 61 ValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
|||||
Db 281 GTGGTGGGTGTACCAATCCATGCTGCAGAAATGAGGATTAATGAATGTGACTCTCTCTA 340
|||||
QY 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100
|||||
Db 341 ATTCACCCAGGTGTACCATCTTTGAAACTCAAGAGCTGCCGCAATGGCTCCTGGGGC 400
|||||
QY 101 GlyThrLeuAspAspPheTyrValLysGlyPheTyrCysAlaGluCysArgAlaGlyTrp 120
|||||
Db 401 GGAACCTCTGGATGACTTCTACGTGAAGGATTTCTACTGCGAAGAGTGCAGGGCAGCTGG 460
|||||
QY 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu 140
|||||
Db 461 TACGGAGGAGACTGTCATGCATGCTGGCCAGGTTCTTCGAGCTTCAAAAGGTCAGATCTTG 520
|||||
QY 141 LeuGluSerTyProLeuAlaHisCysGluTyrThrIleHisAlaLysProGlyPhe 160
|||||
Db 521 TTGAGAGCTATCCCTTAATGCTCACTGTGAATGAGCTATTTCATGCCAGACCTGGGTTT 580
|||||
QY 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp 180
|||||
Db 581 ATCATCCAGTTGAGGTTTGGCATGTTGAGCCTAGAGTTTGACTACATGTGCCAGTATGAC 640
|||||
QY 181 TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGly 200
|||||
Db 641 TATGTGGAGGTCGCGCATGGGATATAGTAGCAGCCCTATTCATCAAGCGTTTCTGTGGC 700
|||||
QY 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220
|||||
Db 701 AACGAGAGGCCAGCTCCCATCANGAGCACTGGGCTCTTCACTCCATGCTCTTTTCCATTCT 760
|||||
QY 221 AspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer 240
|||||
Db 761 GATGGCTCCAAAGAACTTCGATGGCTTTTCACGCTGTTTGTGAGAGATTCACAGCGTGTCTCC 820
|||||
QY 241 SerSerProCysPheHisAspGlyThrCysValLeuAsp-LysAlaGlySerTyrLys-C 260
|||||
Db 821 TCATCCCTTGTTC-CATGATGGCAGATGCCCTCTTGTGACACCACTGGGGTCTTTTAAGGT 879
|||||
QY 260 ySAlaCysLeuAlaGlyTyrThr-GlyGlnArgCysGluAsnLeuLeuGluArgAsn 279
|||||
Db 880 GTCCCTGGCTGGCTGCCTACACTGGGCCGCGCTGTGAAAACCTACTTTGAAGAAAGAAA- 938
|||||
QY 280 CysSerAspPro---GlyGlyProValAsnGlyTyrGlnLysIleThrGlyGlyProGly 298
|||||
Db 939 TGCTCCCGACCTTTTGGGGGGGCCAGTCAATGGGTACCAAGAAATCCCAAAAGGGCCCTGA 998
|||||
```

QY 299 LeuIleAsnGlyArgHisAla-IysIleGlyThrValValSer---PhePheCysAsn-A 317
 :: |||||
 Db 999 ACTTCTCATGAGCGCCCTGTAAAAAATTTGGCGCCCGTGGGGCCCTTCTTTTGGGAACGG 1058
 QY 317 snSerTyrVal-LeuSerGlyAsnGluLysArgThrCys---GlnGlnAsnGlyGlu-Tr 335
 :: |||||
 Db 1059 GTTCATACCTTTCTTGGGGGGGAAGGAAACCAATTTGCCCCCCCCCCCAAAATGGGAAATG 1118
 QY 335 pSerGlyLys 338
 ::|||
 Db 1119 GGCGGGGAAA 1128

RESULT 12

CD514783 879 bp mRNA linear EST 06-JUN-2003
 LOCUS AGENCOURT_14376424 NIH_MGC_181 Homo sapiens cDNA clone
 DEFINITION IMAGE:30396311 5', mRNA sequence.

CD514783
 CD514783.1 GI:31446501

EST.
 SOURCE

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 879)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDM477 row: m column: 24

High quality sequence stop: 613.

FEATURES

source

1..879

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30396311"

/tissue_type="White Matter"

/dev_stage="Unknown"

/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"

/clone_lib="NIH_MGC_181"

/note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV

(destroyed); Library is oligo-dr primed and directionally

cloned (EcoRV site is destroyed upon cloning). Average

insert size 1.42 kb. Library was constructed by

(Invitrogen). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1..4e-128 Length: 879

Score: 1436.00 Matches: 282

Percent Similarity: 97.92% Conservative: 0

Best Local Similarity: 97.92% Mismatches: 2

Query Match: 36.40% Indels: 4

DB: 6 Gaps: 0

US-10-063-692-38 (1-720) x CD514783 (1-879)

QY 310 valValSerPhePheCysAsnAsnSerTyrValLeuSerGlyAsnGluLysArgThrCys 329

|||||

Db 2 GTGGTGCTCTTCTTTTGTAACTCCTATGTTCTTAGTGGCAATGAGAAAGAACTTGC 61

QY 330 GlnGlnAsnGlyGluTrpSerGlyLysGlnProIleCysIleLysAlaCysArgGluPro 349

|||||

Db 62 CAGCAGAATGGAGAGTGGTTCAGGAAACAGCCCATCTGCATAAAAGCCTGCCGAGAACCA 121

|||||

QY 350 LysIleSerAspLeuValArgArgValLeuProMetGlnValGlnSerArgGluThr 369

|||||

Db 122 AGATTTCAGACCTGTGTGAGAGGAGAGTTCCTCCATGCGAGTTTCAGTCAAGGGAGACA 181

|||||

QY 370 ProLeuHisGlnLeuTyrSerAlaAlaPheSerLysGlnLysLeuGlnSerAlaProThr 389

|||||

Db 182 CCATTACACAGCTATCTCAGCGGCTTCAGCAGCAGAACTGCAGAGTGCCCTTACC 241

|||||

QY 390 LysLysProAlaLeuProPheGlyAspLeuProMetGlyTyrGlnHisLeuHisThrGln 409

|||||

Db 242 AGAAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAG 301

|||||

QY 410 LeuGlnTyrGluCysIleSerProPheTyrArgArgLeuGlySerSerArgArgThrCys 429

|||||

Db 302 CTCACGTATGAGTGCATCTCACCCCTTCTACCGCCGCTGGGCAGCAGCAGGAGACATGT 361

|||||

QY 430 LeuArgThrGlyLysTrpSerGlyArgAlaProSerCysIleProIleCysGlyLysIle 449

|||||

Db 362 CTGAGGACTGGGAGTGGAGTGGCGGGCAGCCATCTGCATCCCTATCTCGGGGAAATTT 421

|||||

QY 450 GluAsnIleThrAlaProLysThrGlnGlyLeuArgTrpProTrpGlnAlaIleTyr 469

|||||

Db 422 GAGAACATCACTGCTCCAAAGACCCCAAGGTTGCGCTGGCGTGGCAGCAGCAGGAGCATCTAC 481

|||||

QY 470 ArgArgThrSerGlyValHisAspGlySerLeuHisLysGlyAlaTrpPheLeuValCys 489

|||||

Db 482 AGGAGGACCCAGCGGGTGCATGACGCGCAGCTACACAAAGGAGCGGTGTTCTTAGTCTGC 541

|||||

QY 490 SerGlyAlaLeuValAsnGluArgThrValValAlaAlaHisCysValThrAspLeu 509

|||||

Db 542 AGCGGTGCTGCTGGTGAATGAGCGCACTGTGTGGTGGCTGCCCATCTGTGTTACTGACCTG 601

|||||

QY 510 GlyLysValThrMetIleLysThrAlaAspLeuLysValValLeuGlyLysPheTyrArg 529

|||||

Db 602 NCGAAGGTCAACATGATCAAGCAGCAGACCTGANAGTTGTTTTGGGAAATTTCTACCGG 661

|||||

QY 530 AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleLeuHis 549

|||||

Db 662 GATGATGACCGGGATGAGAGACCATCCAGAGCCTACAGATTTCTCTCATCTTCGCAT 721

|||||

QY 550 ProAsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLysLeuLeuAspLys 569

|||||

Db 722 CCCAACTATGACCCCATCTCTTGTATGCTGACATCCCATCTCTGAGCTCTTAGACACAG 781

|||||

QY 570 AlaArg-IleSerThrArgValGlnProIle-CysLeuAlaAla-SerArgAspLeuSer 588

|||||

Db 782 GCCCGTTATCAGCACCAGCCGAGTCCAGCCCATCTTGCTCGTCCCGCAGTCCGGATCTCAGC 841

|||||

QY 589 ThrSer-PheGlnGlu 593

|||||

Db 842 ACTTCCCTTCCAGGAA 857

|||||

RESULT 13

CD655367 795 bp mRNA linear EST 18-JUN-2003

LOCUS AGENCOURT_14552770 NIA Human H1 Embryonic Stem Cell cDNA Library

DEFINITION (Long) Homo sapiens cDNA clone IMAGE:30426503 5', mRNA sequence.

ACCESSION CD655367

VERSION CD655367.1 GI:31895529

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 795)

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE NIH-MGC <http://mgs.nci.nih.gov/>.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs@mail.nih.gov
Tissue Procurement: Irene Ginis and Mahendra Rao, NIA
cDNA Library Preparation: Yulan Piao and Minoru Ko
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC c lone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM512 row: g column: 24
High quality sequence stop: 676.
Location/Qualifiers

FEATURES

source

1. .795
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30426503"
/tissue_type="Embryonic Stem cells"
/cell_line="WA01"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIA Human H1 Embryonic Stem Cell cDNA Library (Long)"
/notes="Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI;
This is a long-transcript enriched cDNA library (Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199] from WA01 cell line. Undifferentiated human ES cell line WA01/H1 was obtained from WiCell Research Institute, Inc., Madison, WI, cultured according to their instructions, on MSF feeders. They formed round colonies with defined edges and were positive for alkaline phosphatase, SSEA-4, OCT3, OCT4, REX1, UTF, TERT, SOX2, CX43 and CX45. They are negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLK3, SSEA-1, TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days after plating), the ES cells from 4 x 6cm dishes were treated with 1 mg/ml collagenase, type IV (Invitrogen/GIBCO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with Trizol Reagent from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558 (2001). [PMID:11544199] Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTACATCGAGCGCGCCCTTTTCTTTT-3'] from 3.49 of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform extraction, and separated from free linkers by Centricon-100 column. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The average insert size is about 3.6kb."

ORIGIN

Alignment Scores:
Pred. No.: 2,07e-119 Length: 795
Score: 1341.00 Matches: 249
Percent Similarity: 99.21% Conservative: 1
Best Local Similarity: 98.81% Mismatches: 2
Query Match: 33.99% Indels: 2
DB: 6 Gaps: 0

US-10-063-692-38 (1-720) x CD655367 (1-795)

Qy 208 GlnSerIleGlySerSerIleuHisValLeuPheHisSerAspGlySerIysAsnPheAsp 227
Db 13 CAGAGCATAGGATCTCTCACTCCAGCTCTCTTCCACTCCGATCGCTCCAGAAATTTGAC 72
Qy 228 GlyPheHisAlaIleTyrGluGluIleThrAlaCysSerSerProCysPheHisAsp 247

Db 73 GGTTCCTCATGCCATTATGAGGAGATCACAGCATGCTCCTCATCCCTTGTTCATGAC 132
Qy 248 GlyThrCysValLeuAspIysAlaGlySerTyrLysCysAlaCysLeuAlaGlyTyrThr 267
Db 133 GGCAGCTGGCTCTTGACAAGCTGGATCTTAAAGTGTGCTGTCTGGCAGCTATACT 192
Qy 268 GlyGlnArgCysGluAsnLeuLeuGluGluArgAsnCysSerAspProGlyGlyProVal 287
Db 193 GGGCAGCGCTGTGAAATCTCTTGAAGAAAGAACTGCTCAGACCTGGGGCCAGTC 252
Qy 288 AsnGlyTyrGlnLysIleThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaIysIle 307
Db 253 AATGGTACCAGAAAATAACAGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAT 312
Qy 308 GlyThrValValSerPhePheCysAsnAsnSerTyrValLeuSerGlyAsnGluLysArg 327
Db 313 GGCACCGCTGTCTCTTTTGTAACTCTTATGAGTGTCTTAGTGGCAATGAGAAAAA 372
Qy 328 ThrCysGlnGlnAsnGlyGluTrpSerGlyLysGlnProIleCysIleLysAlaCysArg 347
Db 373 ACTTGGCCAGCAAGTGGAGAGTGTTCAGGGAAACAGCCCATCTGCATAAAGCCTGCC 432
Qy 348 GluProLysIleSerAspLeuValArgArgValLeuProMetGlnValGlnSerArg 367
Db 433 GAACCAAGATTTCAGACCTGGTGAGAGGAGAGTTCTTCCGATGCGGTTCACTCAAG 492
Qy 368 GluThrProLeuHisGlnLeuTyrSerAlaAlaPheSerIysGlnLysLeuGlnSerAla 387
Db 493 GAGACACCATTAACAGCTATACTCAGCGGCTTTCAGCAAGCAGAAATCGCAGAGTGC 552
Qy 388 ProThrLysLysProAlaLeuProPheGlyAspLeuProMetGlyTyrGlnHisLeuHis 407
Db 553 CTACCAAGAGCCGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCAT 612
Qy 408 ThrGlnLeuGlnTyrGluCysIleSerProPheTyrArgArgLeuGlySerSerArgArg 427
Db 613 ACCCAGCTCCAGTATGAGTGCATCTCACCGCTTCTACCGCGCTGGGCGCAGCAGGAG 672
Qy 428 ThrCysLeuArgThrGlyLysTrpSerGlyArgAlaProSerCysIleProIleCysGly 447
Db 673 ACATGTCAGAGACTGGGAAGTGGAGTGGCGGCGACCATCTGCATCTCTATCTCGGG 732
Qy 448 LysIleGluAsnIleThrAlaProLysThrGlnGly 459
Db 733 AAATTGAGAC-ATCACTGCTCCAAAGACCAAGGT 767

CF125161 718 bp mRNA linear EST 05-AUG-2003
UI-HF-EL0-avm-p-18-0-UI.r1 NIH_MGC_212 Homo sapiens cDNA clone
IMAGE:30558617 5', mRNA sequence.

CF125161
CF125161.1 GI:33201111
EST.

ORGANISM
Homo sapiens (human)

REFERENCE
1 (bases 1 to 718)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

AUTHORS
Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE
Normalization and subtraction: two approaches to facilitate gene

JOURNAL
discovery

MEDLINE
Genome Res. 6 (9), 791-806 (1996)

PUBMED
97044477

COMMENT
8889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEERF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Mary Hendrix
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Dr. M. Bento Soares, University of Iowa
http://genome.uiowa.edu/distribution/humanfl.html
Seq primer: pYX-5

FEATURES

Location/Qualifiers
1..718
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30558617"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH MGC 212"
/notes="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATAAGGCCA. Tissue was provided by Mary Hendrix."

ORIGIN

Alignment Scores:
Pred. No.: 2,07e-111 Length: 718
Score: 1258.00 Matches: 224
Percent Similarity: 98.68% Conservative: 1
Best Local Similarity: 98.25% Mismatches: 2
Query Match: 31.89% Indels: 1
DB: 7 Gaps: 0

US-10-063-692-38 (1-720) x CF125161 (1-718)

QY 1 MetGluLeuGlyCysTrpThrGln-LeuGlyLeuThrPheLeuGlnLeuLeuLeuLeu 20
DB 37 ATGAGCTGGTGTGGAGCGAGTTGGGGCTACCTTTCTTCAGCTCTTCTCATCTC 96
QY 20 rSerLeuProArgGluTyrThrValLeuAsnGluAlaCysProGlyAlaGluTrpAsnI 40
DB 97 GTCTTGGCCAAAGAGATACAGCTAATTAATGAAGCTGCTGCGAGCAGTGAATAT 156
QY 40 eMetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysProGlyLysArgG 60
DB 157 CATGTGTGGGAGTGTGTGAATATGATCATGATTGAGTGGCTGCTGCCCGGAAAGAGGA 216
QY 60 uValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLe 80
DB 217 AGTCGTGGGTATACCATCCCTTGTGCGAGATGAGGAGATGAGTGTGACTCTCGCCT 276
QY 80 uIleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpG 100
DB 277 GATCCACCCAGGTTGTACCATCTTTGAAACTGCAAGAGCTGCCGAAATGGCTCATGGGG 336
QY 100 yGlyThrLeuAspAspPheTyrValLysGlyPheTyrCysAlaGluCysArgAlaGlyTr 120
DB 337 GGGTACTCTGGATGACTTCTATGTGAAGGGTGTCTACTGTGCAAGTGGCCGACGGCTG 396
QY 120 pTyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLe 140
DB 397 GTACGGAGGAGACTGCATGCGATGTGCCAGGTCTTCGCGAGCCCAAGGGTCAGATTTT 456
QY 140 uLeuGluSerTyrProLeuAsnAlaHisCysGluTyrThrIleHisAlaLysProGlyPh 160
DB 457 GTTGGAAAGCTATCCCTTAATGCTCACTGTGAATGGACCATTCATGCTAAACCTGGTT 516
QY 160 eValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAs 180

DB 517 TGTCTATCCAACTAAGATTTCATGTTGACCTGGAGTTTGACTACATGTGCCAGTATGA 576
QY 180 pTyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysG 200
DB 577 CTATGTTGAGTTTCGTGATGGAGACAATCGCATGGCCAGATCATCAAGCGTGTCTGTGG 636
QY 200 yAsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisE 220
DB 637 CAACGAGCGGTGAGCTCTATCCAGAGCATAGGATTCTCACTCCACGCTCTCTTCTACTC 696
QY 220 rAspGlySerLysAsnPheAsp 227
DB 697 CGATGGCTCCAGAAATTTTGAC 718
RESULT 15
CO397557
LOCUS
DEFINITION
IMAGE:7314174 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1. (bases 1 to 785)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: gcgabs-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
cDNA Library Preparation: Express Genomics
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15366 row: g column: 04
High quality sequence stop: 710.
FEATURES
Location/Qualifiers
1..785
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7314174"
/sex="both"
/tissue_type="Brain - Pooled from several tissues from one
or more individuals"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 254"
/notes="Organ: brain/CNS; Vector: pExpress-1; Site 1:
EcoRV; Site 2: NotI; RNA obtained from brain tissue of 8
wk old animal. Tissues were snap-frozen and kept at -80C
before RNA extraction and purification (Tri-reagent
method). cDNA was primed using oligo-dT primer:
5'-pGATGTTCTAGATCGGCGCGCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 2.18 kb. This
primary library is not normalized (normalized library is
NIH MGC 255) and was constructed by Express Genomics
(Frederick, MD). Note: this is a NIH_MGC library"
ORIGIN
Alignment Scores: 3.11e-108 Length: 785
Pred. No.: 1226.00 Matches: 226

Percent Similarity: 94.92% Conservative: 17
Best Local Similarity: 88.28% Mismatches: 13
Query Match: 31.08% Indels: 0
DB: 7 Gaps: 0

US-10-063-692-38 (1-720) x C0397557 (1-785)

```
QY 417 PropheTyrArgArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTrpSer 436
DB 2 CCCTTCTACACCGCTGGAGAGCAGCAGGAGACATGCTGAGAACTGGGAGTGGAGT 61
QY 437 GlyArgAlaProSerCysIleProIleCysGlyLysIleGluAsnIleThrAlaProLys 456
DB 62 GGGCGGGCCCGCTCTGTATCCAACTCTGTGGAAATCGAGAGCGTTCCTTCCTCCANAG 121
QY 457 ThrGlnGlyLeuArgTrpProTrpGlnAlaAlaIleTyrArgArgThrSerGlyValHis 476
DB 122 ACTCAAGGGACCCGCTGGCCATGGCAGGAGCCATCTACCGGAGGACCACTGGTGTACAT 181
QY 477 AspGlySerLeuHisLysGlyAlaTrpPheLeuValCysSerGlyAlaLeuValAlaGlu 496
DB 182 GACGGTGGTCTGCACAAAGGTGATGGTCTTGCTGAGTGGTCCCTGGTGAATGAG 241
QY 497 ArgThrValValAlaAlaHisCysValThrAspLeuGlyLysValThrMetIleLys 516
DB 242 CGTACTGTGGTGTGGCTGCCACTGTGTACAGAGCTGGGGAAGCTCACCATCATCAAG 301
QY 517 ThrAlaAspLeuLysValValLeuGlyLysPheTyrArgAspAspArgAspGluLys 536
DB 302 ACAGCAGAGCTCAAGGTGTCTTTGGGAAAAATCTACAGGATGATGATGAGATGAGAAG 361
QY 537 ThrIleGlnSerLeuGlnIleSerAlaIleLeuHisProAsnTyrAspProIleLeu 556
DB 362 ACCATCCAGAATTACGGATTTCTGTATCATTTCTGACCCCACTATGACCTATCCTG 421
QY 557 LeuAspAlaAspIleAlaIleLeuLysLeuAspLysAlaArgIleSerThrArgVal 576
DB 422 CTTGACACTGACATCCCGCTTCTGAAGCTCTTAGACAGGCGCGCATCAGTACCCGTGTC 481
QY 577 GlnProIleCysLeuAlaAlaSerArgAspLeuSerThrSerPheGlnGluSerHisIle 596
DB 482 CAACCCATCTGCCCTGCTACCACTCGGACCTCAGCGCCTCTTTTGAGGAGTCTCACATC 541
QY 597 ThrValAlaGlyTrpAsnValLeuAlaAspValArgSerProGlyPheLysAsnAspThr 616
DB 542 ACTGTGGCTGGCTGGAAACATCTCTGGCAGATGTAAAGAGCCCTTGCTTTAAGAAATGACAC 601
QY 617 LeuArgSerGlyValValSerValValAspSerLeuLeuGluGlnHisGluAsp 636
DB 602 CTATATTATGGGATGCTCAAGGTGGTAGACTCAATGCTTTGTGAGGAACAACACGAAGAC 661
QY 637 HisGlyIleProValSerValThrAspAsnMetPheCysAlaSerTrpGluProThrAla 556
DB 662 CATGGCATTCACGTAGTGTCTACGACAAATATCTTCTGTGCCNAACANGACCCAGTACC 721
QY 657 ProSerAspIleCysThrAlaGluThrGlyGlyIleAlaAlaValSer 672
DB 722 CCTTCTAACATCTGCATCTGTAGACAGGGGGCATCGCTGCTTTATCT 769
```

Search completed: May 10, 2005, 01:20:40
Job time : 6017 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 9, 2005, 23:40:28 ; Search time 1063 Seconds
(without alignments)
4141.570 Million cell updates/sec

Perfect score: 3945
Sequence: 1 MELGCTWQLGLTFLQLLLIS.....LSTAFKTVLPFKDWIERNMK 720

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5654200 seqs, 3057283753 residues

Total number of hits satisfying chosen parameters: 11308400

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US10063692/runat_09052005_122336_5254/app_query.fasta_1.903
-DB=Published Applications NA -OFT=Eastap -SURFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdd -LIST=1500 -DOCALLGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=0 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10063692 @CGN 1 1 704 @runat_09052005_122336_5254
-NCPU=6 -ICPU=3 -NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=130 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*

Result No.	Score	Query Match	length	DB	ID	Description
27	3945	100.0	2846	10	US-09-997-428-230	Sequence 230, App
560	3945	100.0	2846	16	US-10-174-587-169	Sequence 169, App
624	3945	100.0	2846	16	US-10-063-743-37	Sequence 37, Appl
739	3945	100.0	2846	19	US-10-972-317-37	Sequence 37, Appl
740	3939	99.8	2306	14	US-10-004-551-3	Sequence 3, Appl
741	3939	99.8	2306	16	US-10-098-871-25	Sequence 25, Appl
742	3932	99.7	2845	15	US-10-101-510-644	Sequence 644, App
743	3500.5	88.7	2632	17	US-10-274-639-38	Sequence 38, Appl
744	3500.5	88.7	2632	17	US-10-333-574-38	Sequence 38, Appl
745	3332.5	79.4	1867	14	US-10-004-551-1	Sequence 1, Appl
746	2946.5	74.7	2259	13	US-10-067-422-2	Sequence 2, Appl
747	2678.5	67.9	2142	15	US-10-037-270-1006	Sequence 1006, Ap
748	2678.5	67.9	2142	17	US-10-117-722-1006	Sequence 1006, Ap
749	2678.5	67.9	2144	15	US-10-037-270-969	Sequence 969, App
750	2678.5	67.9	2144	17	US-10-117-722-969	Sequence 969, App
751	821.5	20.8	997	11	US-09-876-143-1083	Sequence 1083, Ap
752	672	17.0	3467	14	US-10-183-992-3	Sequence 3, Appl
753	672	17.0	3467	18	US-10-480-254-3	Sequence 3, Appl
754	665	16.9	3438	14	US-10-183-992-7	Sequence 7, Appl
755	665	16.9	3438	18	US-10-480-254-7	Sequence 7, Appl
756	665	16.9	3448	18	US-10-638-125-3	Sequence 3, Appl
757	665	16.9	4182	14	US-10-183-992-5	Sequence 5, Appl
758	665	16.9	4182	18	US-10-638-125-1	Sequence 1, Appl
759	665	16.9	4182	18	US-10-480-254-5	Sequence 5, Appl
760	496.5	12.6	432	11	US-09-876-143-696	Sequence 696, App
761	475	12.0	5135	19	US-10-764-420-2328	Sequence 2328, Ap
762	473	12.0	403	10	US-09-918-995-6744	Sequence 6744, Ap
763	471	11.9	3895	16	US-10-148-671-4	Sequence 4, Appl
764	459.5	11.6	369	10	US-09-903-393-1	Sequence 1, Appl
765	429	10.7	2416	19	US-10-764-420-513	Sequence 513, App
766	424	10.7	2037	19	US-10-764-420-513	Sequence 513, App
767	408.5	10.4	3064	15	US-10-101-510-599	Sequence 599, App
768	405	10.3	2475	9	US-09-874-198-3	Sequence 3, Appl
769	405	10.3	2475	9	US-09-874-238-3	Sequence 3, Appl
770	403.5	10.2	2386	9	US-09-808-602-92	Sequence 92, Appl
771	403.5	10.2	2386	9	US-09-800-198-79	Sequence 79, Appl
772	403.5	10.2	2386	17	US-10-172-118-654	Sequence 654, App
773	403.5	10.2	2386	17	US-10-342-887-654	Sequence 654, App
774	403.5	10.2	2493	9	US-09-880-107-2256	Sequence 2256, Ap
775	403.5	10.2	2493	17	US-10-257-021-65	Sequence 65, Appl
776	403.5	10.2	2555	13	US-10-044-090-613	Sequence 613, App
777	403.5	10.2	2555	15	US-10-084-817-23	Sequence 23, Appl
778	403.5	10.2	3064	17	US-10-063-674-2094	Sequence 2094, Ap
779	396.5	10.1	296	18	US-10-723-860-4638	Sequence 4638, Ap
780	396.5	10.1	554	13	US-10-027-632-275184	Sequence 275184,
781	396.5	10.1	554	17	US-10-027-632-275184	Sequence 275184,
782	351	8.9	2647	9	US-09-880-107-2105	Sequence 2105, Ap
783	351	8.9	2647	17	US-10-172-118-655	Sequence 655, App
784	351	8.9	2647	17	US-10-342-887-655	Sequence 655, App
785	350	8.9	2659	13	US-10-044-090-472	Sequence 472, App
786	350	8.9	2659	15	US-10-084-817-15	Sequence 15, Appl
787	348.5	8.8	7149	16	US-10-252-157-101	Sequence 101, App
788	347	8.8	3115	17	US-10-276-774-448	Sequence 448, App
789	347	8.8	3115	17	US-10-296-115-404	Sequence 404, App
790	346	8.8	2647	17	US-10-453-827-883	Sequence 883, App
791	342	8.7	2725	9	US-09-925-301-182	Sequence 182, App
792	340.5	8.6	2908	9	US-09-917-800A-1348	Sequence 1348, Ap
793	340.5	8.6	2908	17	US-10-191-803-812	Sequence 812, App
794	340.5	8.6	2908	17	US-10-152-319A-1421	Sequence 1421, Ap
795	336.5	8.5	3149	17	US-10-172-118-157	Sequence 157, App
796	336.5	8.5	3149	17	US-10-295-027-968	Sequence 968, App
797	336.5	8.5	3149	17	US-10-342-887-157	Sequence 157, App
798	336.5	8.5	3359	18	US-10-729-807-19	Sequence 19, Appl
799	335.5	8.5	2838	17	US-10-072-012-43	Sequence 43, Appl
800	335.5	8.5	3147	10	US-09-776-191-1	Sequence 1, Appl
801	335.5	8.5	3147	10	US-09-776-191-49	Sequence 49, Appl
802	335.5	8.5	3147	14	US-10-099-700A-1	Sequence 1, Appl
803	335.5	8.5	3147	14	US-10-099-700A-3	Sequence 3, Appl
804	335.5	8.5	3147	15	US-10-190-030B-1	Sequence 1, Appl
805	335.5	8.5	3147	15	US-10-190-030B-3	Sequence 3, Appl

806	335.5	8.5	3147	15	US-10-302-840A-1	Sequence 1, Appli	879	289.5	7.3	2544	16	US-10-443-701-3	Sequence 3, Appli
807	335.5	8.5	3147	15	US-10-302-840A-3	Sequence 3, Appli	880	289.5	7.3	2672	10	US-09-776-191-9	Sequence 9, Appli
808	335.5	8.5	3147	15	US-10-267-219-1	Sequence 1, Appli	881	289.5	7.3	2672	17	US-10-156-214A-9	Sequence 9, Appli
809	335.5	8.5	3147	15	US-10-267-219-3	Sequence 3, Appli	882	289.5	7.3	2859	10	US-09-814-353-19992	Sequence 19992, A
810	335.5	8.5	3147	16	US-10-112-221A-1	Sequence 1, Appli	883	289.5	7.3	3104	17	US-09-776-191-7	Sequence 7, Appli
811	335.5	8.5	3147	16	US-10-112-221A-3	Sequence 3, Appli	884	289.5	7.3	3104	17	US-10-156-214A-7	Sequence 7, Appli
812	335.5	8.5	3147	16	US-10-104-271-1	Sequence 1, Appli	885	288.5	7.3	2409	9	US-09-888-615-54	Sequence 54, Appli
813	335.5	8.5	3147	16	US-10-104-271-3	Sequence 3, Appli	885	288.5	7.3	2409	9	US-10-167-749-168	Sequence 168, App
814	335.5	8.5	3147	17	US-10-147-211A-1	Sequence 1, Appli	895	288.5	7.3	3143	14	US-10-170-481A-168	Sequence 168, App
815	335.5	8.5	3147	17	US-10-147-211A-3	Sequence 3, Appli	955	288.5	7.3	3143	17	US-10-210-028-168	Sequence 168, App
816	335.5	8.5	3147	17	US-10-156-214A-1	Sequence 1, Appli	957	288.5	7.3	3143	17	US-10-162-521A-168	Sequence 168, App
817	335.5	8.5	3147	17	US-10-600-187-1	Sequence 1, Appli	962	288.5	7.3	3143	17	US-10-918-851-168	Sequence 168, App
818	335.5	8.5	3147	17	US-10-600-187-18	Sequence 18, Appli	975	288.5	7.3	3143	19	US-10-805-667-168	Sequence 168, App
819	334.5	8.5	3145	16	US-10-252-157-102	Sequence 102, App	976	288.5	7.3	3143	19	US-10-897-359-168	Sequence 168, App
820	331.5	8.4	3696	10	US-09-776-191-63	Sequence 63, Appli	977	288.5	7.3	3143	19	US-10-893-802-168	Sequence 168, App
821	331.5	8.4	3696	15	US-10-157-031-266	Sequence 266, App	978	288.5	7.3	3143	19	US-10-897-360-168	Sequence 168, App
822	331.5	8.4	3696	17	US-10-156-214A-30	Sequence 30, Appli	979	288.5	7.3	3547	19	US-10-926-083-3	Sequence 3, Appli
823	328.5	8.3	4506	17	US-10-467-042-37	Sequence 27, Appli	980	287	7.3	1401	17	US-10-406-031-6	Sequence 6, Appli
824	328.5	8.3	5598	16	US-10-276-934-1	Sequence 1, Appli	981	287	7.3	1404	17	US-10-406-031-4	Sequence 4, Appli
825	328.5	8.3	5667	16	US-10-276-934-2	Sequence 2, Appli	982	287	7.3	2933	19	US-10-741-600-83	Sequence 83, Appli
826	328.5	8.3	6145	16	US-10-276-934-3	Sequence 3, Appli	983	286	7.2	1689	9	US-09-969-271-6	Sequence 6, Appli
827	328.5	8.3	6409	16	US-10-276-934-4	Sequence 4, Appli	984	286	7.2	1726	17	US-10-411-037-25	Sequence 25, Appli
828	328.5	8.3	7323	16	US-10-276-934-5	Sequence 5, Appli	985	286	7.2	1726	17	US-10-411-026-25	Sequence 25, Appli
829	328.5	8.3	8034	16	US-10-276-934-6	Sequence 6, Appli	986	286	7.2	1726	17	US-10-410-962-25	Sequence 25, Appli
830	327.5	8.3	2063	9	US-09-925-302-169	Sequence 169, App	987	286	7.2	1726	17	US-10-411-049-25	Sequence 25, Appli
831	327.5	8.3	2063	9	US-09-925-302-169	Sequence 169, App	988	286	7.2	1726	18	US-10-410-930-25	Sequence 25, Appli
832	324	8.2	2900	17	US-10-600-187-9	Sequence 9, Appli	989	286	7.2	1726	18	US-10-410-977-25	Sequence 25, Appli
833	323	8.2	8010	17	US-10-016-248-3	Sequence 3, Appli	990	286	7.2	1726	18	US-10-411-012-25	Sequence 25, Appli
834	323	8.2	10136	17	US-10-016-248-1	Sequence 1, Appli	991	286	7.2	1726	18	US-10-287-994-25	Sequence 25, Appli
835	319.5	8.1	1365	17	US-10-406-031-18	Sequence 18, Appli	992	286	7.2	1726	18	US-10-410-913-25	Sequence 25, Appli
836	319.5	8.1	1401	17	US-10-406-031-16	Sequence 16, Appli	993	286	7.2	1726	18	US-10-410-980-25	Sequence 25, Appli
837	318.5	8.1	2756	9	US-09-925-301-351	Sequence 351, App	994	286	7.2	2461	17	US-10-172-118-541	Sequence 541, App
838	318.5	8.1	3106	9	US-09-900-751-1	Sequence 1, Appli	995	286	7.2	2461	17	US-10-342-887-541	Sequence 541, App
839	314.5	8.0	1362	17	US-10-406-031-12	Sequence 12, Appli	996	283.5	7.2	1486	19	US-10-764-420-2390	Sequence 2390, Ap
840	314.5	8.0	1365	17	US-10-406-031-10	Sequence 10, Appli	997	281.5	7.1	901	17	US-10-330-051A-21	Sequence 21, Appli
841	312.5	7.9	1843	9	US-09-880-107-3670	Sequence 3670, Ap	998	281	7.1	1467	15	US-10-348-504-43	Sequence 43, Appli
842	312.5	7.9	1843	9	US-10-349-858-17	Sequence 17, Appli	999	281	7.1	1467	16	US-10-407-123-26	Sequence 26, Appli
843	312	7.9	1386	17	US-10-168-407-11	Sequence 11, Appli	1000	280.5	7.1	1184	18	US-09-969-347-210	Sequence 210, App
844	312	7.9	1401	17	US-10-406-031-9	Sequence 9, Appli	1001	280.5	7.1	1184	19	US-10-843-641A-8339	Sequence 8339, Ap
845	312	7.9	1404	17	US-10-406-031-7	Sequence 7, Appli	1002	280.5	7.1	1184	19	US-10-843-641A-8339	Sequence 8339, Ap
846	312	7.9	3096	17	US-10-451-168-29	Sequence 29, Appli	1003	279.5	7.1	2106	18	US-10-617-619-9	Sequence 9, Appli
847	311.5	7.9	2580	17	US-10-104-047-1934	Sequence 1934, Ap	1004	279.5	7.1	3112	14	US-10-097-340-311	Sequence 311, App
848	311	7.9	1386	17	US-10-168-407-9	Sequence 9, Appli	1005	279.5	7.1	7493	18	US-10-617-619-10	Sequence 10, Appli
849	311	7.9	1386	17	US-10-168-407-12	Sequence 12, Appli	1006	279	7.1	2913	9	US-09-888-615-42	Sequence 42, Appli
850	310.5	7.9	1245	17	US-10-670-628-1	Sequence 1, Appli	1007	279	7.1	3522	17	US-10-363-937-23	Sequence 23, Appli
851	310.5	7.9	1257	10	US-09-997-623-3	Sequence 3, Appli	1008	278.5	7.1	877	10	US-09-978-418-33	Sequence 33, Appli
852	310.5	7.9	1257	10	US-09-978-917A-3	Sequence 3, Appli	1009	278.5	7.1	1440	17	US-10-375-741-13	Sequence 13, Appli
853	310.5	7.9	1260	14	US-10-182-263-7	Sequence 7, Appli	1010	278.5	7.1	2462	9	US-09-964-824A-289	Sequence 289, App
854	310.5	7.9	1260	14	US-10-182-263-7	Sequence 7, Appli	1011	278.5	7.1	2462	9	US-09-880-107-2251	Sequence 2251, Ap
855	310.5	7.9	1359	17	US-10-406-031-15	Sequence 15, Appli	1012	278.5	7.1	2462	17	US-10-375-716-25	Sequence 25, Appli
856	310.5	7.9	1383	10	US-09-997-623-1	Sequence 1, Appli	1013	278.5	7.1	2462	17	US-10-349-858-14	Sequence 14, Appli
857	310.5	7.9	1383	10	US-09-978-917A-1	Sequence 1, Appli	1014	278.5	7.1	2462	19	US-10-843-641A-5592	Sequence 5592, Ap
858	310.5	7.9	1386	14	US-10-182-263-8	Sequence 8, Appli	1015	278	7.0	1502	17	US-10-406-031-26	Sequence 26, Appli
859	310.5	7.9	1386	14	US-10-168-407-8	Sequence 8, Appli	1016	278	7.0	1507	15	US-10-101-510-433	Sequence 433, App
860	310.5	7.9	1395	17	US-10-406-031-13	Sequence 13, Appli	1017	278	7.0	1507	17	US-10-349-858-13	Sequence 13, Appli
861	310	7.9	1386	14	US-10-182-263-11	Sequence 11, Appli	1018	278	7.0	1507	18	US-10-283-975A-81	Sequence 81, Appli
862	310	7.9	1386	14	US-10-182-263-12	Sequence 12, Appli	1019	278	7.0	1570	18	US-10-723-860-4988	Sequence 4988, Ap
863	310	7.9	1386	17	US-10-168-407-10	Sequence 10, Appli	1020	278	7.0	1936	17	US-10-401-077-2	Sequence 2, Appli
864	309	7.8	1386	14	US-10-182-263-9	Sequence 9, Appli	1021	277	7.0	1327	14	US-10-167-749-170	Sequence 170, App
865	308	7.8	1386	14	US-10-182-263-10	Sequence 10, Appli	1022	277	7.0	1327	17	US-10-210-028-170	Sequence 170, App
866	301	7.6	2795	19	US-10-741-600-81	Sequence 81, Appli	1092	277	7.0	1327	17	US-10-162-521A-170	Sequence 170, App
867	300.5	7.6	1850	19	US-10-764-420-2429	Sequence 2429, Ap	1097	277	7.0	1327	17	US-10-918-851-170	Sequence 170, App
868	299.5	7.6	1401	17	US-10-406-031-3	Sequence 3, Appli	1109	277	7.0	1327	19	US-10-805-667-170	Sequence 170, App
869	299.5	7.6	1404	17	US-10-406-031-1	Sequence 1, Appli	1110	277	7.0	1327	19	US-10-805-667-170	Sequence 170, App
870	297.5	7.5	2198	16	US-09-974-298-144	Sequence 69, Appli	1111	277	7.0	1327	19	US-10-893-802-170	Sequence 170, App
871	297.5	7.5	2641	9	US-09-917-800A-1575	Sequence 1575, Ap	1112	277	7.0	1327	19	US-10-897-360-170	Sequence 170, App
872	294.5	7.5	1543	9	US-10-152-319A-1544	Sequence 1544, Ap	1113	277	7.0	1327	19	US-09-783-587B-2	Sequence 2, Appli
873	294.5	7.5	1543	9	US-10-152-319A-1544	Sequence 1544, Ap	1114	277	7.0	1338	10	US-09-783-587B-2	Sequence 2, Appli
874	293	7.4	3121	16	US-10-114-153-49	Sequence 49, Appli	1115	277	7.0	1357	9	US-09-954-456-552	Sequence 4, Appli
875	289.5	7.3	2509	14	US-10-193-656-7	Sequence 7, Appli	1116	276.5	7.0	2036	9	US-09-954-456-552	Sequence 552, App
876	289.5	7.3	2519	17	US-09-969-271-5	Sequence 5, Appli	1117	276.5	7.0	2036	9	US-09-880-107-1612	Sequence 1612, Ap
877	289.5	7.3	2519	17	US-10-172-118-540	Sequence 540, App	1118	276.5	7.0	2036	9	US-10-843-641A-3579	Sequence 3579, Ap
878	289.5	7.3	2519	17	US-10-342-887-540	Sequence 540, App	1119	276.5	7.0	2040	18	US-10-617-619-12	Sequence 12, Appli

1120	276.5	7.0	7427	18	US-10-617-619-13	Sequence 13, Appl	1193	263	6.7	1296	13	US-10-076-421-1	Sequence 1, Appl
1121	275.5	7.0	1332	17	US-10-411-037-7	Sequence 7, Appl	1194	263	6.7	1475	9	US-09-735-705-122	Sequence 122, App
1122	275.5	7.0	1332	17	US-10-411-026-7	Sequence 7, Appl	1195	263	6.7	1475	9	US-09-850-716A-122	Sequence 122, App
1123	275.5	7.0	1332	17	US-10-410-962-7	Sequence 7, Appl	1196	263	6.7	1475	9	US-09-897-778-122	Sequence 122, App
1124	275.5	7.0	1332	17	US-10-411-049-7	Sequence 7, Appl	1197	263	6.7	1475	10	US-09-466-396A-122	Sequence 122, App
1125	275.5	7.0	1332	18	US-10-410-930-7	Sequence 7, Appl	1198	263	6.7	1475	14	US-10-007-700-122	Sequence 122, App
1126	275.5	7.0	1332	18	US-10-410-997-7	Sequence 7, Appl	1199	263	6.7	1475	15	US-10-117-982-122	Sequence 122, App
1127	275.5	7.0	1332	18	US-10-411-012-7	Sequence 7, Appl	1200	263	6.7	1475	15	US-10-101-510-159	Sequence 159, App
1128	275.5	7.0	1332	18	US-10-287-994-7	Sequence 7, Appl	1201	263	6.7	1475	17	US-10-313-986-122	Sequence 122, App
1129	275.5	7.0	1332	18	US-10-410-913-7	Sequence 7, Appl	1202	263	6.7	1475	17	US-10-411-037-33	Sequence 33, Appl
1130	275.5	7.0	1332	19	US-10-410-980-7	Sequence 7, Appl	1203	263	6.7	1475	17	US-10-411-026-33	Sequence 33, Appl
1131	275.5	7.0	2016	19	US-10-841-250-7	Sequence 7, Appl	1204	263	6.7	1475	17	US-10-410-962-33	Sequence 33, Appl
1132	275.5	7.0	2422	17	US-10-382-248-33	Sequence 33, Appl	1205	263	6.7	1475	17	US-10-411-048-33	Sequence 33, Appl
1133	275.5	7.0	2422	17	US-10-263-205B-1	Sequence 1, Appl	1206	263	6.7	1475	18	US-10-410-930-33	Sequence 33, Appl
1134	275.5	7.0	2422	18	US-10-738-777-1	Sequence 1, Appl	1207	263	6.7	1475	18	US-10-410-997-33	Sequence 33, Appl
1135	275.5	7.0	4496	15	US-10-234-406-5	Sequence 5, Appl	1208	263	6.7	1475	18	US-10-411-012-33	Sequence 33, Appl
1136	275.5	7.0	6098	14	US-10-109-498-2	Sequence 2, Appl	1209	263	6.7	1475	18	US-10-287-994-33	Sequence 33, Appl
1137	275	7.0	1683	9	US-09-912-559-1	Sequence 1, Appl	1210	263	6.7	1475	18	US-10-410-913-33	Sequence 33, Appl
1138	275	7.0	1683	9	US-09-912-559-2	Sequence 2, Appl	1211	263	6.7	1475	18	US-10-775-972-122	Sequence 122, App
1139	275	7.0	1683	17	US-10-391-213-1	Sequence 1, Appl	1212	263	6.7	1475	19	US-10-410-980-33	Sequence 33, Appl
1140	275	7.0	1683	17	US-10-391-213-2	Sequence 2, Appl	1213	263	6.7	1964	16	US-10-131-985-22	Sequence 22, Appl
1141	275	7.0	1683	17	US-10-391-213-3	Sequence 3, Appl	1214	263	6.7	1964	17	US-10-432-983-2	Sequence 2, Appl
1142	275	7.0	1683	17	US-10-391-215-4	Sequence 4, Appl	1215	263	6.7	1964	19	US-10-901-417-22	Sequence 22, Appl
1143	275	7.0	1683	19	US-10-930-754-1	Sequence 1, Appl	1216	263	6.7	2294	9	US-09-735-705-123	Sequence 123, App
1144	275	7.0	1683	19	US-10-930-754-2	Sequence 2, Appl	1217	263	6.7	2294	9	US-09-850-716A-123	Sequence 123, App
1145	275	7.0	3008	9	US-09-880-107-1668	Sequence 1668, Ap	1218	263	6.7	2294	9	US-09-897-778-123	Sequence 123, App
1146	275	7.0	3008	9	US-10-487-422-89	Sequence 89, Appl	1219	263	6.7	2294	9	US-09-466-396A-123	Sequence 123, App
1147	275	7.0	3022	15	US-10-719-993-421	Sequence 421, App	1220	263	6.7	2294	14	US-10-007-700-123	Sequence 123, App
1148	274	6.9	4276	15	US-10-234-406-7	Sequence 7, Appl	1221	263	6.7	2294	15	US-10-117-983-123	Sequence 123, App
1149	272	6.9	1645	15	US-10-101-510-420	Sequence 420, App	1222	263	6.7	2294	17	US-10-313-986-123	Sequence 123, App
1150	271.5	6.9	1506	14	US-09-873-367C-501	Sequence 501, App	1223	263	6.7	2294	17	US-10-641-643-1217	Sequence 1217, Ap
1151	271.5	6.9	1506	14	US-10-097-340-168	Sequence 168, App	1224	263	6.7	2294	18	US-10-775-972-123	Sequence 123, App
1152	271.5	6.9	1506	14	US-10-282-907-1	Sequence 1, Appl	1225	263	6.7	2294	14	US-10-087-192-593	Sequence 593, App
1153	271.5	6.9	1506	14	US-10-282-907-3	Sequence 3, Appl	1226	263	6.7	2304	14	US-10-171-311-183	Sequence 183, App
1154	271.5	6.9	1506	15	US-10-101-510-167	Sequence 167, App	1227	263	6.7	2304	15	US-10-301-822-160	Sequence 160, App
1155	271.5	6.9	1506	15	US-10-301-822-96	Sequence 96, Appl	1228	263	6.7	2304	17	US-10-388-360-335	Sequence 335, App
1156	271.5	6.9	1506	16	US-10-393-590-55	Sequence 55, Appl	1229	263	6.7	2304	17	US-10-295-027-413	Sequence 413, App
1157	271.5	6.9	1506	16	US-10-393-567-55	Sequence 55, Appl	1230	263	6.7	2304	17	US-10-159-563-131	Sequence 131, App
1158	271.5	6.9	1506	16	US-10-394-087-55	Sequence 55, Appl	1231	263	6.7	2304	17	US-10-159-563-131	Sequence 131, App
1159	271.5	6.9	1506	17	US-10-172-118-814	Sequence 814, App	1232	263	6.7	2304	19	US-10-645-756-37	Sequence 37, Appl
1160	271.5	6.9	1506	17	US-10-295-027-529	Sequence 529, App	1233	263	6.7	2304	19	US-09-971-392-45	Sequence 46, Appl
1161	271.5	6.9	1506	17	US-10-173-999-130	Sequence 130, App	1234	263	6.7	2336	15	US-10-101-510-458	Sequence 458, App
1162	271.5	6.9	1506	17	US-10-342-887-814	Sequence 814, App	1235	263	6.7	2336	16	US-10-252-157-358	Sequence 358, App
1163	271.5	6.9	1506	17	US-10-300-820-11	Sequence 11, Appl	1236	263	6.7	2336	16	US-10-252-157-358	Sequence 358, App
1164	271.5	6.9	1506	18	US-10-757-262-27	Sequence 27, Appl	1237	263	6.7	2655	18	US-10-723-860-5461	Sequence 5461, Ap
1165	271.5	6.9	1506	19	US-10-843-641A-501	Sequence 501, App	1238	262.5	6.7	1413	9	US-09-884-901-2	Sequence 2, Appl
1166	271.5	6.9	3162	17	US-10-210-130-61	Sequence 61, Appl	1239	262.5	6.7	1548	9	US-09-150-811-6	Sequence 6, Appl
1167	270	6.8	200	10	US-09-903-393-2	Sequence 2, Appl	1240	262.5	6.7	1610	15	US-10-073-064-6	Sequence 6, Appl
1168	267	6.8	1389	18	US-10-416-952-1	Sequence 1, Appl	1241	262.5	6.7	2091	15	US-10-841-250-9	Sequence 9, Appl
1169	267	6.8	1437	17	US-10-375-716-26	Sequence 26, Appl	1242	262.5	6.7	2773	17	US-10-349-858-16	Sequence 16, Appl
1170	267	6.8	1437	17	US-10-408-695-1	Sequence 1, Appl	1243	262.5	6.7	2804	14	US-10-132-829-2	Sequence 2, Appl
1171	267	6.8	1437	17	US-10-411-037-9	Sequence 9, Appl	1244	262.5	6.7	2804	16	US-10-133-907-2	Sequence 1, Appl
1172	267	6.8	1437	17	US-10-411-026-9	Sequence 9, Appl	1245	262.5	6.7	3129	18	US-10-865-978-1	Sequence 1, Appl
1173	267	6.8	1437	17	US-10-410-962-9	Sequence 9, Appl	1246	262.5	6.7	3421	17	US-10-276-774-995	Sequence 995, App
1174	267	6.8	1437	17	US-10-410-049-9	Sequence 9, Appl	1247	262.5	6.7	4933	17	US-09-776-191-61	Sequence 61, Appl
1175	267	6.8	1437	18	US-10-410-930-9	Sequence 9, Appl	1248	262.5	6.7	4933	17	US-10-156-214A-28	Sequence 28, Appl
1176	267	6.8	1437	18	US-10-410-997-9	Sequence 9, Appl	1249	262.5	6.7	4933	17	US-10-926-083-1	Sequence 1, Appl
1177	267	6.8	1437	18	US-10-411-012-9	Sequence 9, Appl	1250	262.5	6.7	5753	19	US-10-239-498A-6	Sequence 6, Appl
1178	267	6.8	1437	18	US-10-287-994-9	Sequence 9, Appl	1251	262.5	6.7	13928	17	US-10-362-916-1	Sequence 1, Appl
1179	267	6.8	1437	18	US-10-410-913-9	Sequence 9, Appl	1252	261.5	6.6	2942	9	US-09-118-748-1	Sequence 1, Appl
1180	267	6.8	1437	19	US-10-410-980-9	Sequence 9, Appl	1253	261.5	6.6	2942	15	US-10-101-510-383	Sequence 383, App
1181	265.5	6.7	1359	17	US-10-432-989-3	Sequence 3, Appl	1254	260.5	6.6	2387	18	US-10-398-037-69	Sequence 69, Appl
1182	265.5	6.7	3318	9	US-09-808-602-91	Sequence 91, Appl	1255	260	6.6	2304	17	US-10-282-174-561	Sequence 561, App
1183	265.5	6.7	3318	17	US-09-800-198-78	Sequence 78, Appl	1256	260	6.6	2304	19	US-10-600-009-561	Sequence 561, App
1184	265	6.7	1361	17	US-10-382-248-35	Sequence 35, Appl	1257	259.5	6.6	2976	18	US-10-865-978-33	Sequence 33, Appl
1185	264.5	6.7	1356	9	US-09-808-602-20	Sequence 20, Appl	1258	259.5	6.6	3096	18	US-10-719-993-381	Sequence 381, App
1186	264	6.7	2063	19	US-10-764-420-2110	Sequence 2110, Ap	1259	259	6.6	2359	19	US-10-741-600-437	Sequence 437, App
1187	264	6.7	2328	16	US-10-247-671-34	Sequence 34, Appl	1260	259	6.6	2375	19	US-10-741-600-438	Sequence 438, App
1188	264	6.7	2341	14	US-10-116-802-163	Sequence 163, App	1261	259	6.6	2505	17	US-10-302-172-179	Sequence 179, App
1189	263.5	6.7	1667	9	US-09-808-602-16	Sequence 16, Appl	1262	258.5	6.6	1236	9	US-09-880-503-12	Sequence 12, Appl
1190	263.5	6.7	1667	10	US-09-800-198-16	Sequence 16, Appl	1263	258.5	6.6	1236	17	US-10-407-821-1	Sequence 1, Appl
1191	263.5	6.7	1691	10	US-09-808-602-18	Sequence 18, Appl	1264	258.5	6.6	1236	17	US-10-407-821-1	Sequence 1, Appl
1192	263.5	6.7	1691	10	US-09-800-198-18	Sequence 18, Appl	1265	258.5	6.6	1248	18	US-10-823-911-1	Sequence 1, Appl

1266	255	6.5	1296	18	US-10-372-966-1	Sequence 1, Appli	1339	242	6.1	1022	17	US-10-114-270-133	Sequence 133, App
1267	255	6.5	3546	18	US-10-723-860-1376	Sequence 1376, Ap	1340	242	6.1	1959	15	US-10-101-510-743	Sequence 743, App
1268	255	6.5	3552	18	US-10-473-974-101	Sequence 101, App	1341	242	6.1	1959	15	US-10-283-975A-101	Sequence 101, App
1269	255	6.5	3557	10	US-09-918-715-241	Sequence 241, App	1342	242	6.1	1990	18	US-10-802-432-25	Sequence 25, Appl
1270	255	6.5	3557	18	US-10-474-794-241	Sequence 241, App	1343	242	6.1	2035	15	US-10-101-510-448	Sequence 448, App
1271	255	6.5	3889	18	US-10-723-860-5848	Sequence 5848, Ap	1344	242	6.1	2048	10	US-09-858-909-1	Sequence 1, Appli
1272	253.5	6.4	2487	17	US-10-366-345-9	Sequence 9, Appli	1345	242	6.1	2048	17	US-10-449-132-1	Sequence 1, Appli
1273	252.5	6.4	2487	17	US-09-799-514-3	Sequence 3, Appli	1346	241.5	6.1	1248	9	US-09-815-876-3	Sequence 3, Appli
1274	251.5	6.4	1239	18	US-10-825-911-5	Sequence 5, Appli	1347	241.5	6.1	1639	10	US-09-814-353-21470	Sequence 21470, A
1275	251.5	6.4	3387	9	US-09-888-615-38	Sequence 38, Appli	1348	241.5	6.1	1641	9	US-09-815-876-1	Sequence 1, Appli
1276	251.5	6.4	3711	17	US-10-399-645-23	Sequence 23, Appl	1349	241	6.1	3546	9	US-09-850-048A-3	Sequence 3, Appli
1277	251	6.4	2152	17	US-10-641-643-157	Sequence 157, App	1350	240.5	6.1	846	10	US-09-813-432-11	Sequence 11, Appl
1278	250.5	6.3	1239	18	US-10-372-966-3	Sequence 3, Appli	1351	240.5	6.1	846	17	US-10-174-364-11	Sequence 11, Appl
1279	250.5	6.3	1305	18	US-10-372-966-2	Sequence 2, Appli	1352	240.5	6.1	846	17	US-10-246-583-11	Sequence 11, Appl
1280	250.5	6.3	3316	17	US-10-156-214A-19	Sequence 19, Appl	1353	240.5	6.1	846	18	US-10-689-832-11	Sequence 11, Appl
1281	250	6.3	2245	17	US-10-403-163-49	Sequence 49, Appl	1354	240.5	6.1	3350	17	US-10-016-248-39	Sequence 39, Appl
1282	250	6.3	2245	17	US-10-287-226-399	Sequence 399, App	1355	240.5	6.1	3509	18	US-10-723-860-7933	Sequence 7933, Ap
1283	250	6.3	2245	17	US-10-287-226-657	Sequence 657, App	1356	240.5	6.1	10878	9	US-09-911-842-1	Sequence 1, Appli
1284	250	6.3	2267	9	US-09-964-824A-248	Sequence 248, App	1357	240.5	6.1	10878	13	US-10-150-821-1	Sequence 1, Appli
1285	250	6.3	2267	9	US-09-880-107-2249	Sequence 2249, Ap	1358	240	6.1	880	17	US-10-094-886-127	Sequence 127, App
1286	250	6.3	2267	19	US-10-843-641A-5551	Sequence 5551, Ap	1359	240	6.1	1322	19	US-10-884-163-19	Sequence 19, Appl
1287	249.5	6.3	1212	9	US-09-880-503-15	Sequence 15, Appl	1360	239.5	6.1	1412	18	US-10-764-643-5	Sequence 5, Appli
1288	249.5	6.3	2562	9	US-09-147-947-5	Sequence 5, Appli	1361	239.5	6.1	1412	18	US-10-723-860-810	Sequence 810, App
1289	249.5	6.3	3344	18	US-10-757-262-33	Sequence 33, Appl	1362	239.5	6.1	1441	9	US-09-804-156-3	Sequence 3, Appli
1290	249.5	6.3	3344	18	US-10-723-860-4045	Sequence 4045, Ap	1363	239.5	6.1	1441	13	US-10-067-761-3	Sequence 3, Appli
1291	249.5	6.3	3350	19	US-10-843-299-1	Sequence 1, Appli	1364	239.5	6.1	1441	16	US-10-319-519-3	Sequence 3, Appli
1292	249	6.3	708	17	US-09-776-191-5	Sequence 5, Appli	1365	239.5	6.1	1468	10	US-09-814-353-21812	Sequence 21812, A
1293	249	6.3	708	17	US-10-156-214A-5	Sequence 5, Appli	1366	239.5	6.1	1623	18	US-10-723-860-5415	Sequence 5415, Ap
1294	249	6.3	792	9	US-09-888-615-37	Sequence 37, Appl	1367	239.5	6.1	4882	18	US-10-719-993-211	Sequence 211, App
1295	249	6.3	1869	17	US-10-403-161-47	Sequence 47, Appl	1368	239.5	6.1	10674	17	US-10-295-027-429	Sequence 429, App
1296	249	6.3	1869	17	US-10-403-161-51	Sequence 51, Appl	1369	239.5	6.1	10674	17	US-10-295-027-1080	Sequence 1080, Ap
1297	249	6.3	2038	17	US-10-287-226-403	Sequence 403, App	1370	239.5	6.1	11230	9	US-09-911-842-3	Sequence 3, Appli
1298	249	6.3	2038	17	US-10-099-322-29	Sequence 29, Appl	1371	239.5	6.1	11230	13	US-10-150-821-3	Sequence 3, Appli
1299	249	6.3	2038	17	US-10-044-564-29	Sequence 49, Appl	1372	239	6.1	987	9	US-09-888-615-32	Sequence 32, Appl
1300	249	6.3	2038	17	US-10-403-161-45	Sequence 45, Appl	1373	238	6.0	1234	19	US-10-487-422-84	Sequence 84, Appl
1301	249	6.3	2038	17	US-10-287-226-401	Sequence 401, App	1374	238	6.0	2625	9	US-09-893-238-16	Sequence 18, Appl
1302	249	6.3	2717	13	US-10-044-090-471	Sequence 471, App	1375	238	6.0	4072	9	US-09-893-238-16	Sequence 16, Appl
1303	249	6.3	2914	14	US-10-198-846-10123	Sequence 10123, A	1376	238	6.0	8589	9	US-09-893-238-14	Sequence 14, Appl
1304	248.5	6.3	2388	9	US-09-880-107-2165	Sequence 2165, Ap	1377	237.5	6.0	3430	9	US-09-858-332-14	Sequence 14, Appl
1305	248.5	6.3	2388	10	US-09-873-367C-998	Sequence 998, App	1378	237.5	6.0	11152	17	US-10-028-248A-7	Sequence 7, Appli
1306	248.5	6.3	2388	15	US-10-177-293-26	Sequence 26, App	1379	237.5	6.0	11152	17	US-10-107-782-7	Sequence 7, Appli
1307	248.5	6.3	2388	17	US-10-236-031B-43	Sequence 43, Appl	1380	237.5	6.0	11158	17	US-10-028-248A-5	Sequence 5, Appli
1308	248.5	6.3	2388	17	US-10-172-118-651	Sequence 651, App	1381	237.5	6.0	11158	17	US-10-107-782-5	Sequence 5, Appli
1309	248.5	6.3	2388	17	US-10-240-425-1281	Sequence 1281, Ap	1382	237	6.0	4771	9	US-09-942-366-2	Sequence 2, Appli
1310	248.5	6.3	2388	17	US-10-342-887-651	Sequence 651, App	1383	236.5	6.0	1065	10	US-09-987-455-4	Sequence 4, Appli
1311	248.5	6.3	2388	19	US-10-843-641A-98	Sequence 98, App	1384	236.5	6.0	1065	10	US-09-987-455-7	Sequence 7, Appli
1312	248	6.3	861	16	US-10-340-860A-40	Sequence 40, Appl	1385	236.5	6.0	1065	10	US-09-987-455-2	Sequence 2, Appli
1313	248	6.3	885	17	US-10-330-051A-15	Sequence 15, Appl	1386	236.5	6.0	1128	10	US-09-987-455-5	Sequence 5, Appli
1314	248	6.3	2484	17	US-10-264-049-752	Sequence 752, App	1387	235.5	6.0	978	15	US-10-311-955-1	Sequence 1, Appli
1315	248	6.3	2486	15	US-10-106-698-1989	Sequence 1989, Ap	1388	235.5	6.0	2781	15	US-10-263-538-3	Sequence 3, Appli
1316	247.5	6.3	1787	17	US-10-104-610-7	Sequence 7, Appli	1389	235.5	6.0	2781	18	US-10-669-176-3	Sequence 3, Appli
1317	247.5	6.3	2693	19	US-10-741-600-82	Sequence 82, Appl	1390	235.5	6.0	3404	13	US-10-104-440-3	Sequence 3, Appli
1318	247.5	6.3	2880	17	US-10-112-948-65	Sequence 65, Appl	1391	235.5	6.0	3404	15	US-10-104-610-3	Sequence 3, Appli
1319	247	6.3	3146	17	US-10-016-248-41	Sequence 41, Appl	1392	235.5	6.0	5238	16	US-10-133-013-245	Sequence 245, App
1320	246.5	6.2	885	18	US-10-761-886-1	Sequence 1, Appli	1393	235.5	6.0	5238	16	US-10-247-671-95	Sequence 95, Appl
1321	246.5	6.2	1072	18	US-10-482-926-11	Sequence 11, Appl	1394	235	6.0	1992	9	US-09-729-674-91	Sequence 91, Appl
1322	246.5	6.2	1380	17	US-10-465-156-15	Sequence 15, Appl	1395	235	6.0	1992	10	US-10-913-553-91	Sequence 91, Appl
1323	246.5	6.2	1869	15	US-10-214-932-115	Sequence 115, App	1396	235	6.0	6004	17	US-10-467-433-38	Sequence 38, Appl
1324	246.5	6.2	1947	17	US-10-375-716-24	Sequence 24, Appl	1397	234.5	5.9	2246	19	US-10-764-420-2344	Sequence 2344, Ap
1325	246.5	6.2	1947	18	US-10-283-975A-155	Sequence 155, App	1398	234	5.9	785	17	US-10-072-012-89	Sequence 89, Appl
1326	246.5	6.2	2000	13	US-10-044-090-331	Sequence 331, App	1399	234	5.9	7192	18	US-10-723-860-7819	Sequence 7819, Ap
1327	246	6.2	2716	18	US-10-741-601-19	Sequence 19, Appl	1400	233.5	5.9	870	16	US-10-131-409-19	Sequence 19, Appl
1328	245	6.2	2716	18	US-10-741-600-26	Sequence 26, Appl	1401	233.5	5.9	870	17	US-10-139-854-19	Sequence 19, Appl
1329	245.5	6.2	2707	18	US-10-741-601-20	Sequence 20, Appl	1402	233.5	5.9	870	17	US-10-150-811-19	Sequence 19, Appl
1330	245.5	6.2	2707	19	US-10-741-600-27	Sequence 27, Appl	1403	233.5	5.9	870	17	US-10-150-811-19	Sequence 19, Appl
1331	244.5	6.2	807	9	US-09-981-123-1	Sequence 1, Appli	1404	233.5	5.9	872	17	US-10-300-820-13	Sequence 13, Appl
1332	244.5	6.2	880	16	US-10-029-386-20258	Sequence 20258, A	1405	233.5	5.9	2363	11	US-09-880-107-3690	Sequence 3690, Ap
1333	244	6.2	2991	18	US-10-764-420-2604	Sequence 2604, Ap	1406	233.5	5.9	2363	11	US-09-968-007A-436	Sequence 436, App
1334	243	6.2	5021	9	US-10-473-974-26	Sequence 26, Appl	1407	233.5	5.9	2363	17	US-10-099-322-39	Sequence 39, Appl
1335	243	6.2	5021	18	US-09-285-385C-1	Sequence 1, Appli	1408	233.5	5.9	2363	17	US-10-044-564-39	Sequence 39, Appl
1336	242.5	6.1	699	17	US-10-156-214A-275	Sequence 275, App	1409	233.5	5.9	2363	19	US-10-843-641A-6906	Sequence 6906, Ap
1337	242.5	6.1	2457	9	US-09-850-048A-1	Sequence 1, Appli	1410	233.5	5.9	4134	18	US-10-154-670-18	Sequence 18, Appl
1338	242.5	6.1	11996	18	US-10-603-283-1	Sequence 1, Appli	1411	232.5	5.9	1500	17	US-10-712-332-4	Sequence 4, Appli

1412	232.5	5.9	3919	9	US-09-942-366-4	Sequence 4, Appli	1485	226	5.7	1878	15	US-10-214-932-119	Sequence 119, App
1413	232.5	5.9	6728	18	US-10-723-860-7986	Sequence 7986, Ap	1486	226	5.7	2038	9	US-09-968-415-18	Sequence 18, Appl
1414	232	5.9	2444	16	US-10-316-253-81	Sequence 81, Appl	1487	226	5.7	2038	16	US-10-180-719-18	Sequence 18, Appl
1415	232	5.9	2583	9	US-09-917-800A-1564	Sequence 1564, Ap	1488	226	5.7	2063	10	US-09-888-257A-2	Sequence 2, Appli
1416	232	5.9	2609	18	US-10-399-455-31	Sequence 31, Appl							
1417	231.5	5.9	2175	17	US-10-108-260A-559	Sequence 559, App							
1418	231	5.9	1130	17	US-10-467-042-23	Sequence 23, Appl							
1419	231	5.9	1203	17	US-10-428-275-115	Sequence 115, App							
1420	231	5.9	2590	18	US-10-417-375-139	Sequence 139, App							
1421	231	5.9	2627	18	US-10-417-375-141	Sequence 141, App							
1422	231	5.9	4661	9	US-09-285-385C-3	Sequence 3, Appli							
1423	230.5	5.8	780	17	US-10-165-442-6	Sequence 6, Appli							
1424	230.5	5.8	780	18	US-10-699-393-6	Sequence 6, Appli							
1425	230.5	5.8	873	14	US-10-117-323-2	Sequence 2, Appli							
1426	230.5	5.8	888	17	US-10-165-442-5	Sequence 5, Appli							
1427	230.5	5.8	888	18	US-10-699-393-5	Sequence 5, Appli							
c1428	230	5.8	1078	10	US-09-898-837A-16	Sequence 16, Appl							
1429	230	5.8	1146	17	US-10-428-275-133	Sequence 133, App							
1430	230	5.8	1203	17	US-10-428-275-111	Sequence 111, App							
1431	230	5.8	1203	17	US-10-428-275-117	Sequence 117, App							
1432	230	5.8	1218	17	US-10-428-275-125	Sequence 125, App							
1433	230	5.8	1218	17	US-10-428-275-137	Sequence 137, App							
1434	230	5.8	1314	10	US-09-898-837A-14	Sequence 14, Appl							
c1435	230	5.8	1314	10	US-09-898-837A-17	Sequence 17, Appl							
1436	230	5.8	1314	17	US-10-428-275-131	Sequence 131, App							
1437	230	5.8	1434	14	US-10-177-661-1	Sequence 1, Appli							
1438	230	5.8	1614	9	US-09-888-615-45	Sequence 45, Appl							
1439	230	5.8	1689	17	US-10-156-214A-23	Sequence 23, Appl							
1440	230	5.8	1707	17	US-10-428-275-129	Sequence 129, App							
c1441	230	5.8	1708	17	US-10-428-275-147	Sequence 147, App							
1442	230	5.8	1748	9	US-09-879-792-11	Sequence 11, Appl							
1443	230	5.8	1748	18	US-10-806-370-11	Sequence 11, Appl							
1444	230	5.8	1771	17	US-10-428-275-123	Sequence 123, App							
1445	230	5.8	1779	17	US-10-428-275-119	Sequence 119, App							
1446	230	5.8	2067	17	US-10-156-214A-25	Sequence 25, Appl							
1447	230	5.8	2310	17	US-10-428-275-127	Sequence 127, App							
1448	230	5.8	2393	17	US-10-353-690-99	Sequence 99, Appl							
1449	230	5.8	2432	17	US-10-428-275-103	Sequence 103, App							
1450	229.5	5.8	1059	9	US-09-888-615-36	Sequence 36, Appl							
1451	229.5	5.8	1167	17	US-10-210-130-155	Sequence 155, App							
1452	229	5.8	1187	17	US-10-275-505-22	Sequence 22, Appl							
1453	228.5	5.8	1113	17	US-10-343-953-3	Sequence 3, Appli							
1454	228.5	5.8	1234	14	US-10-076-816-49	Sequence 49, Appl							
1455	228.5	5.8	1272	17	US-10-162-335-85	Sequence 85, Appl							
1456	228.5	5.8	1295	19	US-10-480-988-48	Sequence 48, Appl							
1457	228.5	5.8	7596	16	US-10-004-113-57	Sequence 57, Appl							
1458	228.5	5.8	8064	16	US-10-004-113-56	Sequence 56, Appl							
1459	228	5.8	906	17	US-10-114-270-129	Sequence 129, App							
1460	228	5.8	2432	17	US-10-428-275-139	Sequence 139, App							
1461	228	5.8	2432	17	US-10-428-275-143	Sequence 143, App							
1462	227.5	5.8	888	9	US-09-888-615-26	Sequence 26, Appl							
1463	227.5	5.8	918	15	US-10-239-663-23	Sequence 23, Appl							
1464	227.5	5.8	1460	15	US-10-171-581-291	Sequence 291, App							
1465	227.5	5.8	2255	17	US-10-399-645-29	Sequence 29, Appl							
1466	227	5.8	726	14	US-10-092-004A-1	Sequence 1, Appli							
1467	227	5.8	927	18	US-10-297-987B-26	Sequence 26, Appl							
1468	227	5.8	959	14	US-10-040-647-25	Sequence 25, Appl							
1469	227	5.8	1647	18	US-10-297-987B-25	Sequence 25, Appl							
1470	226.5	5.7	1847	17	US-10-349-858-18	Sequence 18, Appl							
1471	226.5	5.7	2356	19	US-10-843-299-3	Sequence 3, Appli							
1472	226.5	5.7	2614	9	US-09-147-947-3	Sequence 3, Appli							
1473	226.5	5.7	2662	17	US-10-275-505-27	Sequence 27, Appl							
1474	226	5.7	734	18	US-10-297-987B-9	Sequence 9, Appli							
1475	226	5.7	867	9	US-09-888-615-56	Sequence 56, Appl							
1476	226	5.7	1218	17	US-10-274-639-36	Sequence 36, Appl							
1477	226	5.7	1218	17	US-10-333-574-36	Sequence 36, Appl							
1478	226	5.7	1314	17	US-10-295-021-133	Sequence 133, App							
1479	226	5.7	1314	17	US-10-295-027-778	Sequence 778, App							
1480	226	5.7	1314	17	US-10-295-027-790	Sequence 790, App							
1481	226	5.7	1314	17	US-10-295-027-830	Sequence 830, App							
1482	226	5.7	1314	17	US-10-295-027-979	Sequence 979, App							
1483	226	5.7	1314	17	US-10-173-999-88	Sequence 88, Appl							
c1484	226	5.7	1854	17	US-10-296-115-409	Sequence 409, App							

Search completed: May 10, 2005, 04:19:06
Job time : 1128 secs

This Page Blank (uspto)